

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:57 ; Search time 12.9677 Seconds
(without alignments)
44.518 Million cell updates/sec

Title: US-10-009-122-17
Perfect score: 29
Sequence: 1 KVVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	186	1 WRR219	19K globulin precu
2	29	100.0	186	2 JC4784	alpha-globulin pre
3	29	100.0	442	2 H81402	probable integral
4	29	100.0	1144	1 A43271	nitric-oxide synth
5	28	96.6	380	2 F70399	hydrogenase expres
6	27	93.1	447	2 F71039	hypothetical prote
7	26	89.7	33	2 S23094	beta-amyloid prote
8	26	89.7	42	2 PN0512	beta-amyloid prote
9	26	89.7	57	2 A60045	Alzheimer's diseas
10	26	89.7	57	2 F00045	Alzheimer's diseas
11	26	89.7	57	2 D60045	Alzheimer's diseas
12	26	89.7	57	2 G60045	Alzheimer's diseas
13	26	89.7	57	2 B60045	Alzheimer's diseas
14	26	89.7	57	2 F90735	Alzheimer's diseas
15	26	89.7	81	2 A82251	Alzheimer's diseas
16	26	89.7	81	2 G85586	Alzheimer's diseas
17	26	89.7	81	2 H64814	Alzheimer's diseas
18	26	89.7	82	2 PQ0438	Alzheimer's diseas
19	26	89.7	83	2 AC0598	Alzheimer's diseas
20	26	89.7	152	2 T06645	Alzheimer's diseas
21	26	89.7	193	2 B90157	Alzheimer's diseas
22	26	89.7	207	2 B81256	Alzheimer's diseas
23	26	89.7	231	2 H85138	Alzheimer's diseas
24	26	89.7	293	2 D69355	Alzheimer's diseas
25	26	89.7	294	2 H90318	Alzheimer's diseas
26	26	89.7	300	2 T26245	Alzheimer's diseas
27	26	89.7	330	2 B82822	Alzheimer's diseas
28	26	89.7	339	2 B72402	Alzheimer's diseas
29	26	89.7	339	2 B72402	Alzheimer's diseas

hypothetical prote
wax synthase limpo
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
conserved hypotet
hypothetical prote
Alzheimer's diseas
Alzheimer's diseas
Alzheimer's diseas
Alzheimer's diseas
glycogen phosphory
genome polypotein
hypothetical prote
conserved hypotet
hypothetical prote
hypothetical prote
hypothetical prote
PFS system, IIB co
hypothetical prote
hypothetical prote
NADH2 dehydrogenas
NADH2 dehydrogenas
NADH2 dehydrogenas
NADH2 dehydrogenas
NADH2 dehydrogenas
conserved hypotet
probable permease
uncharacterized co
hypothetical prote
probable polysacch
hypothetical prote
hypothetical prote
transcription regu
2-deoxy-D-gluconat
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
NAD-dinitrogen-red
NAD-dinitrogen-red
hypothetical prote
hypothetical prote
hypothetical 21K p
methionyl-tRNA for
capsid protein - b
methionyl-tRNA for
hypothetical prote
NADH2 dehydrogenas
tryptophanyl-tRNA
cell fusion protei
hypD' protein - Br
sorbitol dehydroge
niacitol-phospha
hydrogenase isoenz
pleiotrophic effec
hydrogenase isoenz
hydrogenase expres
hydrogenase homolo
hypothetical prote
hypothetical prote
hypD' protein - Rhi
proton/sodium-glut
proton/sodium-glut
conserved hypotet
probable LPS biosy
lipid A-core surfa
tyrosine-tRNA liga
hypothetical prote
probable selenium-
probable beta-alan

26 89.7 349 2 T26247
26 89.7 352 2 T48903
26 89.7 428 2 T48008
26 89.7 477 2 B28988
26 89.7 520 2 A81548
26 89.7 594 2 F86499
26 89.7 603 2 F72237
26 89.7 617 2 A72123
26 89.7 695 1 A49795
26 89.7 695 2 A27485
26 89.7 695 2 S00550
26 89.7 747 2 JH0773
26 89.7 770 1 QH0744
26 89.7 817 2 A82511
26 89.7 1016 2 S30236
26 86.2 74 2 B64214
25 86.2 109 2 B72213
25 86.2 136 2 T19479
25 86.2 146 2 E75134
25 86.2 148 2 T32362
25 86.2 156 2 H95252
25 86.2 156 2 F98117
25 86.2 159 2 C71080
25 86.2 162 2 T13659
25 86.2 162 2 T13656
25 86.2 162 2 T13563
25 86.2 162 2 T13487
25 86.2 164 2 T13562
25 86.2 188 2 G70475
25 86.2 190 2 A95895
25 86.2 194 2 B97211
25 86.2 200 2 A81632
25 86.2 232 2 A71495
25 86.2 234 2 T23466
25 86.2 247 2 T32514
25 86.2 253 2 D82405
25 86.2 255 2 C87434
25 86.2 257 2 C83982
25 86.2 261 2 D64166
25 86.2 277 2 T31855
25 86.2 286 2 C84857
25 86.2 295 2 JC4744
25 86.2 295 2 I39751
25 86.2 295 2 C70736
25 86.2 302 2 A99074
25 86.2 302 2 B35961
25 86.2 311 2 S73625
25 86.2 316 2 S61237
25 86.2 318 2 A75275
25 86.2 321 2 H71729
25 86.2 328 2 T11938
25 86.2 330 2 H75505
25 86.2 340 1 NMBE5
25 86.2 347 2 S35229
25 86.2 352 2 A92057
25 86.2 352 2 H97272
25 86.2 373 2 AE0847
25 86.2 373 2 A85922
25 86.2 373 2 A91077
25 86.2 373 2 S15200
25 86.2 379 2 T39743
25 86.2 382 2 G83808
25 86.2 384 2 H64161
25 86.2 385 2 S32877
25 86.2 399 2 G97727
25 86.2 399 2 D71728
25 86.2 399 2 A82842
25 86.2 402 2 E86038
25 86.2 402 2 D91191
25 86.2 405 2 A70146
25 86.2 455 2 T34366
25 86.2 469 2 T02325
25 86.2 477 2 T02505

30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102

103	25	86.2	512	2	T19806	hypothetical prote	176	24	82.8	241	2	G71045	hypothetical prote
104	25	86.2	572	2	H96685	probable AMP-bindi	177	24	82.8	245	2	T49889	zinc finger transc
105	25	86.2	604	1	QXLS5M	NADH2 dehydrogenas	178	24	82.8	246	2	E90309	hypothetical prote
106	25	86.2	620	2	H69382	ABC transporter, A	179	24	82.8	248	2	F71849	amino acid ABC tra
107	25	86.2	646	2	AD3409	ABC transporter, AT	180	24	82.8	248	2	C64666	glutamine transpor
108	25	86.2	657	2	G86590	exinuclease ABC eu	181	24	82.8	254	2	T28170	hypothetical prote
109	25	86.2	657	2	B72034	exinuclease ABC, A	182	24	82.8	256	2	AC1561	conserved hypotet
110	25	86.2	657	2	H90523	exinuclease ABC s	183	24	82.8	256	2	AB1203	conserved hypotet
111	25	86.2	660	1	A28153	gelatinase A (EC 3	184	24	82.8	262	2	D88930	protein R11G11.10
112	25	86.2	662	2	S70365	gelatinase A (EC 3	185	24	82.8	262	2	A81055	conserved hypotet
113	25	86.2	662	2	A42496	gelatinase A (EC 3	186	24	82.8	263	2	C69887	hypothetical prote
114	25	86.2	662	2	S34780	gelatinase A (EC 3	187	24	82.8	269	2	A81820	conserved hypotet
115	25	86.2	663	1	S46492	gelatinase A (EC 3	188	24	82.8	276	2	S05343	NAD ADP-ribosyltra
116	25	86.2	676	2	D81654	exinuclease ABC c	189	24	82.8	278	1	S01065	probable dehydroge
117	25	86.2	681	2	T39814	hypothetical prote	190	24	82.8	281	2	F69400	2-deoxy-D-gluconat
118	25	86.2	774	2	F96639	protein T1P9.8 lim	191	24	82.8	283	2	T20734	hypothetical prote
119	25	86.2	774	2	T34496	hypothetical prote	192	24	82.8	286	2	A13105	hypothetical prote
120	25	86.2	804	2	G71546	probable DNA gyras	193	24	82.8	287	2	A12038	carboxyphosphoen
121	25	86.2	812	2	H87386	hypothetical prote	194	24	82.8	300	2	F83621	hypothetical prote
122	25	86.2	1119	2	A86340	protein F2D10.24 (195	24	82.8	301	2	C98181	sitC protein (AF12
123	25	86.2	1147	1	I53165	nitric-oxide synth	196	24	82.8	309	2	T35801	probable polyamine
124	25	86.2	1147	1	I56575	nitric-oxide synth	197	24	82.8	311	2	D64240	methionyl-tRNA for
125	25	86.2	1147	1	S38253	nitric-oxide synth	198	24	82.8	315	2	S59779	probable membrane
126	25	86.2	1147	1	S47647	nitric-oxide synth	199	24	82.8	323	2	AC2119	hypothetical prote
127	25	86.2	1147	2	JC5029	nitric-oxide synth	200	24	82.8	325	1	B40358	NADH2 dehydrogenas
128	25	86.2	1147	2	JC5028	nitric-oxide synth	201	24	82.8	330	2	T29640	mitochondrial carr
129	25	86.2	1147	2	JC5027	nitric-oxide synth	202	24	82.8	331	1	DN0BUL	NADH2 dehydrogenas
130	25	86.2	1147	2	S65440	nitric-oxide synth	203	24	82.8	335	2	A72289	oligopeptide ABC t
131	25	86.2	1324	2	T01508	mismatch repair en	204	24	82.8	337	2	AG0963	hypothetical prote
132	25	86.2	2241	2	T02857	conserved hypotet	205	24	82.8	337	2	T48341	hypothetical prote
133	25	86.2	3623	2	T08618	intrinsic factor-B	206	24	82.8	341	2	S73685	hypothetical prote
134	25	86.2	4152	2	T31102	filamentous hemagg	207	24	82.8	342	2	AE2238	methionyl-tRNA for
135	25	86.2	4919	2	T31105	hypothetical prote	208	24	82.8	344	2	E83562	N-acetyl-gamma-glu
136	24	82.8	20	2	JU0330	hypothetical prote	209	24	82.8	345	2	AB1837	hypothetical prote
137	24	82.8	20	2	A99091	hypothetical prote	210	24	82.8	352	2	E90175	NADH dehydrogenase
138	24	82.8	62	2	E64530	hypothetical prote	211	24	82.8	352	2	AB3079	transcription regu
139	24	82.8	68	2	C71970	hypothetical prote	212	24	82.8	352	2	G98207	hypothetical prote
140	24	82.8	77	2	AC1381	preprotein translo	213	24	82.8	363	2	S56273	probable membrane
141	24	82.8	91	2	H82370	conserved hypotet	214	24	82.8	379	2	T23443	hypothetical prote
142	24	82.8	95	2	AG0277	probable phage-rel	215	24	82.8	380	2	T29248	hypothetical prote
143	24	82.8	106	2	AG2113	hypothetical prote	216	24	82.8	380	2	F86038	probable LPS biosy
144	24	82.8	108	2	C64516	hypothetical prote	217	24	82.8	380	2	E91191	probable LPS biosy
145	24	82.8	138	2	I47205	Ig heavy chain var	218	24	82.8	382	2	A11427	efflux proteins ho
146	24	82.8	141	1	B70457	gliding motility p	219	24	82.8	383	2	AF1893	hydrogenase expres
147	24	82.8	141	2	I47177	Ig H-chain - pig (220	24	82.8	385	2	T31493	hypothetical prote
148	24	82.8	143	1	A44397	cofilin - yeast (S	221	24	82.8	393	2	D86168	hypothetical prote
149	24	82.8	144	2	D72219	conserved hypotet	222	24	82.8	400	2	H69009	hypothetical prote
150	24	82.8	147	2	H82313	hypothetical prote	223	24	82.8	401	2	T44831	probable emulsan r
151	24	82.8	163	2	F86878	hypothetical prote	224	24	82.8	409	2	S29124	membrane glycoprot
152	24	82.8	169	2	AF2630	hypothetical prote	225	24	82.8	415	2	C71467	probable tyrosine
153	24	82.8	171	2	C71244	hypothetical prote	226	24	82.8	416	2	I64039	hypothetical prote
154	24	82.8	174	2	G81349	periplasmic nitrat	227	24	82.8	422	2	E82904	hypothetical prote
155	24	82.8	179	2	AB0652	probable intracell	228	24	82.8	429	2	T28950	hypothetical prote
156	24	82.8	179	2	T45503	hypothetical prote	229	24	82.8	440	1	B29413	ubiquinol-cytochro
157	24	82.8	179	2	S07799	probable membrane	230	24	82.8	442	2	T39683	zeatin-like protei
158	24	82.8	179	2	B90848	probable membrane	231	24	82.8	448	2	A86534	integral membrane
159	24	82.8	179	2	A85706	probable membrane	232	24	82.8	448	2	A72089	ABC transporter, p
160	24	82.8	179	2	S70898	intracellular sept	233	24	82.8	451	2	A81581	probable integral
161	24	82.8	184	2	AH3581	alkyl hydroperoxid	234	24	82.8	451	2	G71561	hypothetical prote
162	24	82.8	193	2	A82435	conserved hypotet	235	24	82.8	452	2	H84016	conserved hypotet
163	24	82.8	195	2	T22032	hypothetical prote	236	24	82.8	455	2	H69837	protein imported
164	24	82.8	197	2	G83597	conserved hypotet	237	24	82.8	456	2	D95384	aromatic amino aci
165	24	82.8	210	2	C97260	probable membrane	238	24	82.8	463	2	S52754	hypothetical prote
166	24	82.8	210	2	S67140	probable membrane	239	24	82.8	466	2	A95179	LPS glycosyltransf
167	24	82.8	214	2	B84217	hypothetical prote	240	24	82.8	466	2	B97030	hypothetical prote
168	24	82.8	216	2	B88065	protein T16A1.3 [i	241	24	82.8	466	2	H98045	hypothetical prote
169	24	82.8	219	1	A35617	HDEL receptor ERD2	242	24	82.8	471	2	T41602	hypothetical prote
170	24	82.8	219	2	A75004	hypothetical prote	243	24	82.8	480	2	B84394	argininosuccinate
171	24	82.8	221	2	G72322	glutaredoxin-relat	244	24	82.8	490	2	A35312	potassium channel
172	24	82.8	222	2	T47768	hypothetical prote	245	24	82.8	500	2	B83364	pyoverdine biosynt
173	24	82.8	225	2	A90260	conserved hypotet	246	24	82.8	500	2	F83418	sodium/proton anti
174	24	82.8	238	2	E75169	hypothetical prote	247	24	82.8	503	2	T34694	probable cationic
175	24	82.8	240	2	G70303	cytochrome c - Aqu	248	24	82.8	507	2	F97765	hypothetical prote

A;Cross-references: UNIPROT:Q9PHV5; UNIPARC:UPI000000C217E; GB:AL139075; GB:AL111168; NID:
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj0560

Query Match 100.0%; Score 29; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||
Db 313 KVVFFA 318

RESULT 4
A43271
nitric-oxide synthase (EC 1.14.13.39), calmodulin-independent - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: A43271; A42166; JN0458; A46186
R;Xie, Q.; Cho, H.J.; Calaycay, J.; Mumford, R.A.; Swiderek, K.M.; Lee, T.D.; Ding, A.;
Science 256, 225-228, 1992
A;Title: Cloning and characterization of inducible nitric oxide synthase from mouse macrophages
A;Reference number: A43271; MUID:92229444; PMID:1373522
A;Accession: A43271
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1144 <XIE>
A;Cross-references: UNIPROT:P29477; UNIPARC:UPI000000D36; GB:M87039; NID:G198406; PIDN:
R;Lyons, C.R.; Orloff, G.J.; Cunningham, J.M.
J. Biol. Chem. 267, 6370-6374, 1992
A;Title: Molecular cloning and functional expression of an inducible nitric oxide synthase
A;Reference number: A42166; MUID:92210618; PMID:1372907
A;Accession: A42166
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1144 <LYO>
A;Cross-references: UNIPARC:UPI000000D36; GB:M84373; NID:G200095; PIDN:AAA39834.1; PID:
R;Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.
Biochem. Biophys. Res. Commun. 191, 767-774, 1993
A;Title: Hepatocytes and macrophages express an identical cytokine inducible nitric oxide
A;Reference number: JN0457; MUID:93221515; PMID:7682072
A;Accession: JN0458
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-278, 'F', 280-682, 'H', 684-937, 939-1144 <WOO>
A;Cross-references: UNIPARC:UPI000017223A
A;Experimental source: liver
R;Lowenstein, C.J.; Glatt, C.S.; Bredt, D.S.; Snyder, S.H.
Proc. Natl. Acad. Sci. U.S.A. 89, 6711-6715, 1992
A;Title: Cloned and expressed macrophage nitric oxide synthase contrasts with the brain
A;Reference number: A46186; MUID:92357701; PMID:1379716
A;Accession: A46186
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-190, 'V', 192-765, 'P', 767-843, 'G', 845-1144 <LOW>
A;Cross-references: UNIPARC:UPI00017223B; GB:M92649; NID:G200109
A;Experimental source: BALB/c, RAW 264.7 cells, macrophage
A;Note: sequence extracted from NCBI backbone (NCBI:P:113541)
C;Genetics:
A;Gene: NOS
C;Function:
A;Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reductase
C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal
P;533-1121/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;535-671/Domain: flavodoxin homology <FLX>
F;194/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 1; Length 1144;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||
Db 514 KVVFFA 519

RESULT 5
F70399
hydrogenase expression/formation protein HypD - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: F70399
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O.
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70399
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-380 <AQF>
A;Cross-references: UNIPROT:O67225; UNIPARC:UPI0000056543; GB:AE000726; NID:G2983612; P:
A;Experimental source: strain VF5
C;Genetics:
A;Gene: HypD
C;Superfamily: [NiFe]-hydrogenase maturation factor, HypD type

Query Match 96.6%; Score 28; DB 2; Length 380;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||
Db 141 KVVFFA 146

RESULT 6
F71039
hypothetical protein PH1606 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Oct-2004
C;Accession: F71039
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki;
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch;
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: F71039
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-447 <KAW>
A;Cross-references: UNIPROT:O59243; UNIPARC:UPI00000630DB; GB:AP000006; NID:G3236133; P:
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1606
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1142

Query Match 93.1%; Score 27; DB 2; Length 447;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||
Db 207 KVVFFA 212

RESULT 7
S23094
beta-amyloid protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C;Accession: S23094
R;Kojima, S.; Omori, M.

FEBS Lett. 304, 57-60, 1992
 A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
 A;Reference number: S23094; MUID:92316198; PMID:1618299
 A;Accession: S23094
 A;Molecule type: protein
 A;Residues: 1-33 <KOU>
 A;Cross-references: UNIPARC:UPI00001777FB
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

Query Match 89.7%; Score 26; DB 2; Length 33;
 Best Local Similarity 83.3%; Pred. No. 14;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |:|:|:|
 Db 21 KLVFFA 26

RESULT 8

PN0512
 beta-amyloid protein - guinea pig (fragment)
 C;Species: Cavia porcellus (guinea pig)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C;Accession: PN0512
 R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.
 Biochem. Biophys. Res. Commun. 193, 624-630, 1993
 A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment
 A;Reference number: PN0512; MUID:93290653; PMID:7685598
 A;Accession: PN0512
 A;Molecule type: protein
 A;Residues: 1-42 <SHI>
 A;Cross-references: UNIPROT:Q7M088; UNIPARC:UPI00000315E8
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C;Keywords: alternative splicing; amyloid

Query Match 89.7%; Score 26; DB 2; Length 42;
 Best Local Similarity 83.3%; Pred. No. 17;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |:|:|:|
 Db 16 KLVFFA 21

RESULT 9

A60045
 Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
 C;Species: Canis lupus familiaris (dog)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C;Accession: A60045
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Accession: A60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56125
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;
 Best Local Similarity 83.3%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |:|:|:|
 Db 21 KLVFFA 26

RESULT 10

F60045
 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
 C;Accession: F60045
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Accession: F60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:G1895; PIDN:CAA39592.1; PID
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;
 Best Local Similarity 83.3%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |:|:|:|
 Db 21 KLVFFA 26

RESULT 11

D60045
 Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C;Accession: D60045
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Accession: D60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56124
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;
 Best Local Similarity 83.3%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |:|:|:|
 Db 21 KLVFFA 26

RESULT 12

E60045
 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
 C;Species: Ovis sp. (sheep)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C;Accession: E60045
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in do
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Accession: E60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56130
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;
 Best Local Similarity 83.3%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |:|:|:|
 Db 21 KLVFFA 26

C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match	89.7%	Score 26;	DB 2;	Length 81;
Best Local Similarity	83.3%;	Pred. No. 32;		
Matches 5;	Conservative	1;	Mismatches	0;
			Indels	0;
			Gaps	0;

Qy 1 KVVFFA 6
Dp 3 KVLFFA 8

RESULT 16

molybdenum cofactor biosynthesis protein D VC1027 [imported] - Vibrio cholerae (strain A82251)
 C:Species: Vibrio cholerae
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 16-Aug-2004
 C/Accession: A82251
 R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
 J. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

A;Title: DNA Sequence
A;Reference number: A8
A;Accession: A82251

A;Molecule type: DNA
A;Residues: 1-81 <HEI>
A;Cross-references: UN
A;Experimental source:

C/Gene: VC1027
A:Map position: 1
C:Superfamily: Molypdo

Query Match
Best Local Similarit
Matches 5. Conse

QY	1	KVFFFA	6
ph	3	KVFFFA	9

RESULT 17
C95596

C;Species: Escherichia
C;Date: 16-Feb-2001 #S
C;Accession: C05596

R;Perna, N.T.; Plunket
iller, L.; Grotbeck, E
Nature 409, 529-533, 2

A;Reference number: A8
A;Accession: G85586
A;Status: preliminary

A;Residues: 1-81 <STO>
A;Cross-references: UN
A;Experimental source:

A;Gene: moad
C;Superfamily: Molybdo

Best Local Similarity
Matches 5; Consequence

Db 3 KVLFFA 8

RESULT 13
G600x5
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
R;Accession: G60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: G60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56126
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
Query Match 89.7% Score 26; DB 2; Length 57;

Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	KVFFFA	6						

RESULT 14

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C:Date: 01-Dec-1992 #sequence revision 01-Dec-1992 #text change 09-Jul-2004

A; Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
 A; Reference number: A50045. MIMD.92017079. PMID.16563157
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A; Author(s): Canney, M.O.; Norris, R.H.; Pascual, R.; Little, S.F.
 A; Journal: Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Accession: B60043
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPROT:Q92149, UNIPARC:UPI00000125049, ENZYME:Y56128, NID:Q2165, BIDN:

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Best Local Similarity 83.3%; Pred. NO. 23;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Cov 1 KATANA 5

Db 21 KLVPFA 26

RESULT 15
F90736
molybdopterin biosynthesis protein D chain [imported] - Escherichia coli (strain O157:H7)
cysGcd_Escherichia coli

C:Accession: F90736
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2004
C:Han, C.G.; Yokoyama, K.; Ishii, K.; Kurokawa, K.; Ohnishi, M.; Makino, K.; R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Han, C.G.

DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic
A/Reference number: A99629; MUID:21156231; PMID:11258796

```
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-81 <HAY>
```

A; Experimental source: strain O157:H7, substrain RMD 0509952
C; Genetics:
A; Gene: ECs0862

```

RESULT 18
H64814
molybdopterin biosynthesis protein D chain [validated] - Escherichia coli (strain K-12)
A;Alternate names: moaD protein; molybdopterin-converting factor 10K chain; molybdopteri
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence revision 17-Sep-1997 #text_change 05-Oct-2004
C;Accession: H64814; S35001; A46585; S31882
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64814
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-81 <BLAT>
A;Cross-references: UNIPROT:P30748; UNIPARC:UPI00001116DF; GB:AE000181; GB:U00096; NID:9
A;Experimental source: strain K-12, substrain MG1655
R;Rivers, S.L.; McNairn, E.; Blasco, F.; Giordano, G.; Boxer, D.H.
Mol. Microbiol. 8, 1071-1081, 1993
A;Title: Molecular genetic analysis of the moa operon of Escherichia coli K-12 required
A;Reference number: S34998; MUID:93368423; PMID:8361352
A;Accession: S35001
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-44, 'R', '46-81 <RIV>
A;Cross-references: UNIPARC:UPI000016P2FD; EMBL:X70420; NID:942007; PIDN:CAA49864.1; PID
A;Experimental source: strain K12
R;Pitterle, D.M.; Rajagopalan, K.V.
J. Biol. Chem. 268, 13498-13505, 1993
A;Title: The biosynthesis of molybdopterin in Escherichia coli. Purification and charact
A;Reference number: A46585; MUID:93293873; PMID:8514782
A;Accession: A46585
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8, 'E', '10-15 <PIT>
A;Cross-references: UNIPARC:UPI00000178EC3
A;Note: sequence extracted from NCBI backbone (NCBIP:134491)
C;Genetics:
A;Gene: moaD
A;Map position: 17.7 min
C;Complex: heterodimer with D chain (PIR:S31883) [validated, MUID:93293873]
C;Function:
A;Description: required for the addition of the Mo-binding dithiolene group to a molybdo
C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein
C;Keywords: heterodimer; molybdopterin biosynthesis
P;81/Modified site: 1-thioglycine (Gly) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 81;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|||
Db 3 KVLFFA 8

RESULT 19
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A;Reference number: PQ0438; MUID:93075180; PMID:1445331
A;Accession: PQ0438
A;Molecule type: DNA
A;Residues: 1-82 <DAV>
A;Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

```

```

Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: C60045
A;Molecule type: mRNA
A;Residues: 12-68 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56129
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 89.7%; Score 26; DB 2; Length 82;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|||
Db 32 KLVFFA 37

RESULT 20
AC0598
molybdopterin converting factor, chain 1 [imported] - Salmonella enterica subsp. enteri
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 16-Aug-2004
C;Accession: AC0598
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
.S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AC0598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <PAR>
A;Cross-references: UNIPARC:UPI000005A0EA; GB:AL513382; PIDN:CAD05253.1; PID:g16502022,
C;Genetics:
A;Gene: STY0839
C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 89.7%; Score 26; DB 2; Length 83;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|||
Db 5 KVLFFA 10

RESULT 21
T06645
hypothetical protein T20K18.220 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06645
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mc
submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15790
A;Accession: T06645
A;Molecule type: DNA
A;Residues: 1-152 <BBV>
A;Cross-references: UNIPROT:Q9ST29; UNIPARC:UPI00000A0722; EMBL:AL049640; GSPDB:GN00062
A;Experimental source: cultivar Columbia; BAC clone T20K18
C;Genetics:
A;Gene: ATSP:T20K18.220
A;Map position: 4
A;Introns: 87/3; 109/3
C;Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match 89.7%; Score 26; DB 2; Length 152;
Best Local Similarity 83.3%; Pred. No. 58;

```

Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KVVFFA 6							
Db	9	KLVFFA 14							
RESULT 22									
B90157									
hypothetical protein SSO0168 [imported] - Sulfolobus solfataricus									
C:Species: Sulfolobus solfataricus									
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004									
C:Accession: B90157									
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-									
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.									
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.									
submitted to GenBank, April 2001									
A:Description: Sulfolobus solfataricus complete genome.									
A:Reference number: A99139									
A:Accession: B90157									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-193 <KUR>									
A:Cross-references: UNIPROT:Q980V9; UNIPARC:UPI00000641A8; GB:AE006641; NID:gl13813299; P									
C:Genetics:									
A:Gene: SSO0168									
Query Match	89.7%;	Score 26;	DB 2;	Length 193;					
Best Local Similarity	83.3%;	Pred. No. 72;							
Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KVVFFA 6							
Db	117	KVFFYA 122							
RESULT 23									
B81256									
phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / phosphoribosyl-ATP diphosphatase (EC 3									
C:Species: Campylobacter jejuni									
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004									
C:Accession: B81256									
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin									
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell									
Nature 403, 665-668, 2000									
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp									
A:Reference number: A81250; MUID:20150912; PMID:10688204									
A:Accession: B81256									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-207 <PAR>									
A:Cross-references: UNIPROT:Q9PM71; UNIPARC:UPI000012C76D; GB:AL1139079; GB:AL1111168; NID									
A:Experimental source: serotype O2, strain NCTC 11168									
C:Genetics:									
A:Gene: hisI; Cj1604									
C:Superfamily: hisI bifunctional enzyme; hisI bifunctional enzyme homology; hisI protein									
C:Keywords: hydrolase									
Query Match	89.7%;	Score 26;	DB 2;	Length 207;					
Best Local Similarity	83.3%;	Pred. No. 77;							
Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KVVFFA 6							
Db	51	KVFFFS 56							
RESULT 24									
H85138									
hypothetical protein AT4gl2900 [imported] - Arabidopsis thaliana									
C:Species: Arabidopsis thaliana (mouse-ear cress)									
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004									
C:Accession: H85138									

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin									
Nature 402, 769-777, 1999									
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.									
A:Reference number: A85001; MUID:20083488; PMID:10617198									
A:Accession: H85138									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-231 <STO>									
A:Cross-references: UNIPROT:Q9SV79; UNIPARC:UPI00000A7E0E; GB:NC_001368; NID:g7267992; i									
C:Genetics:									
A:Gene: AT4gl2900									
A:Map position: 4									
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100									
Query Match	89.7%;	Score 26;	DB 2;	Length 231;					
Best Local Similarity	83.3%;	Pred. No. 85;							
Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KVVFFA 6							
Db	12	KLVFFA 17							
RESULT 25									
D69355									
hypothetical protein AF0844 - Archaeoglobus fulgidus									
C:Species: Archaeoglobus fulgidus									
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004									
C:Accession: D69355									
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson									
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F									
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.									
Nature 390, 364-370, 1997									
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S									
Smith, H.O.; Woese, C.R.; Venter, J.C.									
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae									
A:Reference number: A69250; MUID:98049343; PMID:9389475									
A:Accession: D69355									
A:Status: preliminary; nucleic acid sequence not shown; translation not shown									
A:Molecule type: DNA									
A:Residues: 1-293 <KLE>									
A:Cross-references: UNIPROT:Q29414; UNIPARC:UPI0000056F64; GB:AE001046; GB:AE000782; NIT									
Query Match	89.7%;	Score 26;	DB 2;	Length 293;					
Best Local Similarity	83.3%;	Pred. No. 1.1e+02;							
Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KVVFFA 6							
Db	140	KVLFFA 145							
RESULT 26									
H90318									
Glycerol kinase (glpK-1) [imported] - Sulfolobus solfataricus									
C:Species: Sulfolobus solfataricus									
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004									
C:Accession: H90318									
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan									
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, i									
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.									
submitted to GenBank, April 2001									
A:Description: Sulfolobus solfataricus complete genome.									
A:Reference number: A99139									
A:Accession: H90318									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-294 <KUR>									
A:Cross-references: UNIPROT:Q97XW2; UNIPARC:UPI00000644B6; GB:AE006641; NID:g13814829; i									
C:Genetics:									
A:Gene: glpK-1									
Query Match	89.7%;	Score 26;	DB 2;	Length 294;					

Best Local Similarity 83.3%; Pred. No. 1.1e+02; DB 2; Length 300;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||:
Db 184 KVVYTA 189

RESULT 27
T26245
hypothetical protein W06G6.6 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26245
R:McMurray, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20180
A:Accession: T26245
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-300 <WIL>
A:Cross-references: UNIPROT:Q9XU61; UNIPARC:UPI0000061208; EMBL:Z83129; PIDN: CAB05641.1;
A:Experimental source: clone W06G6
C:Genetics:
A:Gene: CESP:W06G6.6
A:Map position: 5
A:Introns: 171/2; 204/2

Query Match 89.7%; Score 26; DB 2; Length 300;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||:
Db 281 KVVFFA 286

RESULT 28
B82822
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 [similarity] - *Xylella fastidiosa*
C:Species: *Xylella fastidiosa*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: B82822
R:anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: B82822
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-330 <SIM>
A:Cross-references: UNIPROT:Q9PGI8; UNIPARC:UPI00000C2381; GB:AE003884; GB:AE003849; NID
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, P.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrier, H
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facinani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0312
C:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-c
C:Keywords: membrane-associated complex; NAD; oxidoreductase

Query Match 89.7%; Score 26; DB 2; Length 330;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||:
Db 275 KVVFFA 280

RESULT 29
B72402
UDP-N-acetylglucosamine-N-acetyluramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-a
C:Species: *Thermotoga maritima*
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: B72402
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garttett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: B72402
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-339 <ARN>
A:Cross-references: UNIPROT:Q9WY74; UNIPARC:UPI0000012F9EB; GB:AE001707; GB:AE000512; NI
C:Genetics:
A:Gene: TM0232
C:Superfamily: murG protein

Query Match 89.7%; Score 26; DB 2; Length 339;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||:
Db 32 KVVFFA 37

RESULT 30
T26247
hypothetical protein W06G6.8 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26247
R:McMurray, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20180
A:Accession: T26247
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-349 <WIL>
A:Cross-references: UNIPROT:Q9XU59; UNIPARC:UPI0000061209; EMBL:Z83129; PIDN: CAB05643.1;
A:Experimental source: clone W06G6
C:Genetics:
A:Gene: CESP:W06G6.8
A:Map position: 5
A:Introns: 172/2; 210/3; 247/2

Query Match 89.7%; Score 26; DB 2; Length 349;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||:
Db 324 KVVFFA 329

RESULT 31
T48903
wax synthase [imported] - *Simmondsia chinensis*
C:Species: *Simmondsia chinensis*

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C;Accession: T48903
 R;Lardizabal, K.D.; Metz, J.G.; Sakamoto, T.; Hutton, W.C.; Pollard, M.R.; Lassner, M.W.
 Plant Physiol. 122, 645-655, 2000
 A;Title: Purification of a jojoba embryo wax synthase, cloning of its cDNA and production of a recombinant wax synthase
 A;Reference number: Z25002
 A;Accession: T48903
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-352 <LAR>
 A;Cross-references: UNIPROT:Q9XGY6; UNIPARC:UPI00000A1C81; EMBL:AF149919; PIDN:AAD38041.

Query Match 89.7%; Score 26; DB 2; Length 352;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |:|:|:|
 Db 135 KLVFFA 140

RESULT 32
 T48008
 hypothetical protein T17J13.120 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
 C;Accession: T48008
 R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, R.
 submitted to the Protein Sequence Database, February 2000
 A;Reference number: Z24482
 A;Accession: T48008
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-428 <RIE>
 A;Cross-references: UNIPROT:Q9M108; UNIPARC:UPI00000488B7; EMBL:AL138651
 A;Experimental source: cultivar Columbia; BAC clone T17J13
 C;Genetics:
 A;Map position: 3
 A;Introns: 137/3
 A;Note: T17J13.120
 C;Superfamily: N-hydroxycinnamoyl/benzoyl transferase

Query Match 89.7%; Score 26; DB 2; Length 428;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |:|:|:|
 Db 271 KLVFFA 276

RESULT 33
 B28988
 hypothetical protein F1696 (photosynthetic gene cluster) - Rhodobacter capsulatus
 C;Species: Rhodobacter capsulatus
 C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 09-Jul-2004
 C;Accession: B28988
 R;Youvan, D.C.; Bylina, E.J.; Alberti, M.; Begusch, H.; Hearst, J.E.
 Cell 37, 949-957, 1984
 A;Title: Nucleotide and deduced polypeptide sequences of the photosynthetic reaction-center protein
 A;Reference number: A90850; MUID:84259352; PMID:6744416
 A;Accession: B28988
 A;Molecule type: DNA
 A;Residues: 1-477 <YOU>
 A;Cross-references: UNIPROT:P26176; UNIPARC:UPI000013BE54; GB:K01183

Query Match 89.7%; Score 26; DB 2; Length 477;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |:|:|:|
 Db 349 KLVFFA 354

RESULT 34
 A81548
 hypothetical protein CP0705 [imported] - Chlamydophila pneumoniae (strain AR39)
 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C;Accession: A81548
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A;Reference number: A81500; MUID:20150255; PMID:10684935
 A;Accession: A81548
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-520 <REA>
 A;Cross-references: UNIPROT:Q9K207; UNIPARC:UPI00000CCCC9E; GB:AE002229; GB:AE002161; NT
 A;Experimental source: strain AR39, HL cells
 C;Genetics:
 A;Gene: CP0705

Query Match 89.7%; Score 26; DB 2; Length 520;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |:|:|:|
 Db 381 RVVFFA 386

RESULT 35
 F86499
 hypothetical protein CPj0069 [imported] - Chlamydophila pneumoniae (strain J138)
 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: F86499
 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I. Nucleic Acids Res. 28, 2311-2314, 2000
 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A;Reference number: A86491; MUID:20330349; PMID:10871362
 A;Accession: F86499
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-594 <STO>
 A;Cross-references: UNIPROT:Q9JSK0; UNIPARC:UPI00000CCCCBF; GB:BA000008; NID:g8978443; P
 A;Experimental source: strain J138
 C;Genetics:
 A;Gene: CPj0069

Query Match 89.7%; Score 26; DB 2; Length 594;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |:|:|:|
 Db 455 RVVFFA 460

RESULT 36
 F72237
 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
 C;Species: Thermotoga maritima
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: F72237
 R;Nelson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D. C.M.
 Nature 399, 323-329, 1999
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se.
 A;Reference number: A72200; MUID:99287316; PMID:10360571
 A;Accession: F72237
 A;Status: preliminary

A:Molecule type: DNA
A:Residues: 1-603 <ARN>
A:Cross-references: UNIPROT:Q9X1Q9; UNIPARC:UPI00000C125F; GB:AE001902; GB:AE000512; NID:
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1573

Query Match 89.7%; Score 26; DB 2; Length 603;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:|||||: 198
Db 193 KVVFFS 198

RESULT 37
A72123
hypothetical protein CT326 homolog - Chlamydomophila pneumoniae (strain CWL029)
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: A72123
R:Kalmán, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21: 385-389, 1999
A:Title: Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: A72123
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-617 <ARN>
A:Cross-references: UNIPROT:Q9Z9B2; UNIPARC:UPI00000C11C1; GB:AE001592; GB:AE001363; NID:
A:Experimental source: strain CWL029
C:Genetics:
A:Gene: CP0069

Query Match 89.7%; Score 26; DB 2; Length 617;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:|||||: 483
Db 478 RVVFFA 483

RESULT 38
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138: 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a p
A:Reference number: A49795; MUID:91273117; PMID:1905108
A:Accession: A49795
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: UNIPARC:UPI000002A2F2; GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C:Keywords: alternative splicing

Query Match 89.7%; Score 26; DB 1; Length 695;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:|||||: 617
Db 612 KLVFFA 617

RESULT 39
A27485

Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N:Alternate names: Proteinase nexin II
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C:Accession: A27485; S19727; I49485
R:Yamada, T.; Sasaki, H.; Furuha, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149: 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein prec
A:Reference number: A27485; MUID:88106489; PMID:3322280
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:g191568; PIDN:
A:Experimental source: brain
R:de Strooper, B.; van Leeuwen, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129: 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A:Reference number: S19727; MUID:92096458; PMID:1756177
A:Accession: S19727
A:Molecule type: mRNA
A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A:Cross-references: UNIPARC:UPI000002A2F9; EMBL:X59379
R:Izum, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112: 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer'
A:Reference number: I49485; MUID:92209998; PMID:1555768
A:Accession: I49485
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: UNIPARC:UPI00000003B7; GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 89.7%; Score 26; DB 2; Length 695;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:|||||: 617
Db 612 KLVFFA 617

RESULT 40
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7: 1365-1370, 1988
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brai
A:Reference number: S00550; MUID:88312583; PMID:2900758
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2FB; EMBL:X07648; NID:g55616; PII:
R:Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241: 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan cor
A:Reference number: A41245; MUID:88264430; PMID:2968652
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Cross-references: UNIPARC:UPI0000177FD
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349: 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627; PMID:7913895

A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Maller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A:Molecule type: protein
A;Residues: 18-32 <POT>
A;Cross-references: UNIPARC:UPI00001777PE
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor; alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TM>

Query Match 89.7%; Score 26; DB 2; Length 695;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
DB 612 KLVFFA 617

RESULT 41
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A:Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: UNIPARC:UPI00000FC880; GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:JH0773
A;Experimental source: larva
A;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 89.7%; Score 26; DB 2; Length 747;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
DB 664 KLVFFA 669

RESULT 42
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibitor
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular protein precursor splice form APP (770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A33260; A35486; I39452; I39451; I39453; I59562; A44468; A28583; A29302; A60805; JLO038; S06121; A60355; A59011; A38384; S29076; S38252; S38253; S38254; S38255; S38256; S38257; S38258; S38259; S38260; S38261; S38262; S38263; S38264; S38265; S38266; S38267; S38268; S38269; S38270; S38271; S38272; S38273; S38274; S38275; S38276; S38277; S38278; S38279; S38280; S38281; S38282; S38283; S38284; S38285; S38286; S38287; S38288; S38289; S38290; S38291; S38292; S38293; S38294; S38295; S38296; S38297; S38298; S38299; S38300; S38301; S38302; S38303; S38304; S38305; S38306; S38307; S38308; S38309; S38310; S38311; S38312; S38313; S38314; S38315; S38316; S38317; S38318; S38319; S38320; S38321; S38322; S38323; S38324; S38325; S38326; S38327; S38328; S38329; S38330; S38331; S38332; S38333; S38334; S38335; S38336; S38337; S38338; S38339; S38340; S38341; S38342; S38343; S38344; S38345; S38346; S38347; S38348; S38349; S38350; S38351; S38352; S38353; S38354; S38355; S38356; S38357; S38358; S38359; S38360; S38361; S38362; S38363; S38364; S38365; S38366; S38367; S38368; S38369; S38370; S38371; S38372; S38373; S38374; S38375; S38376; S38377; S38378; S38379; S38380; S38381; S38382; S38383; S38384; S38385; S38386; S38387; S38388; S38389; S38390; S38391; S38392; S38393; S38394; S38395; S38396; S38397; S38398; S38399; S38400; S38401; S38402; S38403; S38404; S38405; S38406; S38407; S38408; S38409; S38410; S38411; S38412; S38413; S38414; S38415; S38416; S38417; S38418; S38419; S38420; S38421; S38422; S38423; S38424; S38425; S38426; S38427; S38428; S38429; S38430; S38431; S38432; S38433; S38434; S38435; S38436; S38437; S38438; S38439; S38440; S38441; S38442; S38443; S38444; S38445; S38446; S38447; S38448; S38449; S38450; S38451; S38452; S38453; S38454; S38455; S38456; S38457; S38458; S38459; S38460; S38461; S38462; S38463; S38464; S38465; S38466; S38467; S38468; S38469; S38470; S38471; S38472; S38473; S38474; S38475; S38476; S38477; S38478; S38479; S38480; S38481; S38482; S38483; S38484; S38485; S38486; S38487; S38488; S38489; S38490; S38491; S38492; S38493; S38494; S38495; S38496; S38497; S38498; S38499; S38500; S38501; S38502; S38503; S38504; S38505; S38506; S38507; S38508; S38509; S38510; S38511; S38512; S38513; S38514; S38515; S38516; S38517; S38518; S38519; S38520; S38521; S38522; S38523; S38524; S38525; S38526; S38527; S38528; S38529; S38530; S38531; S38532; S38533; S38534; S38535; S38536; S38537; S38538; S38539; S38540; S38541; S38542; S38543; S38544; S38545; S38546; S38547; S38548; S38549; S38550; S38551; S38552; S38553; S38554; S38555; S38556; S38557; S38558; S38559; S38560; S38561; S38562; S38563; S38564; S38565; S38566; S38567; S38568; S38569; S38570; S38571; S38572; S38573; S38574; S38575; S38576; S38577; S38578; S38579; S38580; S38581; S38582; S38583; S38584; S38585; S38586; S38587; S38588; S38589; S38590; S38591; S38592; S38593; S38594; S38595; S38596; S38597; S38598; S38599; S38600; S38601; S38602; S38603; S38604; S38605; S38606; S38607; S38608; S38609; S38610; S38611; S38612; S38613; S38614; S38615; S38616; S38617; S38618; S38619; S38620; S38621; S38622; S38623; S38624; S38625; S38626; S38627; S38628; S38629; S38630; S38631; S38632; S38633; S38634; S38635; S38636; S38637; S38638; S38639; S38640; S38641; S38642; S38643; S38644; S38645; S38646; S38647; S38648; S38649; S38650; S38651; S38652; S38653; S38654; S38655; S38656; S38657; S38658; S38659; S38660; S38661; S38662; S38663; S38664; S38665; S38666; S38667; S38668; S38669; S38670; S38671; S38672; S38673; S38674; S38675; S38676; S38677; S38678; S38679; S38680; S38681; S38682; S38683; S38684; S38685; S38686; S38687; S38688; S38689; S38690; S38691; S38692; S38693; S38694; S38695; S38696; S38697; S38698; S38699; S38700; S38701; S38702; S38703; S38704; S38705; S38706; S38707; S38708; S38709; S38710; S38711; S38712; S38713; S38714; S38715; S38716; S38717; S38718; S38719; S38720; S38721; S38722; S38723; S38724; S38725; S38726; S38727; S38728; S38729; S38730; S38731; S38732; S38733; S38734; S38735; S38736; S38737; S38738; S38739; S38740; S38741; S38742; S38743; S38744; S38745; S38746; S38747; S38748; S38749; S38750; S38751; S38752; S38753; S38754; S38755; S38756; S38757; S38758; S38759; S38760; S38761; S38762; S38763; S38764; S38765; S38766; S38767; S38768; S38769; S38770; S38771; S38772; S38773; S38774; S38775; S38776; S38777; S38778; S38779; S38780; S38781; S38782; S38783; S38784; S38785; S38786; S38787; S38788; S38789; S38790; S38791; S38792; S38793; S38794; S38795; S38796; S38797; S38798; S38799; S38800; S38801; S38802; S38803; S38804; S38805; S38806; S38807; S38808; S38809; S38810; S38811; S38812; S38813; S38814; S38815; S38816; S38817; S38818; S38819; S38820; S38821; S38822; S38823; S38824; S38825; S38826; S38827; S38828; S38829; S38830; S38831; S38832; S38833; S38834; S38835; S38836; S38837; S38838; S38839; S38840; S38841; S38842; S38843; S38844; S38845; S38846; S38847; S38848; S38849; S38850; S38851; S38852; S38853; S38854; S38855; S38856; S38857; S38858; S38859; S38860; S38861; S38862; S38863; S38864; S38865; S38866; S38867; S38868; S38869; S38870; S38871; S38872; S38873; S38874; S38875; S38876; S38877; S38878; S38879; S38880; S38881; S38882; S38883; S38884; S38885; S38886; S38887; S38888; S38889; S38890; S38891; S38892; S38893; S38894; S38895; S38896; S38897; S38898; S38899; S38900; S38901; S38902; S38903; S38904; S38905; S38906; S38907; S38908; S38909; S38910; S38911; S38912; S38913; S38914; S38915; S38916; S38917; S38918; S38919; S38920; S38921; S38922; S38923; S38924; S38925; S38926; S38927; S38928; S38929; S38930; S38931; S38932; S38933; S38934; S38935; S38936; S38937; S38938; S38939; S38940; S38941; S38942; S38943; S38944; S38945; S38946; S38947; S38948; S38949; S38950; S38951; S38952; S38953; S38954; S38955; S38956; S38957; S38958; S38959; S38960; S38961; S38962; S38963; S38964; S38965; S38966; S38967; S38968; S38969; S38970; S38971; S38972; S38973; S38974; S38975; S38976; S38977; S38978; S38979; S38980; S38981; S38982; S38983; S38984; S38985; S38986; S38987; S38988; S38989; S38990; S38991; S38992; S38993; S38994; S38995; S38996; S38997; S38998; S38999; S39000; S39001; S39002; S39003; S39004; S39005; S39006; S39007; S39008; S39009; S39010; S39011; S39012; S39013; S39014; S39015; S39016; S39017; S39018; S39019; S39020; S39021; S39022; S39023; S39024; S39025; S39026; S39027; S39028; S39029; S39030; S39031; S39032; S39033; S39034; S39035; S39036; S39037; S39038; S39039; S39040; S39041; S39042; S39043; S39044; S39045; S39046; S39047; S39048; S39049; S39050; S39051; S39052; S39053; S39054; S39055; S39056; S39057; S39058; S39059; S39060; S39061; S39062; S39063; S39064; S39065; S39066; S39067; S39068; S39069; S39070; S39071; S39072; S39073; S39074; S39075; S39076; S39077; S39078; S39079; S39080; S39081; S39082; S39083; S39084; S39085; S39086; S39087; S39088; S39089; S39090; S39091; S39092; S39093; S39094; S39095; S39096; S39097; S39098; S39099; S39100; S39101; S39102; S39103; S39104; S39105; S39106; S39107; S39108; S39109; S39110; S39111; S39112; S39113; S39114; S39115; S39116; S39117; S39118; S39119; S39120; S39121; S39122; S39123; S39124; S39125; S39126; S39127; S39128; S39129; S39130; S39131; S39132; S39133; S39134; S39135; S39136; S39137; S39138; S39139; S39140; S39141; S39142; S39143; S39144; S39145; S39146; S39147; S39148; S39149; S39150; S39151; S39152; S39153; S39154; S39155; S39156; S39157; S39158; S39159; S39160; S39161; S39162; S39163; S39164; S39165; S39166; S39167; S39168; S39169; S39170; S39171; S39172; S39173; S39174; S39175; S39176; S39177; S39178; S39179; S39180; S39181; S39182; S39183; S39184; S39185; S39186; S39187; S39188; S39189; S39190; S39191; S39192; S39193; S39194; S39195; S39196; S39197; S39198; S39199; S39200; S39201; S39202; S39203; S39204; S39205; S39206; S39207; S39208; S39209; S39210; S39211; S39212; S39213; S39214; S39215; S39216; S39217; S39218; S39219; S39220; S39221; S39222; S39223; S39224; S39225; S39226; S39227; S39228; S39229; S39230; S39231; S39232; S39233; S39234; S39235; S39236; S39237; S39238; S39239; S39240; S39241; S39242; S39243; S39244; S39245; S39246; S39247; S39248; S39249; S39250; S39251; S39252; S39253; S39254; S39255; S39256; S39257; S39258; S39259; S39260; S39261; S39262; S39263; S39264; S39265; S39266; S39267; S39268; S39269; S39270; S39271; S39272; S39273; S39274; S39275; S39276; S39277; S39278; S39279; S39280; S39281; S39282; S39283; S39284; S39285; S39286; S39287; S39288; S39289; S39290; S39291; S39292; S39293; S39294; S39295; S39296; S39297; S39298; S39299; S39300; S39301; S39302; S39303; S39304; S39305; S39306; S39307; S39308; S39309; S39310; S39311; S39312; S39313; S39314; S39315; S39316; S39317; S39318; S39319; S39320; S39321; S39322; S39323; S39324; S39325; S39326; S39327; S39328; S39329; S39330; S39331; S39332; S39333; S39334; S39335; S39336; S39337; S39338; S39339; S39340; S39341; S39342; S39343; S39344; S39345; S39346; S39347; S39348; S39349; S39350; S39351; S39352; S39353; S39354; S39355; S39356; S39357; S39358; S39359; S39360; S39361; S39362; S39363; S39364; S39365; S39366; S39367; S39368; S39369; S39370; S39371; S39372; S39373; S39374; S39375; S39376; S39377; S39378; S39379; S39380; S39381; S39382; S39383; S39384; S39385; S39386; S39387; S39388; S39389; S39390; S39391; S39392; S39393; S39394; S39395; S39396; S39397; S39398; S39399; S39400; S39401; S39402; S39403; S39404; S39405; S39406; S39407; S39408; S39409; S39410; S39411; S39412; S39413; S39414; S39415; S39416; S39417; S39418; S39419; S39420; S39421; S39422; S39423; S39424; S39425; S39426; S39427; S39428; S39429; S39430; S39431; S39432; S39433; S39434; S39435; S39436; S39437; S39438; S39439; S39440; S39441; S39442; S39443; S39444; S39445; S39446; S39447; S39448; S39449; S39450; S39451; S39452; S39453; S39454; S39455; S39456; S39457; S39458; S39459; S39460; S39461; S39462; S39463; S39464; S39465; S39466; S39467; S39468; S39469; S39470; S39471; S39472; S39473; S39474; S39475; S39476; S39477; S39478; S39479; S39480; S39481; S39482; S39483; S39484; S39485; S39486; S39487; S39488; S39489; S39490; S39491; S39492; S39493; S39494; S39495; S39496; S39497; S39498; S39499; S39500; S39501; S39502; S39503; S39504; S39505; S39506; S39507; S39508; S39509; S39510; S39511; S39512; S39513; S39514; S39515; S39516; S39517; S39518; S39519; S39520; S39521; S39522; S39523; S39524; S39525; S39526; S39527; S39528; S39529; S39530; S39531; S39532; S39533; S39534; S39535; S39536; S39537; S39538; S39539; S39540; S39541; S39542; S39543; S39544; S39545; S39546; S39547; S39548; S39549; S39550; S39551; S39552; S39553; S39554; S39555; S39556; S39557; S39558; S39559; S39560; S39561; S39562; S39563; S39564; S39565; S39566; S39567; S39568; S39569; S39570; S39571; S39572; S39573; S39574; S39575; S39576; S39577; S39578; S39579; S39580; S39581; S39582; S39583; S39584; S39585; S39586; S39587; S39588; S39589; S39590; S39591; S39592; S39593; S39594; S39595; S39596; S39597; S39598; S39599; S39600; S39601; S39602; S39603; S39604; S39605; S39606; S39607; S39608; S39609; S39610; S39611; S39612; S39613; S39614; S39615; S39616; S39617; S39618; S39619; S39620; S39621; S39622; S39623; S39624; S39625; S39626; S39627; S39628; S39629; S39630; S39631; S39632; S39633; S39634; S39635; S39636; S39637; S39638; S39639; S39640; S39641; S39642; S39643; S39644; S39645; S39646; S39647; S39648; S39649; S39650; S39651; S39652; S39653; S39654; S39655; S39656; S39657; S39658; S39659; S39660; S39661; S39662; S39663; S39664; S39665; S39666; S39667; S39668; S39669; S39670; S39671; S39672; S39673; S39674; S39675; S39676; S39677; S39678; S39679; S39680; S39681; S39682; S39683; S39684; S39685; S39686; S39687; S39688; S39689; S39690; S39691; S39692; S39693; S39694; S39695; S39696; S39697; S39698; S39699; S39700; S39701; S39702; S39703; S39704; S39705; S39706; S39707; S39708; S39709; S39710; S39711; S39712; S39713; S39714; S39715; S39716; S39717; S39718; S39719; S39720; S39721; S39722; S39723; S39724; S39725; S39726; S39727; S39728; S39729; S39730; S39731; S39732; S39733; S39734; S39735; S39736; S39737; S39738; S39739; S39740; S39741; S39742; S39743; S39744; S39745; S39746; S39747; S39748; S39749; S39750; S39751; S39752; S39753; S39754; S39755; S39756; S39757; S39758; S39759; S39760; S39761; S39762; S39763; S39764; S39765; S39766; S39767; S39768; S39769; S39770; S39771; S39772; S39773; S39774; S39775; S39776; S39777; S39778; S39779; S39780; S39781; S39782; S39783; S39784; S39785; S39786; S39787; S39788; S39789; S39790; S39791; S39792; S39793; S39794; S39795; S39796; S39797; S39798; S39799; S39800; S39801; S39802; S39803; S39804; S39805; S39806; S39807; S39808; S39809; S39810; S39811; S39812; S39813; S39814; S39815; S39816; S39817; S39818; S39819; S39820; S39821; S398

Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692, 'G', 694-718 <KAM1>
A;Cross-references: UNIPARC:UPI000011F7EB; GB:945135; NID:9257377; PIDN:AAB23645.1; PID:
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCB1 backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: UNIPARC:UPI0000168394; GB:945136; NID:9257379; PIDN:AAB23646.1; PID:
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCB1 backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288, 'V', 365-770 <KAN>
A;Cross-references: UNIPARC:UPI00002A2P2; GB:Y00264; NID:928525; PIDN:CAA68374.1; PID:9
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A;Cross-references: UNIPARC:UPI000016A545; GB:M16765; NID:9178539; PIDN:AAA51722.1; PID:
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756, 'S', 758-770 <GOL>
A;Cross-references: UNIPARC:UPI00001420E5; GB:M15533; NID:9178706; PIDN:AAA35540.1; PID:
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TANI>
A;Cross-references: UNIPARC:UPI000016A46F; GB:M15532; NID:9177957; PIDN:AAA51564.1; PID:
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A;Reference number: S02638; MUID:86296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
A;Cross-references: UNIPARC:UPI0000035AB0
R;Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344, 'I', 365-366 <TAN2>
A;Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
A;Reference number: S00925; MUID:88122639; PMID:2893289

A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344, 'I', 365-770 <PO2>
A;Cross-references: UNIPARC:UPI000002A2P6; GB:X06989; EMBL:X00297; NID:928720; PIDN:CAA
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibito
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: UNIPARC:UPI000014553B; GB:X06981; NID:928816; PIDN:CAA30041.1; PID:
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashto
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-770 <VIT1>
A;Cross-references: UNIPARC:UPI0000174094
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288, 'V', 365-770 <VIT2>
A;Cross-references: UNIPARC:UPI0000174094
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
A;Cross-references: UNIPARC:UPI0000174094
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA

Query Match 89.7%; Score 26; DB 1; Length 770;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
|:||||
DB 687 KLVFFA 692

RESULT 43
A82511
glycogen phosphorylase (EC 2.4.1.1) [similarity] - Vibrio cholerae (strain N16961 serog
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 18-Aug-2003
C;Accession: A82511
R;Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 405, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: A82511
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-817 <HEI>
A;Cross-references: UNIPARC:UPI00000C33CA; GB:AE004345; GB:AE003853; NID:9657390; PID:
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0013
A;Map position: 2
C;Superfamily: glucan phosphorylase
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phosphat

F:564/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 817;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
:|||||
Db 585 RVVFFA 590

RESULT 44

S30236
genome polyprotein - zucchini yellow mosaic virus (strain Singapore) (fragment)
N;Contains: coat protein; nuclear inclusion protein a; RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: zucchini yellow mosaic virus, ZYMV
A;Variety: strain Singapore
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Accession: S30236
R;Wu, M.; Yeong, C.Y.; Lee, S.C.; Wong, S.M.
Nucleic Acids Res. 21, 1317, 1993
A;Title: Nucleotide sequence of the 3' half of zucchini yellow mosaic virus (Singapore isolate)
A;Reference number: S30236; MUID:93219099; PMID:8464715
A;Accession: S30236
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-1016 <WUM>
A;Cross-references: UNIPROT:Q05912; UNIPARC:UPI000008CC69; EMBL:X68509; NID:g288233; PIR:G288233
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1992
C;Superfamily: tobacco etch virus genome polyprotein
C;Keywords: coat protein; genome-linked protein; nucleotidyltransferase; phosphoprotein;
F;9-61/Product: VPg protein #status predicted <VPg>
F;62-494/Product: nuclear inclusion protein a #status predicted <NIA>
F;495-1010/Product: RNA-directed RNA polymerase #status predicted <POL>
F;1011-1016/Product: coat protein (fragment) #status predicted <CP>
F;125/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 1016;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
:|||||
Db 837 KLVFFA 842

RESULT 45

E64214
hypothetical protein homolog MG131 - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: E64214
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: E64214
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-74 <TIGR>
A;Cross-references: UNIPROT:P47377; UNIPARC:UPI000013931D; GB:U39691; GB:I43967; NID:g100000000
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3

Query Match 86.2%; Score 25; DB 2; Length 74;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
:|||||

Db 34 KILFFA 39

RESULT 46

B72213
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: B72213
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.

Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72213
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <ARN>
A;Cross-references: UNIPROT:Q9X292; UNIPARC:UPI000000C120B; GB:AE001815; GB:AE000512; NFI
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1771
C;Superfamily: Bacillus subtilis conserved hypothetical protein yqhy

Query Match 86.2%; Score 25; DB 2; Length 109;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
:|||||
Db 19 KIVFFA 24

RESULT 47

T19479
hypothetical protein C26C6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19479
R;McMurray, A.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19128
A;Accession: T19479
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-136 <WIL>
A;Cross-references: UNIPROT:Q18208; UNIPARC:UPI000007BES9; EMBL:Z72503; PIDN:CAA96598.1
A;Experimental source: clone C26C6
C;Genetics:
A;Gene: CESP:C26C6.6
A;Map position: 1
A;Introns: 22/3; 44/3; 78/1

Query Match 86.2%; Score 25; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
:|||||
Db 24 KVVFF 28

RESULT 48

E75134
hypothetical protein PAB1779 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Dec-2002
C;Accession: E75134
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A;Reference number: A75001

A;Accession: E75134
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 <KAW>
A;Cross-references: UNIPARC:UPI0000063351; GB:AJ248285; GB:AL096836; NID:95458067; PIDN:
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1779
C;Superfamily: uncharacterized conserved protein

Query Match 86.2%; Score 25; DB 2; Length 146;
Best Local Similarity 66.7%; Pred. No. 96;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|||:
Db 39 KVIFVA 44

RESULT 49
T32362
hypothetical protein C08E3.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32362
R;Miller, N.; Kramer, J.; Keppler, D.
A;Description: The sequence of C. elegans cosmid C08E3.
A;Reference number: Z21155
A;Accession: T32362
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-148 <MIL>
A;Cross-references: UNIPROT:O17202; UNIPARC:UPI0000076D24; EMBL:AF025457; PIDN:AAE70972.
A;Experimental source: strain Bristol N2; clone C08E3
C;Genetics:
A;Gene: CESP:C08E3.11
A;Map position: 2
A;Introns: 66/2

Query Match 86.2%; Score 25; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5
|||||
Db 126 KVVFF 130

RESULT 50
H95252
PTS system, IIB component [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: H95252
R;Tetteilin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unay, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: H95252
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <KUR>
A;Cross-references: UNIPROT:Q97N92; UNIPARC:UPI0000051B4E; GB:AE005672; PIDN:AAK76217.1;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP2163
C;Superfamily: phosphotransferase system mannose-specific enzyme II, factor III

Query Match 86.2%; Score 25; DB 2; Length 156;

Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|||:
Db 56 KIVFFS 61

RESULT 51
F98117
hypothetical protein PTS-EII [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: F98117
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: F98117
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <KUR>
A;Cross-references: UNIPROT:Q8DN20; UNIPARC:UPI00000E3754; GB:AE007317; PIDN:RAL00771.1;
C;Genetics:
A;Gene: PTS-EII
C;Superfamily: phosphotransferase system mannose-specific enzyme II, factor III

Query Match 86.2%; Score 25; DB 2; Length 156;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|||:
Db 56 KIVFFS 61

RESULT 52
C71080
hypothetical protein PH0907 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Aug-2004
C;Accession: C71080
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguci
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: C71080
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-159 <KAW>
A;Cross-references: UNIPARC:UPI0000062F34; GB:AF000004; NID:g3236131; PIDN:EAA30001.1;
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBan
C;Genetics:
A;Gene: PH0907
C;Superfamily: uncharacterized conserved protein

Query Match 86.2%; Score 25; DB 2; Length 159;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|||:
Db 54 KVIFVA 59

RESULT 53
T13659
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia sagittata chloroplast

C:Species: chloroplast Pontederia sagittata
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13659
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.
Syst. Biol. 47, 545-567, 1998
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets
A:Reference number: Z17600
A:Accession: T13659
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-162 <GRA>
A:Cross-references: UNIPROT:Q32915; UNIPARC:UPI0000096540; EMBL:U41621; NID:g1174015; PT13659
C:Genetics:
A:Genome: chloroplast
A:Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 13 KVIFFS 18
|||:

RESULT 54
T13656
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia rotundifolia chloroplast
C:Species: chloroplast Pontederia rotundifolia
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13656
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.
Syst. Biol. 47, 545-567, 1998
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets
A:Reference number: Z17600
A:Accession: T13656
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-162 <GRA>
A:Cross-references: UNIPROT:Q32892; UNIPARC:UPI000008CB4C; EMBL:U41620; NID:g1174011; PT13656
C:Genetics:
A:Genome: chloroplast
A:Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 13 KVIFFS 18
|||:

RESULT 55
T13563
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia cordata chloroplast
C:Species: chloroplast Pontederia cordata
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13563
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.
Syst. Biol. 47, 545-567, 1998
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets
A:Reference number: Z17600
A:Accession: T13563
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-162 <GRA>
A:Cross-references: UNIPROT:Q32802; UNIPARC:UPI000008F006; EMBL:U41619; NID:g1174003; PT13563
A:Experimental source: var. ovalle

C:Genetics:
A:Genome: chloroplast
A:Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 13 KVIFFS 18
|||:

RESULT 56
T13487
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Monochoria vaginalis chloroplast
C:Species: chloroplast Monochoria vaginalis
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13487
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.
Syst. Biol. 47, 545-567, 1998
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets
A:Reference number: Z17600
A:Accession: T13487
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-162 <GRA>
A:Cross-references: UNIPROT:Q32648; UNIPARC:UPI00000976F4; EMBL:U41616; NID:g1173991; PT13487
C:Genetics:
A:Genome: chloroplast
A:Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 13 KVIFFS 18
|||:

RESULT 57
T13562
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia cordata chloroplast
C:Species: chloroplast Pontederia cordata
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13562
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.
Syst. Biol. 47, 545-567, 1998
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets
A:Reference number: Z17600
A:Accession: T13562
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-164 <GRA>
A:Cross-references: UNIPROT:Q37011; UNIPARC:UPI000016D3B6; EMBL:U41617; NID:g1173999; PT13562
A:Experimental source: var. cordata
C:Genetics:
A:Genome: chloroplast
A:Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 164;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 13 KVIFFS 18
|||:

Db 13 KVIFPS 18

RESULT 58
G70475
conserved hypothetical protein aq_2049 - Aquifex aeolicus
C/Species: Aquifex aeolicus
C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C/Accession: G70475
R/Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V.
Nature 392, 353-358, 1998
A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A/Reference number: A70300; MUID:98196666; PMID:9537320
A/Accession: G70475
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-188 <AOQ>
A/Cross-references: UNIPROT:O67835; UNIPARC:UPI000005679F; GB:AE000770; NID:g2984274; PT
A/Experimental source: strain VF5
C/Genetics:
A/Gene: aq_2049

Query Match 86.2%; Score 25; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVIFPS 5
Db 79 KVIFPS 83

RESULT 59
A95895
probable permease protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid
C/Species: Sinorhizobium meliloti
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C/Accession: A95895
R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A/Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
A/Reference number: A95842; MUID:21396508; PMID:11481431
A/Accession: A95895
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-190 <KUR>
A/Cross-references: UNIPROT:Q9AWB8; UNIPARC:UPI000000CB514; GB:AL591985; PTDN:CAC48825.1
A/Experimental source: strain 1021, megaplasmid pSymb
R/Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.;
A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A/Reference number: A96039; MUID:21368234; PMID:11474104
A/Contents: annotation
C/Genetics:
A/Gene: SMD20443
A/Genome: plasmid

Query Match 86.2%; Score 25; DB 2; Length 190;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVIFPS 6
Db 116 RIVFPA 121

RESULT 60
B97211
uncharacterized conserved membrane protein CAC2524 [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97211
R;Nolling, J.; Bennett, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
.; Daly, M.J.; Breatton, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-194 <KUR>
A;Cross-references: UNIPROT:Q97G46; UNIPARC:UPI00000CA55C; GB:AE001437; PIDN:AAK80477.1
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2524

Query Match 86.2%; Score 25; DB 2; Length 194;
Best Local Similarity 86.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
||:||||
DB 165 KIUFFA 170

RESULT 61
AE1632
hypothetical protein homolog lin1598 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE1632
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloech
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, I
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; i
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlan
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1632
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-200 <GLA>
A;Cross-references: UNIPROT:Q92BF2; UNIPARC:UPI0000127CE2; GB:AL592022; PIDN:CAC96829.1
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin1598
C;Superfamily: conserved hypothetical protein YDR196c

Query Match 86.2%; Score 25; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFF 5
|||||
DB 109 KVVFFF 113

RESULT 62
A71495
probable polysaccharide transporter - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: A71495
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchel
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tri
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: A71495
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-232 <ARN>

A;Cross-references: UNIPROT:O84601; UNIPARC:UPI00000D336C; GB:AE001330; GB:AE001273; NID: D82405
 A;Experimental source: serotype D, strain UW-3/Cx
 C;Genetics:
 A;Gene: exbB
 C;Superfamily: biopolymer transport protein

Query Match 86.2%; Score 25; DB 2; Length 232;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 ||:||:
 Db 21 KVVFFS 26

RESULT 63

T23466

hypothetical protein K08E4.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T23466

R;Percy, C.

submitted to the EMBL Data Library, December 1995

A;Reference number: Z19744

A;Accession: T23466

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-234 <WIL>

A;Cross-references: UNIPROT:Q21336; UNIPARC:UPI00000765B4; EMBL:Z68316; PIDN:CAA92683.1;
 A;Experimental source: clone K08E4

C;Genetics:

A;Gene: CESP:K08E4.6

A;Map position: 4

A;Introns: 54/3; 154/3

Query Match 86.2%; Score 25; DB 2; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
 |||||
 Db 109 KVVFF 113

RESULT 64

T32514

hypothetical protein C44B12.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004

C;Accession: T32514

R;Tin-Wollam, A.

submitted to the EMBL Data Library, December 1997

A;Description: The sequence of C. elegans cosmid C44B12.

A;Reference number: Z21183

A;Accession: T32514

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-247 <TIN>

A;Cross-references: UNIPROT:O44145; UNIPARC:UPI00001793B3; EMBL:AF036692; PIDN:AAB88324.
 A;Experimental source: strain Bristol N2; clone C44B12

C;Genetics:

A;Gene: CESP:C44B12.1

A;Map position: 4

A;Introns: 28/3; 82/1; 164/1; 192/1

Query Match 86.2%; Score 25; DB 2; Length 247;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 ||:||:
 Db 224 KVVFFS 229

RESULT 65

D82405

transcription regulator LuxR family VCA0888 [imported] - Vibrio cholerae (strain N16961

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: D82405

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.

chardson, D.; Emolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I.

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: D82405

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-253 <HEI>

A;Cross-references: UNIPROT:Q9KL60; UNIPARC:UPI00000C36AA; GB:AE004416; GB:AE003853; NID:

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VCA0888

A;Map position: 2

Query Match 86.2%; Score 25; DB 2; Length 253;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 ||:||:
 Db 51 KVVFFS 56

RESULT 66

C87434

2-deoxy-D-gluconate 3-dehydrogenase [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004

C;Accession: C87434

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo-

n, J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: C87434

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-255 <STO>

A;Cross-references: UNIPROT:Q9A872; UNIPARC:UPI00000C73DC; GB:AE005673; NID:gl3422867; I

C;Genetics:

A;Gene: CC1492

C;Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 86.2%; Score 25; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
 |||||
 Db 117 KVVFF 121

RESULT 67

C83982

hypothetical protein BH2659 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C;Accession: C83982

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A;Reference number: A83650; MUID:20512592; PMID:11058132

A;Accession: C83982


```

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <STO>
A;Cross-references: UNIPROT:Q9K9I8; UNIPARC:UPI00000C3F80; GB:AP001516; GB:BA000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2659

Query Match      86.2%; Score 25; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFF 5
        |||||
Db      4 KVVFF 8

RESULT 68
D64166
hypothetical protein HI1086 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: D64166
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.;
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.F.; Glodek, A.; Kelley, J.M.; Weidman, J.;
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: D64166
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-261 <TIGR>
A;Cross-references: UNIPROT:P45030; UNIPARC:UPI000013BFAD; GB:U32788; GB:L42023; NID:g18
A;Note: best homolog was a hypothetical protein from Escherichia coli
C;Superfamily: conserved hypothetical protein HI1086

Query Match      86.2%; Score 25; DB 2; Length 261;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
        | ||||
Db     205 KAVFFA 210

RESULT 69
T31855
hypothetical protein C02E7.12 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31855
R;Fulton, B.; Wohlmann, P.
submitted to the EMBL Data Library, June 1998
A;Description: The sequence of C. elegans cosmid C02E7.
A;Reference number: Z21093
A;Accession: T31855
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-277 <FUL>
A;Cross-references: UNIPARC:UPI000017B71A; EMBL:AF016446; PIDN:AAC24170.1; GSPDB:GN00023
A;Experimental source: strain Bristol N2; clone C02E7
C;Genetics:
A;Gene: CESP:C02E7.12
A;Map position: 5
A;Introns: 45/2; 146/3

Query Match      86.2%; Score 25; DB 2; Length 277;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6

```

```

Db     112 KIVFFA 117
        |:|:|

RESULT 70
C84857
hypothetical protein At2g42710 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: C84857
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84857
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <STO>
A;Cross-references: UNIPROT:Q9SJ15; UNIPARC:UPI00000A82D6; GB:AE002093; NID:g4512681; P
C;Genetics:
A;Gene: At2g42710
A;Map position: 2
C;Superfamily: ribosomal protein Llp/L10e

Query Match      86.2%; Score 25; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
        || |||
Db     241 KVAFFA 246

RESULT 71
JC4744
NAD-dinitrogen-reductase ADP-D-ribosyltransferase (EC 2.4.2.37) - rice
C;Species: Oryza sativa (rice)
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 02-Aug-2002
C;Accession: JC4744
R;Inoue, A.; Shigematsu, T.; Hidaka, M.; Maseki, H.; Uozumi, T.
Gene 170, 101-106, 1996
A;Title: Cloning, sequencing and transcriptional regulation of the draT and draG genes
A;Reference number: JC4744; MUID:96200864; PMID:8621068
A;Accession: JC4744
A;Molecule type: DNA
A;Residues: 1-295 <INO>
A;Cross-references: UNIPARC:UPI00000BDA45; DDBJ:D55631; NID:g862322; PID:g862323
C;Comment: This enzyme is responsible for the post-translation regulation of nitroge
C;Genetics:
A;Gene: draT
C;Superfamily: Azospirillum NAD+-nitrogenase ADP-D-ribosyltransferase
C;Keywords: Glycosyltransferase; NAD; pentosyltransferase

Query Match      86.2%; Score 25; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFF 5
        |||||
Db     262 KVVFF 266

RESULT 72
I39751
NAD-dinitrogen-reductase ADP-D-ribosyltransferase (EC 2.4.2.37) - Azospirillum brasil
C;Species: Azospirillum brasilense
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: I39751
R;Zhang, Y.; Burris, R.H.; Roberts, G.P.
J. Bacteriol. 174, 3364-3369, 1992
A;Title: Cloning, sequencing, mutagenesis, and functional characterization of draT and

```

A:Reference number: I39751; MUID:92250433; PMID:1577701
 A:Accession: I39751
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-295 <RES>
 A:Cross-references: UNIPROT:Q43903; UNIPARC:UPI0000080CDE; GB:M87319; NID:g142411; PIDN:
 C:Genetics:
 A:Gene: drat

C:Superfamily: Azospirillum NAD+-nitrogenase ADP-D-ribosyltransferase
 C:Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 86.2%; Score 25; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
 |||||
 Db 262 KVVFF 266

RESULT 73

C70736
 hypothetical protein Rv3406 - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: C70736

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.T.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Sqaes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: C70736
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA

A:Residues: 1-295 <COL>
 A:Cross-references: UNIPROT:Q50719; UNIPARC:UPI000013C263; GB:Z77165; GB:AL123456; NID:9
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: Rv3406

Query Match 86.2%; Score 25; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
 |||||
 Db 43 KVVFF 47

RESULT 74

A99074
 hypothetical protein ABC-MSP [imported] - Streptococcus pneumoniae (strain R6)
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: A99074

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; B
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: A99074
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-302 <KUR>
 A:Cross-references: UNIPROT:Q8DNN8; UNIPARC:UPI00000836B3; GB:AE007317; PIDN:AAL00422.1;
 C:Genetics:
 A:Gene: ABC-MSP
 C:Superfamily: inner membrane protein uga

Query Match 86.2%; Score 25; DB 2; Length 302;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFF 6
 |||||
 Db 118 KVVFF 123

RESULT 75

B35961
 hypothetical 21K protein - Pseudomonas syringae pv. savastanoi
 C:Species: Pseudomonas syringae pv. savastanoi
 C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
 C:Accession: B35961

R;Roberto, F.F.; Klee, H.; White, F.; Nordeen, R.; Kosuge, T.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5797-5801, 1990

A:Title: Expression and fine structure of the gene encoding N(epsilon)-((indole-3-acetyl)
 A:Reference number: A35961; MUID:90332869; PMID:2377619

A:Accession: B35961
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-302 <ROB>
 A:Cross-references: UNIPROT:P18205; UNIPARC:UPI000013B36E; GB:M35373; NID:g151286; PIDN:

Query Match 86.2%; Score 25; DB 2; Length 302;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 6
 :|||
 Db 197 QVVFF 202

Search completed: December 29, 2005, 17:49:20
 Job time : 13.9677 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.29032 Seconds
(without alignments)
13.656 Million cell updates/sec

Title: US-10-009-122-17

Perfect score: 29

Sequence: 1 KVPFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 300 summaries

Database : Published Applications AA_New:
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/PT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	89.7	19	6	US-10-923-605-5
2	26	89.7	19	6	US-10-934-818-5
3	26	89.7	40	7	US-11-016-706-36
4	26	89.7	40	7	US-11-098-674-12
5	26	89.7	42	6	US-10-923-605-1
6	26	89.7	42	6	US-10-934-818-1
7	26	89.7	42	7	US-11-016-706-37
8	26	89.7	43	6	US-10-934-818-6
9	26	89.7	43	6	US-10-250-581-1
10	26	89.7	43	6	US-10-250-581-1
11	26	89.7	770	6	US-10-982-545-15
12	26	89.7	770	6	US-10-789-273-38
13	25	86.2	660	7	US-11-186-284-125
14	25	86.2	708	6	US-10-821-234-917
15	24	82.8	229	6	US-10-131-826A-410
16	24	82.8	269	6	US-10-467-657-330
17	24	82.8	311	6	US-10-793-626-2450
18	24	82.8	400	6	US-10-793-626-1056
19	24	82.8	3623	6	US-10-995-561-593
20	23	79.3	50	6	US-10-467-657-7892
21	23	79.3	167	7	US-11-210-316-18
22	23	79.3	239	6	US-10-467-657-432
23	23	79.3	265	6	US-10-793-626-2500
24	23	79.3	347	6	US-10-467-657-2014
25	23	79.3	402	6	US-10-467-657-9070
26	23	79.3	402	6	US-10-467-657-9070
27	23	79.3	402	6	US-10-467-657-9070
28	23	79.3	402	6	US-10-467-657-9070
29	23	79.3	402	6	US-10-467-657-9070
30	23	79.3	402	6	US-10-467-657-9070
31	23	79.3	402	6	US-10-467-657-9070
32	23	79.3	402	6	US-10-467-657-9070
33	23	79.3	402	6	US-10-467-657-9070
34	23	79.3	402	6	US-10-467-657-9070
35	23	79.3	402	6	US-10-467-657-9070
36	23	79.3	402	6	US-10-467-657-9070
37	23	79.3	402	6	US-10-467-657-9070
38	23	79.3	402	6	US-10-467-657-9070
39	23	79.3	402	6	US-10-467-657-9070
40	23	79.3	402	6	US-10-467-657-9070
41	23	79.3	402	6	US-10-467-657-9070
42	23	79.3	402	6	US-10-467-657-9070
43	23	79.3	402	6	US-10-467-657-9070
44	23	79.3	402	6	US-10-467-657-9070
45	23	79.3	402	6	US-10-467-657-9070
46	23	79.3	402	6	US-10-467-657-9070
47	23	79.3	402	6	US-10-467-657-9070
48	23	79.3	402	6	US-10-467-657-9070
49	23	79.3	402	6	US-10-467-657-9070
50	23	79.3	402	6	US-10-467-657-9070
51	23	79.3	402	6	US-10-467-657-9070
52	23	79.3	402	6	US-10-467-657-9070
53	23	79.3	402	6	US-10-467-657-9070
54	23	79.3	402	6	US-10-467-657-9070
55	23	79.3	402	6	US-10-467-657-9070
56	23	79.3	402	6	US-10-467-657-9070
57	23	79.3	402	6	US-10-467-657-9070
58	23	79.3	402	6	US-10-467-657-9070
59	23	79.3	402	6	US-10-467-657-9070
60	23	79.3	402	6	US-10-467-657-9070
61	23	79.3	402	6	US-10-467-657-9070
62	23	79.3	402	6	US-10-467-657-9070
63	23	79.3	402	6	US-10-467-657-9070
64	23	79.3	402	6	US-10-467-657-9070
65	23	79.3	402	6	US-10-467-657-9070
66	23	79.3	402	6	US-10-467-657-9070
67	23	79.3	402	6	US-10-467-657-9070
68	23	79.3	402	6	US-10-467-657-9070
69	23	79.3	402	6	US-10-467-657-9070
70	23	79.3	402	6	US-10-467-657-9070
71	23	79.3	402	6	US-10-467-657-9070
72	23	79.3	402	6	US-10-467-657-9070
73	23	79.3	402	6	US-10-467-657-9070
74	23	79.3	402	6	US-10-467-657-9070
75	23	79.3	402	6	US-10-467-657-9070
76	23	79.3	402	6	US-10-467-657-9070
77	23	79.3	402	6	US-10-467-657-9070
78	23	79.3	402	6	US-10-467-657-9070
79	23	79.3	402	6	US-10-467-657-9070
80	23	79.3	402	6	US-10-467-657-9070
81	23	79.3	402	6	US-10-467-657-9070
82	23	79.3	402	6	US-10-467-657-9070
83	23	79.3	402	6	US-10-467-657-9070
84	23	79.3	402	6	US-10-467-657-9070
85	23	79.3	402	6	US-10-467-657-9070
86	23	79.3	402	6	US-10-467-657-9070
87	23	79.3	402	6	US-10-467-657-9070
88	23	79.3	402	6	US-10-467-657-9070
89	23	79.3	402	6	US-10-467-657-9070
90	23	79.3	402	6	US-10-467-657-9070
91	23	79.3	402	6	US-10-467-657-9070
92	23	79.3	402	6	US-10-467-657-9070
93	23	79.3	402	6	US-10-467-657-9070
94	23	79.3	402	6	US-10-467-657-9070
95	23	79.3	402	6	US-10-467-657-9070
96	23	79.3	402	6	US-10-467-657-9070
97	23	79.3	402	6	US-10-467-657-9070
98	23	79.3	402	6	US-10-467-657-9070

Sequence 2120, Ap
Sequence 959, Ap
Sequence 22, Appl
Sequence 13, Appl
Sequence 26, Appl
Sequence 230, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 7886, Ap
Sequence 5436, Ap
Sequence 2836, Ap
Sequence 3436, Ap
Sequence 1372, Ap
Sequence 45, Appl
Sequence 106, Ap
Sequence 24, Appl
Sequence 104, Ap
Sequence 1930, Ap
Sequence 2868, Ap
Sequence 104, Ap
Sequence 347, Ap
Sequence 348, Ap
Sequence 7, Appl
Sequence 114, Ap
Sequence 4746, Ap
Sequence 9209, Ap
Sequence 1701, Ap
Sequence 2486, Ap
Sequence 2420, Ap
Sequence 2232, Ap
Sequence 6318, Ap
Sequence 6932, Ap
Sequence 4, Appl
Sequence 568, Ap
Sequence 4838, Ap
Sequence 1322, Ap
Sequence 544, Ap
Sequence 543, Ap
Sequence 16, Appl
Sequence 2476, Ap
Sequence 2734, Ap
Sequence 234, Ap
Sequence 19, Appl
Sequence 376, Ap
Sequence 7996, Ap
Sequence 572, Ap
Sequence 836, Ap
Sequence 7420, Ap
Sequence 1, Appl
Sequence 308, Ap
Sequence 69, Appl
Sequence 112, Ap
Sequence 1075, Ap
Sequence 678, Ap
Sequence 7094, Ap
Sequence 8028, Ap
Sequence 76, Appl
Sequence 7104, Ap
Sequence 198, Ap
Sequence 178, Ap
Sequence 350, Ap
Sequence 225, Ap
Sequence 1067, Ap
Sequence 7120, Ap
Sequence 1673, Ap
Sequence 94, Appl
Sequence 2948, Ap
Sequence 6, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 64, Appl
Sequence 4, Appl
Sequence 9, Appl

99	21	72.4	1165	7	US-11-192-219-2	Sequence 2, Appli	172	20	69.0	329	6	US-10-524-647-80	Sequence 80, Appli
100	21	72.4	1217	7	US-11-074-176-252	Sequence 252, App	173	20	69.0	335	6	US-10-467-657-3818	Sequence 3818, Ap
101	21	72.4	7968	7	US-11-186-731-5	Sequence 5, Appli	174	20	69.0	341	6	US-10-524-647-27	Sequence 27, Appl
102	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	175	20	69.0	348	6	US-10-821-234-1402	Sequence 1402, Ap
103	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	176	20	69.0	355	6	US-10-454-437-102	Sequence 102, App
104	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	177	20	69.0	356	7	US-11-012-762-46	Sequence 46, Appl
105	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	178	20	69.0	362	7	US-11-012-762-62	Sequence 62, Appl
106	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	179	20	69.0	364	6	US-10-131-826A-186	Sequence 186, App
107	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	180	20	69.0	370	6	US-10-821-234-1105	Sequence 1105, Ap
108	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	181	20	69.0	370	7	US-11-073-605-2	Sequence 2, Appli
109	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	182	20	69.0	386	7	US-11-075-400-14	Sequence 14, Appl
110	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	183	20	69.0	386	7	US-11-012-762-44	Sequence 44, Appl
111	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	184	20	69.0	389	7	US-11-069-642-18	Sequence 18, Appl
112	20	69.0	42	6	US-10-250-581-16	Sequence 19, Appl	185	20	69.0	395	6	US-10-467-657-1950	Sequence 1950, Ap
113	20	69.0	42	6	US-10-250-581-19	Sequence 19, Appl	186	20	69.0	396	6	US-10-510-386-238	Sequence 238, App
114	20	69.0	43	7	US-11-075-400-28	Sequence 28, Appl	187	20	69.0	399	6	US-10-510-386-30	Sequence 30, Appl
115	20	69.0	52	6	US-10-467-657-2216	Sequence 2216, Ap	188	20	69.0	413	6	US-10-467-657-1858	Sequence 1858, Ap
116	20	69.0	54	6	US-10-467-657-4978	Sequence 4978, Ap	189	20	69.0	418	6	US-10-467-657-5788	Sequence 5788, Ap
117	20	69.0	56	6	US-10-467-657-1050	Sequence 1050, Ap	190	20	69.0	423	6	US-10-525-710-44	Sequence 44, Appl
118	20	69.0	76	6	US-10-467-657-5690	Sequence 5690, Ap	191	20	69.0	436	6	US-10-467-657-7694	Sequence 7694, Ap
119	20	69.0	80	6	US-10-986-501-200	Sequence 200, App	192	20	69.0	443	6	US-10-793-626-1860	Sequence 1860, Ap
120	20	69.0	86	6	US-10-467-657-3962	Sequence 3962, Ap	193	20	69.0	444	6	US-10-467-657-362	Sequence 362, App
121	20	69.0	91	6	US-10-821-234-1703	Sequence 1703, Ap	194	20	69.0	445	6	US-10-454-437-312	Sequence 312, App
122	20	69.0	98	6	US-10-467-657-3376	Sequence 3376, Ap	195	20	69.0	445	7	US-11-082-389-376	Sequence 376, App
123	20	69.0	107	6	US-10-467-657-2102	Sequence 2102, Ap	196	20	69.0	445	7	US-11-180-997-4	Sequence 32, Appl
124	20	69.0	115	6	US-10-793-626-1554	Sequence 1554, Ap	197	20	69.0	456	6	US-10-467-657-4150	Sequence 4150, Ap
125	20	69.0	115	6	US-10-432-483-10	Sequence 10, Appl	198	20	69.0	456	6	US-10-467-657-6352	Sequence 6352, Ap
126	20	69.0	123	6	US-10-793-626-430	Sequence 430, App	199	20	69.0	463	6	US-10-467-657-7604	Sequence 7604, Ap
127	20	69.0	123	6	US-10-467-657-5166	Sequence 5166, Ap	200	20	69.0	465	6	US-10-793-626-2928	Sequence 2928, Ap
128	20	69.0	126	6	US-10-793-626-2766	Sequence 2766, Ap	201	20	69.0	475	7	US-11-180-997-4	Sequence 4, Appli
129	20	69.0	127	7	US-11-106-796-10	Sequence 10, Appl	202	20	69.0	485	7	US-10-204-029-7	Sequence 7, Appli
130	20	69.0	129	6	US-10-501-039-8	Sequence 8, Appli	203	20	69.0	489	6	US-10-467-657-7846	Sequence 7846, Ap
131	20	69.0	134	6	US-10-793-626-2374	Sequence 2374, Ap	204	20	69.0	490	7	US-11-074-176-316	Sequence 316, App
132	20	69.0	137	6	US-10-793-626-530	Sequence 530, App	205	20	69.0	492	6	US-10-793-626-770	Sequence 770, App
133	20	69.0	139	6	US-10-467-657-5728	Sequence 5728, Ap	206	20	69.0	495	7	US-11-074-176-60	Sequence 60, Appl
134	20	69.0	144	6	US-10-793-626-2478	Sequence 2478, Ap	207	20	69.0	496	7	US-11-067-121-12	Sequence 12, Appl
135	20	69.0	165	6	US-10-467-657-4990	Sequence 4990, Ap	208	20	69.0	508	7	US-11-075-185-26	Sequence 26, Appl
136	20	69.0	175	6	US-10-965-694-23	Sequence 23, Appl	209	20	69.0	522	6	US-10-995-561-1030	Sequence 1030, Ap
137	20	69.0	182	6	US-10-467-657-3510	Sequence 3510, Ap	210	20	69.0	555	6	US-10-454-437-100	Sequence 100, App
138	20	69.0	183	6	US-10-467-657-6906	Sequence 6906, Ap	211	20	69.0	558	6	US-10-467-657-4258	Sequence 4258, Ap
139	20	69.0	183	6	US-10-467-657-8138	Sequence 8138, Ap	212	20	69.0	578	6	US-10-858-730-103	Sequence 103, App
140	20	69.0	196	6	US-10-793-626-630	Sequence 630, App	213	20	69.0	582	7	US-11-090-439-58	Sequence 58, Appl
141	20	69.0	200	6	US-10-524-198-2	Sequence 2, Appli	214	20	69.0	585	7	US-11-012-762-6	Sequence 6, Appli
142	20	69.0	200	7	US-11-073-605-3	Sequence 3, Appli	215	20	69.0	592	6	US-10-467-657-4888	Sequence 3, Appli
143	20	69.0	204	6	US-10-467-657-5874	Sequence 5874, Ap	216	20	69.0	601	7	US-11-103-957-3	Sequence 3, Appli
144	20	69.0	210	6	US-10-986-501-126	Sequence 126, App	217	20	69.0	615	6	US-10-995-561-940	Sequence 940, App
145	20	69.0	216	6	US-10-467-657-8102	Sequence 8102, Ap	218	20	69.0	626	6	US-10-467-657-1196	Sequence 1196, Ap
146	20	69.0	220	6	US-10-467-657-3154	Sequence 3154, Ap	219	20	69.0	637	7	US-11-080-991-48	Sequence 48, Appl
147	20	69.0	221	6	US-10-467-657-290	Sequence 290, App	220	20	69.0	662	6	US-10-995-561-943	Sequence 943, App
148	20	69.0	221	6	US-10-467-657-5750	Sequence 5750, Ap	221	20	69.0	690	6	US-10-131-826A-306	Sequence 306, App
149	20	69.0	231	6	US-10-689-742-132	Sequence 132, App	222	20	69.0	702	6	US-10-995-561-942	Sequence 942, App
150	20	69.0	234	6	US-10-467-657-6144	Sequence 6144, Ap	223	20	69.0	721	6	US-10-467-9628-49	Sequence 49, Appl
151	20	69.0	272	6	US-10-632-150-46	Sequence 46, Appl	224	20	69.0	738	7	US-11-147-047-48	Sequence 48, Appl
152	20	69.0	272	7	US-11-073-457-46	Sequence 46, Appl	225	20	69.0	741	6	US-10-467-657-6266	Sequence 6266, Ap
153	20	69.0	272	7	US-11-073-460-46	Sequence 46, Appl	226	20	69.0	747	7	US-11-018-018-1	Sequence 1, Appli
154	20	69.0	288	6	US-10-467-657-1272	Sequence 1272, Ap	227	20	69.0	747	7	US-11-047-757-1	Sequence 1, Appli
155	20	69.0	291	7	US-11-102-883-22	Sequence 22, Appl	228	20	69.0	754	6	US-10-995-561-941	Sequence 941, App
156	20	69.0	292	7	US-11-102-883-24	Sequence 24, Appl	229	20	69.0	797	6	US-10-995-561-802	Sequence 802, App
157	20	69.0	294	6	US-10-467-657-7686	Sequence 7686, Ap	230	20	69.0	852	6	US-10-467-657-5004	Sequence 5004, Ap
158	20	69.0	296	6	US-10-965-972-8	Sequence 8, Appli	231	20	69.0	916	6	US-10-467-657-4242	Sequence 4242, Ap
159	20	69.0	296	7	US-11-012-978-7	Sequence 7, Appli	232	20	69.0	928	6	US-10-841-129-2	Sequence 2, Appli
160	20	69.0	314	7	US-11-018-018-4	Sequence 4, Appli	233	20	69.0	928	6	US-10-841-129-4	Sequence 4, Appli
161	20	69.0	314	7	US-11-047-757-4	Sequence 4, Appli	234	20	69.0	984	7	US-11-055-822-508	Sequence 508, App
162	20	69.0	315	6	US-10-524-647-25	Sequence 25, Appl	235	20	69.0	984	7	US-11-055-822-594	Sequence 594, App
163	20	69.0	317	6	US-10-995-561-798	Sequence 798, App	236	20	69.0	989	6	US-10-821-234-975	Sequence 975, App
164	20	69.0	319	6	US-10-467-657-640	Sequence 640, App	237	20	69.0	1070	7	US-11-147-047-49	Sequence 49, Appl
165	20	69.0	321	6	US-10-467-657-2504	Sequence 2504, Ap	238	20	69.0	1278	6	US-10-995-561-952	Sequence 952, App
166	20	69.0	322	6	US-11-073-605-4	Sequence 4, Appli	239	20	69.0	1451	7	US-11-102-217-2	Sequence 2, Appli
167	20	69.0	324	6	US-10-467-657-7692	Sequence 7692, Ap	240	20	69.0	1857	7	US-11-102-217-2	Sequence 1, Appli
168	20	69.0	324	6	US-10-467-657-8440	Sequence 8440, Ap	241	20	69.0	2261	6	US-10-995-561-600	Sequence 600, App
169	20	69.0	325	6	US-10-454-437-142	Sequence 142, App	242	20	69.0	2261	7	US-11-055-309A-9	Sequence 9, Appli
170	20	69.0	329	6	US-10-524-647-2	Sequence 2, Appli	243	20	69.0	2261	7	US-11-055-309A-10	Sequence 10, Appl
171	20	69.0	329	6	US-10-524-647-23	Sequence 23, Appl	244	20	69.0	2504	6	US-10-647-956A-8	Sequence 8, Appli

245 19 65.5 9 6 US-10-982-891-44 Sequence 44, Appl
246 19 65.5 13 6 US-10-511-559-836 Sequence 836, App
247 19 65.5 13 6 US-10-511-559-837 Sequence 837, App
248 19 65.5 13 6 US-10-511-559-838 Sequence 838, App
249 19 65.5 13 6 US-10-511-559-839 Sequence 839, App
250 19 65.5 13 6 US-10-511-559-840 Sequence 840, App
251 19 65.5 13 6 US-10-511-559-841 Sequence 841, App
252 19 65.5 13 6 US-10-511-559-842 Sequence 842, App
253 19 65.5 19 6 US-10-467-657-8712 Sequence 8712, App
254 19 65.5 27 6 US-10-986-501-347 Sequence 347, App
255 19 65.5 28 6 US-10-250-581-2 Sequence 2, Appli
256 19 65.5 28 6 US-10-250-581-2 Sequence 2, Appli
257 19 65.5 30 6 US-10-467-657-6336 Sequence 6336, App
258 19 65.5 38 6 US-10-467-657-1296 Sequence 1296, App
259 19 65.5 40 6 US-10-250-581-3 Sequence 3, Appli
260 19 65.5 40 6 US-10-250-581-3 Sequence 3, Appli
261 19 65.5 42 6 US-10-467-657-8811 Sequence 8811, App
262 19 65.5 42 6 US-10-250-581-4 Sequence 4, Appli
263 19 65.5 42 6 US-10-250-581-4 Sequence 4, Appli
264 19 65.5 76 7 US-11-000-463-318 Sequence 318, App
265 19 65.5 76 7 US-11-000-463-318 Sequence 318, App
266 19 65.5 83 6 US-10-467-657-5366 Sequence 5366, App
267 19 65.5 95 6 US-10-467-657-2518 Sequence 2518, App
268 19 65.5 98 6 US-10-467-657-6988 Sequence 6988, App
269 19 65.5 100 7 US-11-123-896-137 Sequence 137, App
270 19 65.5 102 6 US-10-793-626-2592 Sequence 2592, App
271 19 65.5 102 6 US-10-485-788A-650 Sequence 650, App
272 19 65.5 102 7 US-11-053-076-132 Sequence 122, App
273 19 65.5 105 6 US-10-131-826A-470 Sequence 470, App
274 19 65.5 107 6 US-10-793-626-1586 Sequence 1586, App
275 19 65.5 107 6 US-10-467-657-1018 Sequence 1018, App
276 19 65.5 108 6 US-10-467-657-4266 Sequence 4266, App
277 19 65.5 114 6 US-10-821-234-1140 Sequence 1140, App
278 19 65.5 114 6 US-10-467-657-1414 Sequence 1414, App
279 19 65.5 114 6 US-10-467-657-3162 Sequence 3162, App
280 19 65.5 114 6 US-10-467-657-3754 Sequence 3754, App
281 19 65.5 114 6 US-10-467-657-5012 Sequence 5012, App
282 19 65.5 114 6 US-10-467-657-5012 Sequence 5012, App
283 19 65.5 116 6 US-10-467-657-8574 Sequence 8574, App
284 19 65.5 116 6 US-10-467-657-5514 Sequence 5514, App
285 19 65.5 131 6 US-10-467-657-5308 Sequence 5308, App
286 19 65.5 137 7 US-11-193-512-31 Sequence 31, Appl
287 19 65.5 138 6 US-10-793-626-1254 Sequence 1254, App
288 19 65.5 138 7 US-11-137-465-37 Sequence 37, Appl
289 19 65.5 139 6 US-10-467-657-28 Sequence 28, Appl
290 19 65.5 139 6 US-10-467-657-8188 Sequence 8188, App
291 19 65.5 140 7 US-11-083-800-7 Sequence 7, Appli
292 19 65.5 144 6 US-10-793-626-1640 Sequence 1640, App
293 19 65.5 144 6 US-10-793-626-1358 Sequence 1358, App
294 19 65.5 156 6 US-10-467-657-1280 Sequence 1280, App
295 19 65.5 157 7 US-11-116-144-167 Sequence 167, App
296 19 65.5 160 6 US-10-793-626-750 Sequence 750, App
297 19 65.5 182 6 US-10-980-388-89 Sequence 89, Appl
298 19 65.5 186 6 US-10-467-657-3918 Sequence 3918, App
299 19 65.5 192 6 US-10-467-657-5588 Sequence 5588, App
300 19 65.5 193 7 US-11-102-240-142 Sequence 142, App

ALIGNMENTS

RESULT 1
US-10-923-605-5
; Sequence 5, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923, 605
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322, 289

; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-923-605-5

Query Match 89.7%; Score 26; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 2

US-10-934-818-5
; Sequence 5, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934, 818
; CURRENT FILING DATE: 2004-09-02
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/067, 740
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5

Query Match 89.7%; Score 26; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 3

US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.

; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-36

Query Match 89.7%; Score 26; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 4
US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

Query Match 89.7%; Score 26; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 5
US-10-923-605-1
; Sequence 1, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605

; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-923-605-1

Query Match 89.7%; Score 26; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 6
US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1

Query Match 89.7%; Score 26; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 7
US-11-016-706-37
; Sequence 37, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24

; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-37

Query Match 89.7%; Score 26; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 8
US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match 89.7%; Score 26; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.9;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 9
US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs...
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 89.7%; Score 26; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.9;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 10
US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs...
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 89.7%; Score 26; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.9;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 11
US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hvild
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease

Qy 1 KVFPPA 6
| | | | |
Db 531 KAVPPA 536

RESULT 14

US-10-821-234-917
; Sequence 917, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Suean
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 917
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-917

Query Match 86.2%; Score 25; DB 6; Length 708;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFPPA 6
| | | | |
Db 579 KAVPPA 584

RESULT 15

US-10-131-826A-410
; Sequence 410, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DePorge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 410
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-410

Query Match 82.8%; Score 24; DB 6; Length 229;
Best Local Similarity 80.0%; Pred. No. 79;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPP 5
| | | | |
Db 118 KVIFF 122

RESULT 16

US-10-467-657-330
; Sequence 330, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 330
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-330

Query Match 82.8%; Score 24; DB 6; Length 269;
Best Local Similarity 80.0%; Pred. No. 92;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPP 5
| | | | |
Db 11 KVIFF 15

RESULT 17

US-10-793-626-2450
; Sequence 2450, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258

; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2450
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2450

Query Match 82.8%; Score 24; DB 6; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
|:|:|
DB 296 VVFFA 300

RESULT 18
US-10-793-626-1056
; Sequence 1056, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1056
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1056

Query Match 82.8%; Score 24; DB 6; Length 400;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVUFF 5
|:|:|
DB 7 KIVFF 11

RESULT 19
US-10-995-561-593
; Sequence 593, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 593
; LENGTH: 3623
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-593

Query Match 82.8%; Score 24; DB 6; Length 3623;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVUFF 5
|:|:|
DB 2544 KVUFF 2548

RESULT 20
US-10-467-657-7892
; Sequence 7892, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7892
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7892

Query Match 79.3%; Score 23; DB 6; Length 50;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVUFF 5
|:|:|
DB 33 KIVFF 37

RESULT 21
US-11-210-316-18
; Sequence 18, Application US/11210316
; Publication No. US20050282278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (34)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (85)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:

```
; NAME/KEY: UNSURE
; LOCATION: (98)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (112)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (151)
; OTHER INFORMATION: Xaa = any amino acid
US-11-210-316-18
```

```
Query Match      79.3%; Score 23; DB 7; Length 167;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 KVFFA 6
       |||||
Db     105 VIFFA 109
```

```
RESULT 22
US-10-467-657-432
; Sequence 432, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 432
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-432
```

```
Query Match      79.3%; Score 23; DB 6; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KVFFA 6
       |||||
Db     128 KVIFA 133
```

```
RESULT 23
US-10-793-626-2500
; Sequence 2500, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2500
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2500
```

```
Query Match      79.3%; Score 23; DB 6; Length 265;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KVFFFA 6
       |||||
Db     230 KVFFMA 235
```

```
RESULT 24
US-10-467-657-2014
; Sequence 2014, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2014
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2014
```

```
Query Match      79.3%; Score 23; DB 6; Length 347;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 VFFFA 6
       :|||
Db     73 IVFFA 77
```

```
RESULT 25
US-10-467-657-9070
; Sequence 9070, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9070
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9070
```

```
Query Match      79.3%; Score 23; DB 6; Length 402;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
```

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
:|||||
Db 264 IVFFA 268

RESULT 26

US-10-467-657-2120
; Sequence 2120, Application US/10467657
; Publication No. US20050260581A1

GENERAL INFORMATION:

; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: Seqwin99, version 1.04

; SEQ ID NO 2120

; LENGTH: 426

; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-2120

Query Match 79.3%; Score 23; DB 6; Length 426;

Best Local Similarity 80.0%; Pred. No. 2.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
:|||||
Db 414 IVFFA 418

RESULT 27

US-10-995-561-959

; Sequence 959, Application US/10995561

; Publication No. US20050272054A1

GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 959

; LENGTH: 481

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-995-561-959

Query Match 79.3%; Score 23; DB 6; Length 481;

Best Local Similarity 66.7%; Pred. No. 2.6e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:|:|
Db 275 KVVFA 280

RESULT 28

US-11-210-316-22

; Sequence 22, Application US/11210316

; Publication No. US20050282278A1

GENERAL INFORMATION:

; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.

; APPLICANT: Kinney, Anthony J.

; TITLE OF INVENTION: Plant Sugar Transport Proteins

; FILE REFERENCE: BB11630SDIV

; CURRENT APPLICATION NUMBER: US/11/210,316

; CURRENT FILING DATE: 2005-08-24

; PRIOR APPLICATION NUMBER: US/10/051,902

; PRIOR FILING DATE: 2002-01-17

; PRIOR APPLICATION NUMBER: 60/083,044

; PRIOR FILING DATE: 1998-04-24

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 22

; LENGTH: 510

; TYPE: PRT

; ORGANISM: Oryza sativa

FEATURE:

; NAME/KEY: UNSURE

; LOCATION: (102)

; OTHER INFORMATION: Xaa = any amino acid

US-11-210-316-22

Query Match 79.3%; Score 23; DB 7; Length 510;

Best Local Similarity 80.0%; Pred. No. 2.8e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
|:|:|
Db 96 VVFFA 100

RESULT 29

US-10-689-742-13

; Sequence 13, Application US/10689742

; Publication No. US20050250180A1

GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; APPLICANT: McCoy, John M

; APPLICANT: LaValle, Edward R

; APPLICANT: Racie, Lisa A

; APPLICANT: Evans, Cheryl

; APPLICANT: Merberg, David

; APPLICANT: Treacy, Maurice

; APPLICANT: Spaulding, Vikki

; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

; FILE REFERENCE: 00766.000091.10

; CURRENT APPLICATION NUMBER: US/10/689,742

; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 09/746,783

; PRIOR FILING DATE: 2000-12-21

; NUMBER OF SEQ ID NOS: 231

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 13

; LENGTH: 524

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-689-742-13

Query Match 79.3%; Score 23; DB 6; Length 524;

Best Local Similarity 80.0%; Pred. No. 2.9e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
:|||||
Db 404 IVFFA 408

RESULT 30

US-11-210-316-26

; Sequence 26, Application US/11210316

; Publication No. US20050282278A1

; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: B81163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; PRIOR FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-210-316-26

Query Match 79.3%; Score 23; DB 7; Length 539;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6
|:|:|
Db 121 VVFFA 125

RESULT 31
US-10-131-826A-230
; Sequence 230, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 230
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-230

Query Match 79.3%; Score 23; DB 6; Length 677;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6
|:|:|
Db 557 VVFFA 561

RESULT 32
US-10-873-528-2
; Sequence 2, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2233
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-2

Query Match 79.3%; Score 23; DB 6; Length 2233;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFFFA 6
|:|:|
Db 1895 KVFFFA 1900

RESULT 33
US-11-098-674-1
; Sequence 1, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

```
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-098-674-1

Query Match      75.9%; Score 22; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.3e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
Db      1 KLVFF 5

RESULT 34
US-10-467-657-7886
; Sequence 7886, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7886
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7886

Query Match      75.9%; Score 22; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      14 KVVFFA 19

RESULT 35
US-10-467-657-5436
; Sequence 5436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5436
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5436

Query Match      75.9%; Score 22; DB 6; Length 47;
Best Local Similarity 80.0%; Pred. No. 47;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
Db      36 KVVFF 40

RESULT 36
US-10-793-626-2836
; Sequence 2836, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2836
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2836

Query Match      75.9%; Score 22; DB 6; Length 182;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      14 KVVFFS 19

RESULT 37
US-10-467-657-3436
; Sequence 3436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3436
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3436

Query Match      75.9%; Score 22; DB 6; Length 190;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      46 KVVFFA 51
```

```

; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 05/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 106
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-11-082-389-106

Query Match 75.9%; Score 22; DB 7; Length 440;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5
Db 333 RVVFF 337

RESULT 41
US-10-793-626-24
; Sequence 24, Application US/10793626
; Publication No. US2005025478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 24
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-24

Query Match 75.9%; Score 22; DB 6; Length 482;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFF 6
Db 388 KVLFF 393

; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF PRECLAMPSIA
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PF SEQ_genes Version 1.0
; SEQ ID NO 1372
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1372

Query Match 75.9%; Score 22; DB 6; Length 211;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFF 6
Db 33 KTVFF 38

RESULT 39
US-10-957-569-45
; Sequence 45, Application US/10957569
; Publication No. US20050246785A1
; GENERAL INFORMATION:
; APPLICANT: COOK, Zhihong et al.
; TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
; TITLE OF INVENTION: THEROP
; FILE REFERENCE: 2750-1577PUS3
; CURRENT APPLICATION NUMBER: US/10/957,569
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/950,321
; PRIOR FILING DATE: 2004-09-23
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 45
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-957-569-45

Query Match 75.9%; Score 22; DB 6; Length 278;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5
Db 55 KVLFF 59

RESULT 40
US-11-082-389-106
; Sequence 106, Application US/11082389
; Publication No. US2005024935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor

```

```
RESULT 42
US-11-080-991-104
; Sequence 104, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; AND OVARIAN CANCER
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-104
```

```
Query Match 75.9%; Score 22; DB 7; Length 522;
Best Local Similarity 60.0%; Pred. No. 4.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 VVFFA 6
Db 260 IIFFA 264
```

```
RESULT 43
US-10-793-626-1930
; Sequence 1930, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUB480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1930
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1930
```

```
Query Match 75.9%; Score 22; DB 6; Length 528;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVPF 5
Db 477 KLVFF 481
```

```
RESULT 44
US-10-467-657-2868
; Sequence 2868, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
```

```
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2868
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2868
```

```
Query Match 75.9%; Score 22; DB 6; Length 533;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 VVFFA 6
Db 371 IIFFA 375
```

```
RESULT 45
US-11-082-389-104
; Sequence 104, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGI-131PCPN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 104
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-104
```

```
Query Match 75.9%; Score 22; DB 7; Length 569;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```


Qy 1 KVVFF 5
:||||
Db 462 RVVFF 466

RESULT 46

US-11-000-463-347
; Sequence 347, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 347
; LENGTH: 1061
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-347

Query Match 75.9%; Score 22; DB 7; Length 1061;
Best Local Similarity 83.3%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
:||||
Db 131 KVDFFA 136

RESULT 47

US-11-000-463-348
; Sequence 348, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-348

Query Match 75.9%; Score 22; DB 7; Length 1091;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
:||||
Db 131 KVDFFA 136

RESULT 48

US-11-075-185-7
; Sequence 7, Application US/11075185
; Publication No. US20050266434A1
; GENERAL INFORMATION:
; APPLICANT: REEVES, CHRISTOPHER D
; APPLICANT: JULIEN, BRYAN
; APPLICANT: REID, RALPH
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
; FILE REFERENCE: 010099.03
; CURRENT APPLICATION NUMBER: US/11/075,185
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/568,290
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 3507
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-11-075-185-7

Query Match 75.9%; Score 22; DB 7; Length 3507;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
:||||
Db 565 KVVFFA 570

RESULT 49

US-10-510-386-114
; Sequence 114, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne

```
/ APPLICANT: Clausen, Ib Groth
/ APPLICANT: Jorgensen, Steen Troels
/ APPLICANT: Olsen, Peter Bjarke
/ APPLICANT: Rasmussen, Michael Dolberg
/ TITLE OF INVENTION: Improved Bacillus Host Cell
/ FILE REFERENCE: 10294.204-US
/ CURRENT APPLICATION NUMBER: US/10/510,386
/ CURRENT FILING DATE: 2004-10-04
/ NUMBER OF SEQ ID NOS: 248
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 114
/ LENGTH: 83
/ TYPE: PRT
/ ORGANISM: Bacillus licheniformis
US-10-510-386-114

Query Match          72.4%; Score 21; DB 6; Length 83;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 VVFFA 6
Db      17 VLFFA 21

RESULT 50
US-10-467-657-4746
/ Sequence 4746, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SpA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 4746
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4746

Query Match          72.4%; Score 21; DB 6; Length 98;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
Db      62 KIVFY 66

RESULT 51
US-10-467-657-9209
/ Sequence 9209, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SpA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 2486
/ LENGTH: 140
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2486

/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pt_seq_genes Version 1.0
/ SEQ ID NO 1701
/ LENGTH: 137
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-1701

Query Match          72.4%; Score 21; DB 6; Length 137;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVVFF 5
Db      28 KVTFF 32

RESULT 53
US-10-467-657-2486
/ Sequence 2486, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SpA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 2486
/ LENGTH: 140
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2486
```

Query Match 72.4%; Score 21; DB 6; Length 140;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5
|||:
Db 89 KVIYF 93

RESULT 54
US-10-467-657-2420
; Sequence 2420, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2420
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2420

Query Match 72.4%; Score 21; DB 6; Length 155;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6
:||||
Db 18 MVFFA 22

RESULT 55
US-10-467-657-2232
; Sequence 2232, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2232
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2232

Query Match 72.4%; Score 21; DB 6; Length 179;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
||| |

Db 107 KVVSPA 112

RESULT 56
US-10-467-657-6318
; Sequence 6318, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6318
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6318

Query Match 72.4%; Score 21; DB 6; Length 210;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFF 5
| |||
Db 116 KAVFF 120

RESULT 57
US-10-467-657-6932
; Sequence 6932, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6932
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6932

Query Match 72.4%; Score 21; DB 6; Length 211;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6
:||||
Db 19 LVFFA 23

RESULT 58
US-10-131-826A-4
; Sequence 4, Application US/10131826A
; Publication No. US20050245730A1

```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria A.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 4
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-4

Query Match 72.4%; Score 21; DB 6; Length 215;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
Db 166 LVFFA 170

RESULT 59
US-10-467-657-568
; Sequence 568, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838

Query Match 72.4%; Score 21; DB 6; Length 228;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
Db 156 LVFFA 160

RESULT 60
US-10-467-657-4838
; Sequence 4838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838

Query Match 72.4%; Score 21; DB 6; Length 228;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
Db 156 LVFFA 160

RESULT 61
US-10-821-234-1322
; Sequence 1322, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1322
; LENGTH: 233
; TYPE: PRT

```

```
; ORGANISM: Homo sapiens
US-10-821-234-1322

Query Match      72.4%; Score 21; DB 6; Length 233;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VVFFA 6
Db      166 LVFFA 170

RESULT 62
US-10-995-561-544
; Sequence 544, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 544
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(266)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-995-561-544

Query Match      72.4%; Score 21; DB 6; Length 266;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KVVPF 5
Db      152 KVTFP 156

RESULT 63
US-10-995-561-543
; Sequence 543, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 543
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(267)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-995-561-543

Query Match      72.4%; Score 21; DB 6; Length 267;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KVVPF 5
Db      153 KVTFP 157

RESULT 64
US-11-055-822-16
; Sequence 16, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberbauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BG1-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 16
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-16

Query Match      72.4%; Score 21; DB 7; Length 312;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVPF 5
Db      133 EVVFP 137

RESULT 65
US-10-793-626-2476
; Sequence 2476, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2476
; LENGTH: 330
```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2476

Query Match 72.4%; Score 21; DB 6; Length 330;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVPF 5
|::||
Db 3 KIMFF 7

RESULT 66
US-10-793-626-2734
; Sequence 2734, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P034800S
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2734
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2734

Query Match 72.4%; Score 21; DB 6; Length 330;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVPF 5
|::||
Db 3 KIMFF 7

RESULT 67
US-10-485-517-234
; Sequence 234, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629W0
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 234
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-234

Query Match 72.4%; Score 21; DB 6; Length 337;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVPF 5
|::||
Db 175 KVAFP 179

RESULT 68
US-10-878-556A-19
; Sequence 19, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/cn03_human
; DATABASE ENTRY DATE: 2001-10-16
US-10-878-556A-19

Query Match 72.4%; Score 21; DB 6; Length 338;
Best Local Similarity 60.0%; Pred. No. 5.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVPF 5
|::||
Db 76 KLIFP 80

RESULT 69
US-10-131-826A-376
; Sequence 376, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115

```

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 376
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-376

Query Match          72.4%; Score 21; DB 6; Length 344;
Best Local Similarity 60.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 5
Db 279 KLIPF 283

RESULT 70
US-10-467-657-7996
; Sequence 7996, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7996
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7996

Query Match          72.4%; Score 21; DB 6; Length 355;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 5 KTTFFA 10

RESULT 71
US-11-055-822-572
; Sequence 572, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor

```

```

; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 572
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-572

Query Match          72.4%; Score 21; DB 7; Length 358;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 61 KIVVFA 66

RESULT 72
US-11-055-822-836
; Sequence 836, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08

```

```
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 836
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-836

Query Match      72.4%; Score 21; DB 7; Length 358;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:| |||
Db      61 KIVVFA 66

RESULT 73
US-10-467-657-7420
; Sequence 7420, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7420
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7420

Query Match      72.4%; Score 21; DB 6; Length 406;
Best Local Similarity 66.7%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:| |||
Db      310 KTAFFA 315

RESULT 74
US-10-878-556A-1
; Sequence 1, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (307)..(307)
```

```
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: hsugp:006101-3-0
; DATABASE ENTRY DATE: 2003-02-16
US-10-878-556A-1

Query Match      72.4%; Score 21; DB 6; Length 414;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 VVFFA 6
      |:| |||
Db      59 VMFFA 63

RESULT 75
US-11-194-246-308
; Sequence 308, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND ME
; TITLE OF INVENTION: USE
; FILE REFERENCE: 00592.US1 (M&R 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 308
; LENGTH: 432
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-308

Query Match      72.4%; Score 21; DB 7; Length 432;
Best Local Similarity 60.0%; Pred. No. 6.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
      |:| |||
Db      4 KILFF 8

Search completed: December 29, 2005, 18:50:21
Job time : 4.29032 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds
(without alignments)
37.818 Million cell updates/sec

Title: US-10-009-122-17
Perfection score: 29
Sequence: 1 KVPFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

- Database : Published Applications AA_Main:
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	29	100.0	6	3	US-09-867-847-18
2	29	100.0	6	3	US-09-867-847-26
3	29	100.0	6	3	US-09-915-092-8
4	29	100.0	6	3	US-09-915-092-16
5	29	100.0	6	3	US-09-747-408-9
6	29	100.0	6	3	US-09-747-408-17
7	29	100.0	6	5	US-10-728-028-8
8	29	100.0	6	5	US-10-728-028-16
9	29	100.0	6	5	US-10-825-958-16
10	29	100.0	6	5	US-10-825-958-24
11	29	100.0	37	4	US-10-641-924-7
12	29	100.0	37	4	US-10-642-255-7
13	29	100.0	60	4	US-10-437-963-173619
14	29	100.0	87	4	US-10-437-963-133986
15	29	100.0	109	4	US-10-437-963-105773
16	29	100.0	135	4	US-10-437-963-141578
17	29	100.0	175	4	US-10-437-963-132124
18	29	100.0	186	5	US-10-481-032A-214
19	29	100.0	186	5	US-10-481-032A-228
20	29	100.0	188	4	US-10-437-963-172476
21	29	100.0	198	4	US-10-437-963-172452
22	29	100.0	416	6	US-10-055-475-14
23	29	100.0	416	6	US-11-042-922-14
24	29	100.0	514	4	US-10-055-475-13
25	29	100.0	514	6	US-11-042-922-13
26	29	100.0	925	4	US-10-408-765A-2031
27	29	100.0	925	4	US-10-755-889-234

28	100.0	925	5	US-10-370-715B-8	Sequence 8, Appli
29	100.0	925	5	US-10-631-467-680	Sequence 680, App
30	100.0	925	5	US-10-631-467-747	Sequence 747, App
31	100.0	1144	3	US-09-870-759-124	Sequence 124, App
32	100.0	1144	3	US-09-751-708A-124	Sequence 124, App
33	100.0	1144	4	US-10-428-817A-120	Sequence 120, App
34	100.0	1144	5	US-10-937-758A-101	Sequence 101, App
35	100.0	1144	5	US-10-631-467-1388	Sequence 1388, App
36	100.0	1144	5	US-10-631-467-1464	Sequence 1464, App
37	100.0	1640	4	US-10-437-963-109646	Sequence 109646, App
38	96.6	6	3	US-09-867-847-11	Sequence 11, Appli
39	96.6	6	3	US-09-867-847-19	Sequence 19, Appli
40	96.6	6	3	US-09-915-092-1	Sequence 1, Appli
41	96.6	6	3	US-09-915-092-9	Sequence 9, Appli
42	96.6	6	3	US-09-747-408-1	Sequence 1, Appli
43	96.6	6	3	US-09-747-408-10	Sequence 10, Appli
44	96.6	6	5	US-10-728-028-1	Sequence 1, Appli
45	96.6	6	5	US-10-728-028-9	Sequence 9, Appli
46	96.6	6	5	US-10-825-958-9	Sequence 9, Appli
47	96.6	6	5	US-10-825-958-17	Sequence 17, Appli
48	96.6	58	4	US-10-425-115-280164	Sequence 280164, App
49	96.6	90	4	US-10-424-599-165325	Sequence 165325, App
50	96.6	93	4	US-10-424-599-240310	Sequence 240310, App
51	96.6	99	5	US-10-450-763-56957	Sequence 56957, A
52	93.1	564	6	US-11-097-143-12723	Sequence 12723, A
53	93.1	1443	6	US-11-097-143-32208	Sequence 32208, A
54	89.7	6	3	US-09-867-847-7	Sequence 7, Appli
55	89.7	6	3	US-09-867-847-20	Sequence 20, Appli
56	89.7	6	3	US-09-972-475-9	Sequence 9, Appli
57	89.7	6	3	US-09-915-092-10	Sequence 10, Appli
58	89.7	6	3	US-09-915-092-28	Sequence 28, Appli
59	89.7	6	3	US-09-956-625-25	Sequence 25, Appli
60	89.7	6	3	US-09-747-408-3	Sequence 3, Appli
61	89.7	6	3	US-09-747-408-11	Sequence 11, Appli
62	89.7	6	4	US-10-463-729-9	Sequence 9, Appli
63	89.7	6	5	US-10-728-028-10	Sequence 10, Appli
64	89.7	6	5	US-10-728-028-27	Sequence 27, Appli
65	89.7	6	5	US-10-728-028-28	Sequence 28, Appli
66	89.7	6	5	US-10-825-958-7	Sequence 7, Appli
67	89.7	6	5	US-10-825-958-18	Sequence 18, Appli
68	89.7	6	5	US-10-666-095-3	Sequence 3, Appli
69	89.7	7	3	US-09-867-847-12	Sequence 12, Appli
70	89.7	7	3	US-09-867-847-27	Sequence 27, Appli
71	89.7	7	3	US-09-867-847-28	Sequence 28, Appli
72	89.7	7	3	US-09-972-475-7	Sequence 7, Appli
73	89.7	7	3	US-09-915-092-2	Sequence 2, Appli
74	89.7	7	3	US-09-915-092-17	Sequence 17, Appli
75	89.7	7	3	US-09-915-092-18	Sequence 18, Appli
76	89.7	7	3	US-09-915-092-18	Sequence 18, Appli
77	89.7	7	3	US-09-747-408-18	Sequence 2, Appli
78	89.7	7	3	US-09-747-408-19	Sequence 19, Appli
79	89.7	7	4	US-10-463-729-7	Sequence 7, Appli
80	89.7	7	5	US-10-728-028-2	Sequence 2, Appli
81	89.7	7	5	US-10-728-028-17	Sequence 17, Appli
82	89.7	7	5	US-10-728-028-18	Sequence 18, Appli
83	89.7	7	5	US-10-825-958-10	Sequence 10, Appli
84	89.7	7	5	US-10-825-958-25	Sequence 25, Appli
85	89.7	7	5	US-10-825-958-26	Sequence 26, Appli
86	89.7	7	5	US-10-810-881A-128	Sequence 128, App
87	89.7	7	5	US-10-505-313-269	Sequence 269, App
88	89.7	8	3	US-09-850-061A-44	Sequence 44, Appli
89	89.7	8	3	US-09-972-475-5	Sequence 5, Appli
90	89.7	8	4	US-10-235-483-1	Sequence 1, Appli
91	89.7	8	4	US-10-463-729-5	Sequence 5, Appli
92	89.7	8	4	US-10-281-092-42	Sequence 42, Appli
93	89.7	8	4	US-10-721-774-44	Sequence 44, Appli
94	89.7	8	5	US-10-810-861A-125	Sequence 125, App
95	89.7	8	5	US-10-817-979-73	Sequence 73, Appli
96	89.7	9	3	US-09-867-847-9	Sequence 9, Appli
97	89.7	9	3	US-09-899-815-2	Sequence 2, Appli
98	89.7	9	3	US-09-747-408-20	Sequence 20, Appli
99	89.7	9	4	US-10-235-483-64	Sequence 64, Appli
100	89.7	9	4	US-10-619-454-3	Sequence 3, Appli

101	26	89.7	9	4	US-10-619-454-25	Sequence 25, Appl	174	26	89.7	12	6	US-11-012-797A-33	Sequence 33, Appl
102	26	89.7	9	4	US-10-619-454-28	Sequence 28, Appl	175	26	89.7	13	4	US-10-281-458-1	Sequence 1, Appl
103	26	89.7	9	4	US-10-619-454-57	Sequence 57, Appl	176	26	89.7	13	5	US-10-625-854-127	Sequence 127, App
104	26	89.7	9	4	US-10-619-454-157	Sequence 157, App	177	26	89.7	13	5	US-10-625-854-140	Sequence 140, App
105	26	89.7	10	3	US-09-867-847-29	Sequence 29, Appl	178	26	88.7	14	3	US-09-992-800-5	Sequence 5, Appl
106	26	89.7	10	3	US-09-915-092-19	Sequence 19, Appl	179	26	89.7	14	3	US-09-992-994-5	Sequence 5, Appl
107	26	89.7	10	3	US-10-889-999-20	Sequence 20, Appl	180	26	89.7	14	4	US-10-385-065-5	Sequence 5, Appl
108	26	89.7	10	5	US-10-889-999-21	Sequence 21, Appl	181	26	89.7	14	5	US-10-810-881A-114	Sequence 114, App
109	26	89.7	10	5	US-10-889-999-22	Sequence 22, Appl	182	26	89.7	14	5	US-10-505-313-2	Sequence 2, Appl
110	26	89.7	10	5	US-10-889-999-23	Sequence 23, Appl	183	26	89.7	14	5	US-10-625-854-115	Sequence 115, App
111	26	89.7	10	5	US-10-889-999-24	Sequence 24, Appl	184	26	89.7	14	5	US-10-625-854-128	Sequence 128, App
112	26	89.7	10	5	US-10-890-070-20	Sequence 20, Appl	185	26	89.7	14	5	US-10-625-854-141	Sequence 141, App
113	26	89.7	10	5	US-10-890-070-21	Sequence 21, Appl	186	26	89.7	14	6	US-11-063-350-5	Sequence 5, Appl
114	26	89.7	10	5	US-10-890-070-22	Sequence 22, Appl	187	26	89.7	15	3	US-09-972-475-14	Sequence 14, Appl
115	26	89.7	10	5	US-10-890-070-23	Sequence 23, Appl	188	26	89.7	15	3	US-09-996-357-9	Sequence 9, Appl
116	26	89.7	10	5	US-10-890-070-24	Sequence 24, Appl	189	26	89.7	15	4	US-10-235-483-56	Sequence 56, Appl
117	26	89.7	10	5	US-10-890-000-20	Sequence 20, Appl	190	26	89.7	15	4	US-10-235-483-57	Sequence 57, Appl
118	26	89.7	10	5	US-10-890-000-21	Sequence 21, Appl	191	26	89.7	15	4	US-10-235-483-58	Sequence 58, Appl
119	26	89.7	10	5	US-10-890-000-22	Sequence 22, Appl	192	26	89.7	15	4	US-10-235-483-60	Sequence 60, Appl
120	26	89.7	10	5	US-10-890-000-23	Sequence 23, Appl	193	26	89.7	15	4	US-10-235-483-61	Sequence 61, Appl
121	26	89.7	10	5	US-10-890-000-24	Sequence 24, Appl	194	26	89.7	15	4	US-10-235-483-62	Sequence 62, Appl
122	26	89.7	10	5	US-10-823-463-20	Sequence 20, Appl	195	26	89.7	15	4	US-10-235-483-63	Sequence 63, Appl
123	26	89.7	10	5	US-10-823-463-21	Sequence 21, Appl	196	26	89.7	15	4	US-10-235-483-65	Sequence 65, Appl
124	26	89.7	10	5	US-10-823-463-22	Sequence 22, Appl	197	26	89.7	15	4	US-10-463-729-14	Sequence 14, Appl
125	26	89.7	10	5	US-10-823-463-23	Sequence 23, Appl	198	26	89.7	15	5	US-10-625-854-103	Sequence 103, App
126	26	89.7	10	5	US-10-823-463-24	Sequence 24, Appl	199	26	89.7	15	5	US-10-625-854-116	Sequence 116, App
127	26	89.7	10	5	US-10-728-028-19	Sequence 19, Appl	200	26	89.7	15	5	US-10-625-854-129	Sequence 129, App
128	26	89.7	10	5	US-10-822-968-20	Sequence 20, Appl	201	26	89.7	15	5	US-10-625-854-142	Sequence 142, App
129	26	89.7	10	5	US-10-822-968-21	Sequence 21, Appl	202	26	89.7	16	5	US-10-625-854-91	Sequence 91, Appl
130	26	89.7	10	5	US-10-822-968-22	Sequence 22, Appl	203	26	89.7	16	5	US-10-625-854-104	Sequence 104, App
131	26	89.7	10	5	US-10-822-968-23	Sequence 23, Appl	204	26	89.7	16	5	US-10-625-854-117	Sequence 117, App
132	26	89.7	10	5	US-10-822-968-24	Sequence 24, Appl	205	26	89.7	16	5	US-10-625-854-130	Sequence 130, App
133	26	89.7	10	5	US-10-777-792-20	Sequence 20, Appl	206	26	89.7	16	5	US-10-625-854-143	Sequence 143, App
134	26	89.7	10	5	US-10-777-792-21	Sequence 21, Appl	207	26	89.7	17	3	US-09-992-800-3	Sequence 3, Appl
135	26	89.7	10	5	US-10-777-792-22	Sequence 22, Appl	208	26	89.7	17	3	US-09-992-994-3	Sequence 3, Appl
136	26	89.7	10	5	US-10-777-792-23	Sequence 23, Appl	209	26	89.7	17	3	US-09-998-491-8	Sequence 8, Appl
137	26	89.7	10	5	US-10-777-792-24	Sequence 24, Appl	210	26	89.7	17	4	US-10-385-065-3	Sequence 3, Appl
138	26	89.7	10	5	US-10-825-958-27	Sequence 27, Appl	211	26	89.7	17	4	US-10-451-367-26	Sequence 26, Appl
139	26	89.7	10	5	US-10-890-071-20	Sequence 20, Appl	212	26	89.7	17	4	US-10-475-281-8	Sequence 8, Appl
140	26	89.7	10	5	US-10-890-071-21	Sequence 21, Appl	213	26	89.7	17	4	US-10-810-919-3	Sequence 3, Appl
141	26	89.7	10	5	US-10-890-071-22	Sequence 22, Appl	214	26	89.7	17	5	US-10-684-346-24	Sequence 24, Appl
142	26	89.7	10	5	US-10-890-071-23	Sequence 23, Appl	215	26	89.7	17	5	US-10-997-078-46	Sequence 46, Appl
143	26	89.7	10	5	US-10-890-071-24	Sequence 24, Appl	216	26	89.7	17	5	US-10-997-700-19	Sequence 19, Appl
144	26	89.7	10	5	US-10-890-024-20	Sequence 20, Appl	217	26	89.7	17	6	US-11-063-350-3	Sequence 3, Appl
145	26	89.7	10	5	US-10-890-024-21	Sequence 21, Appl	218	26	89.7	17	6	US-11-066-697-950	Sequence 950, App
146	26	89.7	10	5	US-10-890-024-22	Sequence 22, Appl	219	26	89.7	17	6	US-11-066-697-983	Sequence 983, App
147	26	89.7	10	5	US-10-890-024-23	Sequence 23, Appl	220	26	89.7	19	3	US-09-825-242-5	Sequence 5, Appl
148	26	89.7	10	5	US-10-890-024-24	Sequence 24, Appl	221	26	89.7	19	4	US-10-429-216-5	Sequence 5, Appl
149	26	89.7	10	5	US-10-928-926-20	Sequence 20, Appl	222	26	89.7	19	4	US-10-816-022-5	Sequence 5, Appl
150	26	89.7	10	5	US-10-928-926-21	Sequence 21, Appl	223	26	89.7	19	4	US-10-816-529-5	Sequence 5, Appl
151	26	89.7	10	5	US-10-928-926-22	Sequence 22, Appl	224	26	89.7	19	4	US-10-815-353-5	Sequence 5, Appl
152	26	89.7	10	5	US-10-928-926-23	Sequence 23, Appl	225	26	89.7	19	4	US-10-815-391-5	Sequence 5, Appl
153	26	89.7	10	5	US-10-928-926-24	Sequence 24, Appl	226	26	89.7	19	5	US-10-828-548-5	Sequence 5, Appl
154	26	89.7	10	6	US-11-058-757-20	Sequence 20, Appl	227	26	89.7	19	5	US-10-816-380-5	Sequence 5, Appl
155	26	89.7	10	6	US-11-058-757-21	Sequence 21, Appl	228	26	89.7	19	5	US-10-889-999-75	Sequence 75, Appl
156	26	89.7	10	6	US-11-058-757-22	Sequence 22, Appl	229	26	89.7	19	5	US-10-890-070-75	Sequence 75, Appl
157	26	89.7	10	6	US-11-058-757-23	Sequence 23, Appl	230	26	89.7	19	5	US-10-890-000-75	Sequence 75, Appl
158	26	89.7	10	6	US-11-058-757-24	Sequence 24, Appl	231	26	89.7	19	5	US-10-788-666-5	Sequence 5, Appl
159	26	89.7	11	3	US-09-988-842-9	Sequence 9, Appl	232	26	89.7	19	5	US-10-923-471-5	Sequence 5, Appl
160	26	89.7	11	3	US-09-988-842-25	Sequence 25, Appl	233	26	89.7	19	5	US-10-823-463-75	Sequence 75, Appl
161	26	89.7	11	4	US-10-235-483-14	Sequence 14, Appl	234	26	89.7	19	5	US-10-923-469-5	Sequence 5, Appl
162	26	89.7	11	4	US-10-050-200-33	Sequence 33, Appl	235	26	89.7	19	5	US-10-933-559-5	Sequence 5, Appl
163	26	89.7	11	4	US-10-237-673-20	Sequence 20, Appl	236	26	89.7	19	5	US-10-815-404-5	Sequence 5, Appl
164	26	89.7	11	5	US-10-464-117-13	Sequence 13, Appl	237	26	89.7	19	5	US-10-934-609-5	Sequence 5, Appl
165	26	89.7	11	5	US-10-772-230-9	Sequence 9, Appl	238	26	89.7	19	5	US-10-923-474-5	Sequence 5, Appl
166	26	89.7	12	3	US-10-772-230-25	Sequence 25, Appl	239	26	89.7	19	5	US-10-884-892-5	Sequence 5, Appl
167	26	89.7	12	3	US-09-867-847-8	Sequence 8, Appl	240	26	89.7	19	5	US-10-822-968-75	Sequence 75, Appl
168	26	89.7	12	4	US-10-481-180-671	Sequence 671, App	241	26	89.7	19	5	US-10-777-792-75	Sequence 75, Appl
169	26	89.7	12	5	US-10-810-881A-115	Sequence 115, App	242	26	89.7	19	5	US-10-890-071-75	Sequence 75, Appl
170	26	89.7	12	5	US-10-810-881A-117	Sequence 117, App	243	26	89.7	19	5	US-10-890-024-75	Sequence 75, Appl
171	26	89.7	12	5	US-10-508-586-2	Sequence 2, Appl	244	26	89.7	19	5	US-10-934-818-5	Sequence 5, Appl
172	26	89.7	12	5	US-10-508-586-3	Sequence 3, Appl	245	26	89.7	19	5	US-10-923-267-5	Sequence 5, Appl
173	26	89.7	12	5	US-10-625-854-139	Sequence 139, App	246	26	89.7	19	5	US-10-928-926-75	Sequence 75, Appl

247 26 89.7 19 6 US-11-058-757-75 Sequence 75, Appl
248 26 89.7 19 6 US-11-108-102-5 Sequence 5, Appl
249 26 89.7 20 3 US-09-908-943A-25 Sequence 25, Appl
250 26 89.7 20 3 US-10-481-180-710 Sequence 710, Appl
251 26 89.7 20 5 US-10-801-487-25 Sequence 25, Appl
252 26 89.7 20 5 US-10-801-938-25 Sequence 25, Appl
253 26 89.7 20 5 US-10-801-509-25 Sequence 25, Appl
254 26 89.7 20 5 US-10-801-486-25 Sequence 25, Appl
255 26 89.7 20 5 US-10-801-493-25 Sequence 25, Appl
256 26 89.7 24 5 US-10-728-246-6 Sequence 6, Appl
257 26 89.7 24 5 US-10-481-180-724 Sequence 724, Appl
258 26 89.7 26 3 US-09-792-079-11 Sequence 11, Appl
259 26 89.7 26 4 US-10-153-279-11 Sequence 11, Appl
260 26 89.7 28 3 US-09-867-847-4 Sequence 4, Appl
261 26 89.7 28 3 US-09-865-294-66 Sequence 66, Appl
262 26 89.7 28 3 US-09-792-079-5 Sequence 5, Appl
263 26 89.7 28 4 US-10-159-279-5 Sequence 5, Appl
264 26 89.7 28 4 US-10-363-082-2 Sequence 2, Appl
265 26 89.7 28 4 US-10-433-385-7 Sequence 7, Appl
266 26 89.7 28 4 US-10-390-472-4 Sequence 4, Appl
267 26 89.7 28 4 US-10-741-205-36 Sequence 36, Appl
268 26 89.7 28 4 US-10-416-262B-7 Sequence 7, Appl
269 26 89.7 28 4 US-10-481-180-735 Sequence 735, Appl
270 26 89.7 28 4 US-10-478-308-4 Sequence 4, Appl
271 26 89.7 28 4 US-10-478-307-4 Sequence 4, Appl
272 26 89.7 28 5 US-10-861-614-66 Sequence 66, Appl
273 26 89.7 28 5 US-10-825-958-4 Sequence 4, Appl
274 26 89.7 28 6 US-11-091-309-3 Sequence 3, Appl
275 26 89.7 28 6 US-11-066-697-959 Sequence 959, Appl
276 26 89.7 28 6 US-11-066-697-955 Sequence 955, Appl
277 26 89.7 28 6 US-11-066-697-976 Sequence 976, Appl
278 26 89.7 28 6 US-11-066-697-992 Sequence 992, Appl
279 26 89.7 28 6 US-11-066-697-1003 Sequence 1003, Appl
280 26 89.7 30 3 US-09-861-847-1 Sequence 1, Appl
281 26 89.7 30 4 US-10-301-488A-1 Sequence 1, Appl
282 26 89.7 30 4 US-10-666-423-1 Sequence 1, Appl
283 26 89.7 30 4 US-10-617-876-9 Sequence 9, Appl
284 26 89.7 30 4 US-10-619-454-24 Sequence 24, Appl
285 26 89.7 30 4 US-10-301-448-1 Sequence 1, Appl
286 26 89.7 30 4 US-10-775-562-5 Sequence 5, Appl
287 26 89.7 32 4 US-10-732-862A-99 Sequence 99, Appl
288 26 89.7 33 3 US-09-930-915A-295 Sequence 295, Appl
289 26 89.7 33 4 US-10-082-014-84 Sequence 84, Appl
290 26 89.7 33 4 US-10-372-076-85 Sequence 85, Appl
291 26 89.7 33 4 US-10-732-862A-98 Sequence 98, Appl
292 26 89.7 33 4 US-10-806-006-295 Sequence 85, Appl
293 26 89.7 33 4 US-10-677-074-85 Sequence 85, Appl
294 26 89.7 33 4 US-10-805-913-295 Sequence 295, Appl
295 26 89.7 33 4 US-10-481-180-746 Sequence 746, Appl
296 26 89.7 35 3 US-09-867-847-3 Sequence 3, Appl
297 26 89.7 35 3 US-09-972-475-16 Sequence 16, Appl
298 26 89.7 35 4 US-10-463-729-16 Sequence 16, Appl
299 26 89.7 35 5 US-10-825-958-3 Sequence 3, Appl
300 26 89.7 35 5 US-10-825-958-3 Sequence 3, Appl

ALIGNMENTS

RESULT-1
US-09-867-847-18
; Sequence 18, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867, 847
; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-18

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 2

US-09-867-847-26
; Sequence 26, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION

US-09-867-847-26

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 3

US-09-915-092-8
; Sequence 8, Application US/09915092
; Publication No. US2002011571A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert

	<pre>; APPLICANT: Migneault, David ; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND ; FILE REFERENCE: NBI-139 ; CURRENT APPLICATION NUMBER: US/09/915,092 ; PRIOR FILING DATE: 2001-07-24 ; PRIOR APPLICATION NUMBER: 60/220,808 ; PRIOR FILING DATE: 2000-07-25 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 8 ; LENGTH: 6 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-915-092-8</pre>				
	<pre>Query Match 100.0%; Score 29; DB 3; Length 6; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>				
	<pre>QY 1 KVVFFA 6 Db 1 KVVFFA 6</pre>				
	<pre>RESULT 4 US-09-915-092-16 ; Sequence 16, Application US/09915092 ; Publication No. US2002011571A1 ; GENERAL INFORMATION: ; APPLICANT: Gervais, Francine ; APPLICANT: Kong, Xianqi ; APPLICANT: Chalifour, Robert ; APPLICANT: Migneault, David ; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND ; FILE REFERENCE: NBI-139 ; CURRENT APPLICATION NUMBER: US/09/915,092 ; CURRENT FILING DATE: 2001-07-24 ; PRIOR APPLICATION NUMBER: 60/220,808 ; PRIOR FILING DATE: 2000-07-25 ; NUMBER OF SEQ ID NOS: 28 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 16 ; LENGTH: 6 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-915-092-16</pre>				
	<pre>Query Match 100.0%; Score 29; DB 3; Length 6; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>				
	<pre>QY 1 KVVFFA 6 Db 1 KVVFFA 6</pre>				
	<pre>RESULT 5 US-09-747-408-9 ; Sequence 9, Application US/09747408 ; Publication No. US20030003141A1 ; GENERAL INFORMATION: ; APPLICANT: Green, Allan M. ; APPLICANT: Gervais, Francine ; TITLE OF INVENTION: Compounds And Methods For Modulating ; TITLE OF INVENTION: Cerebral Amyloid Angiopathy ; FILE REFERENCE: NBI-088 ; CURRENT APPLICATION NUMBER: US/09/747,408 ; CURRENT FILING DATE: 2000-12-22 ; PRIOR APPLICATION NUMBER: 60/171,877 ; PRIOR FILING DATE: 1999-12-23 ; NUMBER OF SEQ ID NOS: 24</pre>				
	<pre>Query Match 100.0%; Score 29; DB 3; Length 6; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>				
	<pre>QY 1 KVVFFA 6 Db 1 KVVFFA 6</pre>				
	<pre>RESULT 6 US-09-747-408-17 ; Sequence 17, Application US/09747408 ; Publication No. US20030003141A1 ; GENERAL INFORMATION: ; APPLICANT: Green, Allan M. ; APPLICANT: Gervais, Francine ; TITLE OF INVENTION: Compounds And Methods For Modulating ; TITLE OF INVENTION: Cerebral Amyloid Angiopathy ; FILE REFERENCE: NBI-088 ; CURRENT APPLICATION NUMBER: US/09/747,408 ; CURRENT FILING DATE: 2000-12-22 ; PRIOR APPLICATION NUMBER: 60/171,877 ; PRIOR FILING DATE: 1999-12-23 ; NUMBER OF SEQ ID NOS: 24 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 17 ; LENGTH: 6 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-747-408-17</pre>				
	<pre>Query Match 100.0%; Score 29; DB 3; Length 6; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>				
	<pre>QY 1 KVVFFA 6 Db 1 KVVFFA 6</pre>				
	<pre>RESULT 7 US-10-728-028-8 ; Sequence 8, Application US/10728028 ; Publication No. US20050048000A1 ; GENERAL INFORMATION: ; APPLICANT: Gervais, Francine ; APPLICANT: Kong, Xianqi ; APPLICANT: Chalifour, Robert ; APPLICANT: Migneault, David ; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND ; TITLE OF INVENTION: USES THEREOF ; FILE REFERENCE: NBI-139CP ; CURRENT APPLICATION NUMBER: US/10/728,028 ; CURRENT FILING DATE: 2003-12-03 ; PRIOR APPLICATION NUMBER: 60/443291 ; PRIOR FILING DATE: 2003-01-29 ; PRIOR APPLICATION NUMBER: 09/915092 ; PRIOR FILING DATE: 2001-07-24 ; PRIOR APPLICATION NUMBER: 60/220808 ; PRIOR FILING DATE: 2000-07-25 ; NUMBER OF SEQ ID NOS: 28 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 8 ; LENGTH: 6 ; TYPE: PRT ; ORGANISM: Artificial Sequence</pre>				
	<pre>Query Match 100.0%; Score 29; DB 3; Length 6; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>				
	<pre>QY 1 KVVFFA 6 Db 1 KVVFFA 6</pre>				
	<pre>RESULT 8 US-10-728-028-8 ; Sequence 8, Application US/10728028 ; Publication No. US20050048000A1 ; GENERAL INFORMATION: ; APPLICANT: Gervais, Francine ; APPLICANT: Kong, Xianqi ; APPLICANT: Chalifour, Robert ; APPLICANT: Migneault, David ; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND ; TITLE OF INVENTION: USES THEREOF ; FILE REFERENCE: NBI-139CP ; CURRENT APPLICATION NUMBER: US/10/728,028 ; CURRENT FILING DATE: 2003-12-03 ; PRIOR APPLICATION NUMBER: 60/443291 ; PRIOR FILING DATE: 2003-01-29 ; PRIOR APPLICATION NUMBER: 09/915092 ; PRIOR FILING DATE: 2001-07-24 ; PRIOR APPLICATION NUMBER: 60/220808 ; PRIOR FILING DATE: 2000-07-25 ; NUMBER OF SEQ ID NOS: 28 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 8 ; LENGTH: 6 ; TYPE: PRT ; ORGANISM: Artificial Sequence</pre>				
	<pre>Query Match 100.0%; Score 29; DB 3; Length 6; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>				
	<pre>QY 1 KVVFFA 6 Db 1 KVVFFA 6</pre>				

```

; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-8
Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 8
US-10-728-028-16
; Sequence 16, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6.
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-16
Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 9
US-10-825-958-16
; Sequence 16, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6.
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-825-958-16
Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 10
US-10-825-958-24
; Sequence 24, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6.
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-825-958-24
Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 11
US-10-641-924-7
; Sequence 7, Application US/10641924
; Publication No. US20040096881A1
; GENERAL INFORMATION:
; APPLICANT: Blasko, Eric
; APPLICANT: Kauser, Katalin
; APPLICANT: Parkinson, John
; TITLE OF INVENTION: eNOS Mutants Useful for Gene Therapy
; FILE REFERENCE: 53035AUSM1
; CURRENT APPLICATION NUMBER: US/10/641,924
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,638
; PRIOR FILING DATE: 2002-08-16

```

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-641-924-7

Query Match 100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||
Db 18 KVVFFA 23

RESULT 12
US-10-642-255-7
; Sequence 7, Application US/10642255
; Publication No. US20040120930A1
; GENERAL INFORMATION:
; APPLICANT: Dole, William P.
; APPLICANT: Kauser, Katalin
; APPLICANT: Qian, Hu Sheng
; APPLICANT: Rubanyi, Gabor
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant
; FILE REFERENCE: 52339AUSM1
; CURRENT APPLICATION NUMBER: US/10/642,255
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,637
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-642-255-7

Query Match 100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||
Db 18 KVVFFA 23

RESULT 13
US-10-437-963-173619
; Sequence 173619, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 173619
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Oryza sativa

; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_71639C.1.pep
US-10-437-963-173619

Query Match 100.0%; Score 29; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||
Db 4 KVVFFA 9

RESULT 14
US-10-437-963-133986
; Sequence 133986, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133986
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35803C.1.pep
US-10-437-963-133986

Query Match 100.0%; Score 29; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||
Db 6 KVVFFA 11

RESULT 15
US-10-437-963-105773
; Sequence 105773, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 105773
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_102988C.1.pep
US-10-437-963-105773

Query Match 100.0%; Score 29; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
| | | | |
Db 4 KVVFFA 9

RESULT 16

US-10-437-963-141578

; Sequence 141578, Application US/10437963
; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 141578

; LENGTH: 135

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_42668C.1.pep

US-10-437-963-141578

Query Match 100.0%; Score 29; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
| | | | |
Db 4 KVVFFA 9

RESULT 17

US-10-437-963-122124

; Sequence 122124, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 122124

; LENGTH: 175

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(175)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_25081C.1.pep
US-10-437-963-122124

Query Match 100.0%; Score 29; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
| | | | |
Db 4 KVVFFA 9

RESULT 18

US-10-481-032A-214

; Sequence 214, Application US/10481032A

; Publication No. US20050177901A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Tong

; APPLICANT: Cheng, Wenqiong

; APPLICANT: Briggs, Steven

; APPLICANT: Cooper, Bret

; APPLICANT: Goff, Stephen A.

; APPLICANT: Moughamer, Todd

; APPLICANT: Glazebrook, Jane

; APPLICANT: Katagiri, Fumiaki

; APPLICANT: Kreps, Joel

; APPLICANT: Provart, Nicolas

; APPLICANT: Ricke, Darrell

; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES

; FILE REFERENCE: 60148USPCT

; CURRENT APPLICATION NUMBER: US/10/481.032A

; CURRENT FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: US 60/300,112

; PRIOR FILING DATE: 2001-06-22

; PRIOR APPLICATION NUMBER: US 60/325,277

; PRIOR FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: US 60/342,327

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: PCT/IB02/02450

; PRIOR FILING DATE: 2002-06-21

; NUMBER OF SEQ ID NOS: 1201

; SOFTWARE: PatentIn Ver. 2.2

; SEQ ID NO 214

; LENGTH: 186

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-481-032A-214

Query Match 100.0%; Score 29; DB 5; Length 186;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
| | | | |
Db 4 KVVFFA 9

RESULT 19

US-10-481-032A-228

; Sequence 228, Application US/10481032A

; Publication No. US20050177901A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Tong

; APPLICANT: Cheng, Wenqiong

; APPLICANT: Briggs, Steven

; APPLICANT: Cooper, Bret

; APPLICANT: Goff, Stephen A.

; APPLICANT: Moughamer, Todd

; APPLICANT: Glazebrook, Jane

; APPLICANT: Katagiri, Fumiaki

```
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Rickes, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US/10/481,032A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 228
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-481-032A-228
```

```
Query Match 100.0%; Score 29; DB 5; Length 186;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVFFA 6
    |||||
Db 4 KVVFFA 9
```

```
RESULT 20
US-10-437-963-172476
; Sequence 172476, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172476
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(188)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70608C.1.pap
US-10-437-963-172476
```

```
Query Match 100.0%; Score 29; DB 4; Length 188;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVFFA 6
    |||||
Db 4 KVVFFA 9
```

RESULT 21

```
US-10-437-963-172452
; Sequence 172452, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172452
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(198)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70587C.1.pap
US-10-437-963-172452
```

```
Query Match 100.0%; Score 29; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVFFA 6
    |||||
Db 4 KVVFFA 9
```

```
RESULT 22
US-10-055-475-14
; Sequence 14, Application US/10055475
; Publication No. US20030022855A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalakrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
; CURRENT APPLICATION NUMBER: US/10/055,475
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 416
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-055-475-14
```

```
Query Match 100.0%; Score 29; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVFFA 6
    |||||
Db 57 KVVFFA 62
```



```
RESULT 23
US-11-042-922-14
; Sequence 14, Application US/11042922
; Publication No. US20050186211A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalakrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.2689)
; CURRENT APPLICATION NUMBER: US/11/042,922
; CURRENT FILING DATE: 2005-01-24
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 416
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-042-922-14
Query Match      100.0%; Score 29; DB 6; Length 416;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 57 KVVFFA 62

RESULT 24
US-10-055-475-13
; Sequence 13, Application US/10055475
; Publication No. US20030022855A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalakrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
; CURRENT APPLICATION NUMBER: US/10/055,475
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 514
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-055-475-13
Query Match      100.0%; Score 29; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 57 KVVFFA 62

RESULT 25
US-11-042-922-13
; Sequence 13, Application US/11042922
; Publication No. US20050186211A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalakrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.2689)
; CURRENT APPLICATION NUMBER: US/11/042,922
; CURRENT FILING DATE: 2005-01-24
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 514
; TYPE: PRT
; ORGANISM: sus scrofa
US-11-042-922-13
Query Match      100.0%; Score 29; DB 6; Length 514;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 57 KVVFFA 62

RESULT 26
US-10-408-765A-2031
; Sequence 2031, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2031
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2031
Query Match      100.0%; Score 29; DB 4; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 292 KVVFFA 297

RESULT 27
US-10-755-889-234
; Sequence 234, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
```

```
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 234
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-234

Query Match          100.0%; Score 29; DB 4; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      292 KVVFFA 297

RESULT 28
US-10-370-715B-8
; Sequence 8, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patent Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: F1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 8
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-8

Query Match          100.0%; Score 29; DB 5; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      292 KVVFFA 297

RESULT 29
US-10-631-467-680
; Sequence 680, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive P
; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
```

```
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 680
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-680

Query Match          100.0%; Score 29; DB 5; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      292 KVVFFA 297

RESULT 30
US-10-631-467-747
; Sequence 747, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive i
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 747
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-747

Query Match          100.0%; Score 29; DB 5; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      292 KVVFFA 297

RESULT 31
US-09-870-759-124
; Sequence 124, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-870-759-124

Query Match          100.0%; Score 29; DB 3; Length 1144;
```

Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 32
US-09-751-708A-124
; Sequence 124, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-751-708A-124

Query Match 100.0%; Score 29; DB 3; Length 1144;
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 33
US-10-428-817A-120
; Sequence 120, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-428-817A-120

Query Match 100.0%; Score 29; DB 4; Length 1144;
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 34
US-10-937-758A-101
; Sequence 101, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-937-758A-101

Query Match 100.0%; Score 29; DB 5; Length 1144;
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 35
US-10-631-467-1388
; Sequence 1388, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1388
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1388

Query Match 100.0%; Score 29; DB 5; Length 1144;
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 36
US-10-631-467-1464
; Sequence 1464, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive

```
; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1464
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1464

Query Match          100.0%; Score 29; DB 5; Length 1144;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |||||
Db      514 KVVFFA 519

RESULT 37
US-10-437-963-109646
; Sequence 109646, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109646
; LENGTH: 1640
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_13784C.1.pep
US-10-437-963-109646

Query Match          100.0%; Score 29; DB 4; Length 1640;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |||||
Db      1596 KVVFFA 1601

RESULT 38
US-09-867-847-11
; Sequence 11, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP

; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1464
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1464

Query Match          100.0%; Score 29; DB 5; Length 1144;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |||||
Db      514 KVVFFA 519

RESULT 37
US-10-437-963-109646
; Sequence 109646, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109646
; LENGTH: 1640
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_13784C.1.pep
US-10-437-963-109646

Query Match          100.0%; Score 29; DB 4; Length 1640;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |||||
Db      1596 KVVFFA 1601

RESULT 38
US-09-867-847-11
; Sequence 11, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP

; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-19

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:|||
Db      1 KIVFFA 6

RESULT 39
US-09-867-847-19
; Sequence 19, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-19

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:|||
Db      1 KIVFFA 6

RESULT 40
US-09-915-092-1
; Sequence 1, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
```

```

; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-1

```

```

Query Match      96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVVFFA 6
        |:||||
Db      1 KVVFFA 6

```

RESULT 41

```

US-09-915-092-9
; Sequence 9, Application US/09915092
; Publication No. US2002011571A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-9

```

```

Query Match      96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVVFFA 6
        |:||||
Db      1 KVVFFA 6

```

RESULT 42

```

US-09-747-408-1
; Sequence 1, Application US/09747408
; Publication No. US2003003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877

```

```

; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-1

```

```

Query Match      96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVVFFA 6
        |:||||
Db      1 KVVFFA 6

```

RESULT 43

```

US-09-747-408-10
; Sequence 10, Application US/09747408
; Publication No. US2003003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-10

```

```

Query Match      96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVVFFA 6
        |:||||
Db      1 KVVFFA 6

```

RESULT 44

```

US-10-728-028-1
; Sequence 1, Application US/10728028
; Publication No. US2005004800A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6

```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-1
```

```
Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
      |:|||||
Db      1 KIVFFA 6
```

```
RESULT 45
US-10-728-028-9
; Sequence 9, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; PRIOR FILING DATE: 2003-12-03
; PRIOR FILING DATE: 2003-01-29
; PRIOR FILING DATE: 2001-07-24
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-9
```

```
Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
      |:|||||
Db      1 KIVFFA 6
```

```
RESULT 46
US-10-825-958-9
; Sequence 9, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-9
```

```
Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
      |:|||||
Db      1 KIVFFA 6
```

```
RESULT 47
US-10-825-958-17
; Sequence 17, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-17
```

```
Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
      |:|||||
Db      1 KIVFFA 6
```

```
RESULT 48
US-10-425-115-280164
; Sequence 280164, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
```

; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 280164
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_187087C.1.pep
US-10-425-115-280164

Query Match 96.6%; Score 28; DB 4; Length 58;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 28 KIVFFA 33

RESULT 49

US-10-424-599-165325
; Sequence 165325, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424.599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 165325
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_120303C.1.pep
US-10-424-599-165325

Query Match 96.6%; Score 28; DB 4; Length 90;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 21 KIVFFA 26

RESULT 50

US-10-424-599-240310
; Sequence 240310, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424.599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240310
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59027C.1.pep

US-10-424-599-240310

Query Match 96.6%; Score 28; DB 4; Length 93;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 34 KIVFFA 39

RESULT 51

US-10-450-763-56957
; Sequence 56957, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450.763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56957
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: DOMAIN
; LOCATION: (13)..(62)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354Z, p-value=2.452e-13, raw score
; OTHER INFORMATION: 9.06
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(99)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-56957

Query Match 96.6%; Score 28; DB 5; Length 99;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 63 KIVFFA 68

RESULT 52

US-11-097-143-12723
; Sequence 12723, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28

```
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12723
; LENGTH: 564
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-12723

Query Match          93.1%; Score 27; DB 6; Length 564;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
        |::|||
Db       53 KIIFFA 58
```

```
RESULT 53
US-11-097-143-32208
; Sequence 32208, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32208
; LENGTH: 1443
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-32208
```

```
Query Match          93.1%; Score 27; DB 6; Length 1443;
Best Local Similarity 66.7%; Pred. No. 4.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
        |::|||
Db      1204 KIIFFA 1209
```

```
RESULT 54
US-09-867-847-7
; Sequence 7, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangdi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-7

Query Match          89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
        |::|||
Db       1 KLVFFA 6
```

```
RESULT 55
US-09-867-847-20
; Sequence 20, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangdi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-20

Query Match          89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```



```
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Antifibrillogenic agents
US-09-956-625-25

Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      1 KLVFFA 6
      |:||||

RESULT 60
US-09-747-408-3
; Sequence 3, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-3

Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      1 KLVFFA 6
      |:||||

RESULT 61
US-09-747-408-11
; Sequence 11, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-11

Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
Db      1 KLVFFA 6
      |:||||

RESULT 62
US-10-463-729-9
; Sequence 9, Application US/10463729
; Publication No. US20040005307A1
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/463,729
; FILING DATE: 17-JUNE-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-463-729-9

Query Match      89.7%; Score 26; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      1 KLVFFA 6
      |:||||

RESULT 63
US-10-728-028-10
; Sequence 10, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
```

; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-10

Query Match 89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 64
US-10-728-028-27
; Sequence 27, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-27

Query Match 89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 65
US-10-728-028-28
; Sequence 28, Application US/10728028

; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-28

Query Match 89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 66
US-10-825-958-7
; Sequence 7, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-7

Query Match 89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

```
RESULT 67
US-10-825-958-18
; Sequence 18, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-18

Query Match      89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
       |:||||
Db      1 KLVFFA 6

RESULT 68
US-10-666-095-3
; Sequence 3, Application US/10666095
; Publication No. US20050119187A1
; GENERAL INFORMATION:
; APPLICANT: Hammer, Robert P.
; APPLICANT: Fu, Yanwen
; APPLICANT: Aucoin, Jed P.
; APPLICANT: Miller, Tod J.
; APPLICANT: McLaughlin, Mark L.
; APPLICANT: McCarley, Robin L.
; TITLE OF INVENTION: Anti-fibril Peptides
; FILE REFERENCE: 0212.1 Hammer
; CURRENT APPLICATION NUMBER: US/10/666,095
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,081
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-666-095-3

Query Match      89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
       |:||||
Db      1 KLVFFA 6

RESULT 69
US-09-867-847-12
; Sequence 12, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-12

Query Match      89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
       |:||||
Db      2 KLVFFA 7

RESULT 70
US-09-867-847-27
; Sequence 27, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-27

Query Match      89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
       |:||||
Db      2 KLVFFA 7
```

```
Db      1 KLVFFA 6

RESULT 69
US-09-867-847-12
; Sequence 12, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-12

Query Match      89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
       |:||||
Db      2 KLVFFA 7

RESULT 70
US-09-867-847-27
; Sequence 27, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-27

Query Match      89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
       |:||||
Db      2 KLVFFA 7
```

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 71

US-09-867-847-28
; Sequence 28, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 28
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD RES
; LOCATION: (7)
; OTHER INFORMATION: AMIDATION
US-09-867-847-28

Query Match 89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 72

US-09-972-475-7
; Sequence 7, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Pondeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267

; FILING DATE: <Unknown>
; APPLICATION NUMBER: USN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-972-475-7

Query Match 89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 73

US-09-915-092-2
; Sequence 2, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-2

Query Match 89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 74

US-09-915-092-17
; Sequence 17, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND

```
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-17
```

```
Query Match      89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
      |:||||
Db      1 KLVFFA 6
```

```
RESULT 75
US-09-915-092-18
; Sequence 18, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-18
```

```
Query Match      89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFFA 6
      |:||||
Db      1 KLVFFA 6
```

```
Search completed: December 29, 2005, 18:49:48
Job time : 67.2903 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds
(without alignments)
24.763 Million cell updates/sec

Title: US-10-009-122-17

Perfect score: 29

Sequence: 1 KVVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	2	US-09-747-408-9
2	29	100.0	6	2	US-09-747-408-17
3	29	100.0	77	2	US-09-513-999C-6921
4	29	100.0	1144	1	US-08-147-812-5
5	29	100.0	1144	1	US-08-319-866-12
6	29	100.0	1144	2	US-09-123-708-2
7	29	100.0	1144	2	US-09-123-624-2
8	29	100.0	1144	2	US-09-661-258-5
9	29	100.0	1144	2	US-08-809-917-12
10	29	100.0	1144	2	US-09-419-371-12
11	28	96.6	6	2	US-09-747-408-1
12	28	96.6	6	2	US-09-747-408-10
13	28	96.6	123	2	US-09-902-540-13513
14	26	89.7	6	1	US-08-612-785B-9
15	26	89.7	6	2	US-08-703-675C-32
16	26	89.7	6	2	US-08-617-267C-9
17	26	89.7	6	2	US-09-747-408-3
18	26	89.7	6	2	US-09-747-408-11
19	26	89.7	7	1	US-08-127-904-14
20	26	89.7	7	1	US-08-612-785B-7
21	26	89.7	7	2	US-08-703-675C-30
22	26	89.7	7	2	US-08-617-267C-7
23	26	89.7	7	2	US-08-264-709A-13
24	26	89.7	7	2	US-09-747-408-2
25	26	89.7	7	2	US-09-747-408-18
26	26	89.7	7	2	US-09-747-408-19
27	26	89.7	7	4	PCT-US94-10475-14

28	89.7	8	1	US-08-612-785B-5	Sequence 5, Appli
29	89.7	8	1	US-08-630-645-1	Sequence 1, Appli
30	89.7	8	2	US-08-703-675C-28	Sequence 28, Appli
31	89.7	8	2	US-08-617-267C-5	Sequence 5, Appli
32	89.7	8	2	US-09-095-106A-44	Sequence 44, Appli
33	89.7	8	2	US-08-766-596A-1	Sequence 1, Appli
34	89.7	8	2	US-09-668-314C-73	Sequence 73, Appli
35	89.7	8	4	PCT-US96-10220-1	Sequence 1, Appli
36	89.7	9	2	US-08-766-596A-64	Sequence 64, Appli
37	89.7	9	2	US-09-747-408-20	Sequence 20, Appli
38	89.7	10	2	US-08-970-833-3	Sequence 3, Appli
39	89.7	10	2	US-09-724-961-20	Sequence 20, Appli
40	89.7	10	2	US-09-724-961-21	Sequence 21, Appli
41	89.7	10	2	US-09-724-961-22	Sequence 22, Appli
42	89.7	10	2	US-09-724-961-23	Sequence 23, Appli
43	89.7	10	2	US-09-724-961-24	Sequence 24, Appli
44	89.7	10	2	US-09-580-018-20	Sequence 20, Appli
45	89.7	10	2	US-09-580-018-21	Sequence 21, Appli
46	89.7	10	2	US-09-580-018-22	Sequence 22, Appli
47	89.7	10	2	US-09-580-018-23	Sequence 23, Appli
48	89.7	10	2	US-09-580-018-24	Sequence 24, Appli
49	89.7	10	2	US-09-724-551-20	Sequence 20, Appli
50	89.7	10	2	US-09-724-551-21	Sequence 21, Appli
51	89.7	10	2	US-09-724-551-22	Sequence 22, Appli
52	89.7	10	2	US-09-724-551-23	Sequence 23, Appli
53	89.7	10	2	US-09-724-551-24	Sequence 24, Appli
54	89.7	10	2	US-09-724-940-20	Sequence 20, Appli
55	89.7	10	2	US-09-724-940-21	Sequence 21, Appli
56	89.7	10	2	US-09-724-940-22	Sequence 22, Appli
57	89.7	10	2	US-09-724-940-23	Sequence 23, Appli
58	89.7	10	2	US-09-724-940-24	Sequence 24, Appli
59	89.7	11	1	US-08-630-645-14	Sequence 14, Appli
60	89.7	11	2	US-08-766-596A-14	Sequence 14, Appli
61	89.7	11	2	US-09-988-842-9	Sequence 9, Appli
62	89.7	11	2	US-09-988-842-25	Sequence 25, Appli
63	89.7	11	4	PCT-US96-10220-14	Sequence 14, Appli
64	89.7	14	2	US-09-594-366-5	Sequence 5, Appli
65	89.7	14	2	US-09-992-800-5	Sequence 5, Appli
66	89.7	15	1	US-08-612-785B-14	Sequence 14, Appli
67	89.7	15	1	US-08-612-785B-37	Sequence 37, Appli
68	89.7	15	2	US-08-617-267C-14	Sequence 14, Appli
69	89.7	15	2	US-08-766-596A-56	Sequence 56, Appli
70	89.7	15	2	US-08-766-596A-57	Sequence 57, Appli
71	89.7	15	2	US-08-766-596A-58	Sequence 58, Appli
72	89.7	15	2	US-08-766-596A-60	Sequence 60, Appli
73	89.7	15	2	US-08-766-596A-61	Sequence 61, Appli
74	89.7	15	2	US-08-766-596A-62	Sequence 62, Appli
75	89.7	15	2	US-08-766-596A-63	Sequence 63, Appli
76	89.7	15	2	US-08-766-596A-65	Sequence 65, Appli
77	89.7	17	2	US-09-264-709A-2	Sequence 2, Appli
78	89.7	17	2	US-09-594-366-3	Sequence 3, Appli
79	89.7	17	2	US-09-623-548A-950	Sequence 950, App
80	89.7	17	2	US-09-623-548A-983	Sequence 983, App
81	89.7	17	2	US-09-992-800-3	Sequence 3, Appli
82	89.7	17	2	US-09-657-276-950	Sequence 950, App
83	89.7	17	2	US-09-657-276-983	Sequence 983, App
84	89.7	19	2	US-08-970-833-11	Sequence 11, Appli
85	89.7	19	2	US-09-723-384-5	Sequence 5, Appli
86	89.7	19	2	US-09-724-961-75	Sequence 75, Appli
87	89.7	19	2	US-09-724-552-5	Sequence 5, Appli
88	89.7	19	2	US-09-580-018-75	Sequence 75, Appli
89	89.7	19	2	US-09-723-927-5	Sequence 5, Appli
90	89.7	19	2	US-09-724-489-5	Sequence 5, Appli
91	89.7	19	2	US-09-724-477-5	Sequence 5, Appli
92	89.7	19	2	US-09-723-762-5	Sequence 5, Appli
93	89.7	19	2	US-09-201-430-5	Sequence 5, Appli
94	89.7	19	2	US-09-724-551-75	Sequence 75, Appli
95	89.7	19	2	US-10-815-353-5	Sequence 5, Appli
96	89.7	19	2	US-10-816-529-5	Sequence 5, Appli
97	89.7	19	2	US-10-815-391-5	Sequence 5, Appli
98	89.7	19	2	US-10-816-022-5	Sequence 5, Appli
99	89.7	19	2	US-09-724-940-75	Sequence 75, Appli
100	89.7	19	2	US-10-934-609-5	Sequence 5, Appli

101	26	89.7	19	2	US-10-884-892-5	Sequence 5, Appl	174	26	89.7	38	2	US-09-623-548A-1002	Sequence 1002, Ap
102	26	89.7	20	2	US-08-970-833-10	Sequence 10, Appl	175	26	89.7	38	2	US-09-657-276-975	Sequence 975, App
103	26	89.7	20	2	US-09-724-953-33	Sequence 33, Appl	176	26	89.7	38	2	US-09-657-276-1002	Sequence 1002, Ap
104	26	89.7	20	2	US-09-724-567-33	Sequence 33, Appl	177	26	89.7	39	1	US-08-304-585-5	Sequence 5, Appl
105	26	89.7	20	2	US-09-979-952-33	Sequence 33, Appl	178	26	89.7	39	1	US-08-302-808-2	Sequence 2, Appl
106	26	89.7	20	2	US-09-585-817-33	Sequence 33, Appl	179	26	89.7	39	1	US-08-609-090-7	Sequence 7, Appl
107	26	89.7	26	1	US-08-304-585-7	Sequence 7, Appl	180	26	89.7	39	1	US-08-682-245A-1	Sequence 1, Appl
108	26	89.7	28	1	US-08-346-849-4	Sequence 4, Appl	181	26	89.7	39	1	US-08-986-948-2	Sequence 2, Appl
109	26	89.7	28	1	US-08-302-808-7	Sequence 7, Appl	182	26	89.7	40	1	US-07-744-767A-1	Sequence 1, Appl
110	26	89.7	28	1	US-08-609-090-2	Sequence 2, Appl	183	26	89.7	40	1	US-08-235-400-2	Sequence 2, Appl
111	26	89.7	28	1	US-08-986-948-7	Sequence 7, Appl	184	26	89.7	40	1	US-08-476-464A-2	Sequence 2, Appl
112	26	89.7	28	1	US-08-293-284A-4	Sequence 4, Appl	185	26	89.7	40	1	US-08-304-585-1	Sequence 1, Appl
113	26	89.7	28	1	US-08-461-216-2	Sequence 2, Appl	186	26	89.7	40	1	US-08-304-585-8	Sequence 8, Appl
114	26	89.7	28	2	US-09-388-890-2	Sequence 2, Appl	187	26	89.7	40	1	US-08-302-808-3	Sequence 3, Appl
115	26	89.7	28	2	US-09-388-890-3	Sequence 3, Appl	188	26	89.7	40	1	US-08-433-734-1	Sequence 1, Appl
116	26	89.7	28	2	US-09-388-890-4	Sequence 4, Appl	189	26	89.7	40	1	US-08-609-090-8	Sequence 8, Appl
117	26	89.7	28	2	US-09-388-890-5	Sequence 5, Appl	190	26	89.7	40	1	US-07-737-371E-69	Sequence 69, Appl
118	26	89.7	28	2	US-09-388-890-6	Sequence 6, Appl	191	26	89.7	40	1	US-08-682-245A-2	Sequence 2, Appl
119	26	89.7	28	2	US-09-388-890-7	Sequence 7, Appl	192	26	89.7	40	1	US-08-986-948-3	Sequence 3, Appl
120	26	89.7	28	2	US-09-388-890-8	Sequence 8, Appl	193	26	89.7	40	1	US-08-461-216-1	Sequence 1, Appl
121	26	89.7	28	2	US-09-388-890-9	Sequence 9, Appl	194	26	89.7	40	2	US-08-959-148-1	Sequence 1, Appl
122	26	89.7	28	2	US-09-388-890-10	Sequence 10, Appl	195	26	89.7	40	2	US-09-242-724-22	Sequence 22, Appl
123	26	89.7	28	2	US-09-388-890-12	Sequence 12, Appl	196	26	89.7	40	2	US-08-723-661B-1	Sequence 1, Appl
124	26	89.7	28	2	US-09-388-890-13	Sequence 13, Appl	197	26	89.7	40	2	US-09-062-365-3	Sequence 3, Appl
125	26	89.7	28	2	US-09-388-890-14	Sequence 14, Appl	198	26	89.7	40	2	US-09-133-866-1	Sequence 1, Appl
126	26	89.7	28	2	US-09-264-709A-1	Sequence 1, Appl	199	26	89.7	40	2	US-09-861-847A-7	Sequence 7, Appl
127	26	89.7	28	2	US-08-723-661B-2	Sequence 2, Appl	200	26	89.7	40	2	US-09-861-847A-8	Sequence 8, Appl
128	26	89.7	28	2	US-09-660-954-2	Sequence 2, Appl	201	26	89.7	40	2	US-09-988-842-3	Sequence 3, Appl
129	26	89.7	28	2	US-09-660-954-3	Sequence 3, Appl	202	26	89.7	40	2	US-10-455-218-1	Sequence 1, Appl
130	26	89.7	28	2	US-09-660-954-4	Sequence 4, Appl	203	26	89.7	40	2	US-10-151-614-1	Sequence 1, Appl
131	26	89.7	28	2	US-09-660-954-5	Sequence 5, Appl	204	26	89.7	40	2	US-09-623-548A-956	Sequence 956, App
132	26	89.7	28	2	US-09-660-954-6	Sequence 6, Appl	205	26	89.7	40	2	US-09-623-548A-962	Sequence 962, App
133	26	89.7	28	2	US-09-660-954-7	Sequence 7, Appl	206	26	89.7	40	2	US-09-623-548A-968	Sequence 968, App
134	26	89.7	28	2	US-09-660-954-8	Sequence 8, Appl	207	26	89.7	40	2	US-09-623-548A-978	Sequence 978, App
135	26	89.7	28	2	US-09-660-954-9	Sequence 9, Appl	208	26	89.7	40	2	US-09-623-548A-989	Sequence 989, App
136	26	89.7	28	2	US-09-660-954-10	Sequence 10, Appl	209	26	89.7	40	2	US-09-623-548A-995	Sequence 995, App
137	26	89.7	28	2	US-09-660-954-12	Sequence 12, Appl	210	26	89.7	40	2	US-09-623-548A-1005	Sequence 1005, Ap
138	26	89.7	28	2	US-09-660-954-13	Sequence 13, Appl	211	26	89.7	40	2	US-09-657-276-956	Sequence 956, App
139	26	89.7	28	2	US-09-660-954-14	Sequence 14, Appl	212	26	89.7	40	2	US-09-657-276-962	Sequence 962, App
140	26	89.7	28	2	US-08-898-300-4	Sequence 4, Appl	213	26	89.7	40	2	US-09-657-276-968	Sequence 968, App
141	26	89.7	28	2	US-08-824-513-4	Sequence 4, Appl	214	26	89.7	40	2	US-09-657-276-978	Sequence 978, App
142	26	89.7	28	2	US-09-623-548A-959	Sequence 959, App	215	26	89.7	40	2	US-09-657-276-989	Sequence 989, App
143	26	89.7	28	2	US-09-623-548A-965	Sequence 965, App	216	26	89.7	40	2	US-09-657-276-995	Sequence 995, App
144	26	89.7	28	2	US-09-623-548A-976	Sequence 976, App	217	26	89.7	40	2	US-09-657-276-1005	Sequence 1005, Ap
145	26	89.7	28	2	US-09-623-548A-992	Sequence 992, App	218	26	89.7	40	2	US-09-962-955D-36	Sequence 36, App
146	26	89.7	28	2	US-09-623-548A-1003	Sequence 1003, Ap	219	26	89.7	40	4	PCT-US92-06700-1	Sequence 1, Appl
147	26	89.7	28	2	US-09-657-276-959	Sequence 959, App	220	26	89.7	41	1	US-07-819-361-1	Sequence 1, Appl
148	26	89.7	28	2	US-09-657-276-965	Sequence 965, App	221	26	89.7	41	1	US-08-302-808-4	Sequence 4, Appl
149	26	89.7	28	2	US-09-657-276-976	Sequence 976, App	222	26	89.7	41	1	US-08-682-245A-3	Sequence 3, Appl
150	26	89.7	28	2	US-09-657-276-992	Sequence 992, App	223	26	89.7	41	1	US-08-986-948-4	Sequence 4, Appl
151	26	89.7	28	2	US-09-657-276-1003	Sequence 1003, Ap	224	26	89.7	42	1	US-07-744-767A-2	Sequence 2, Appl
152	26	89.7	28	2	US-09-865-294A-66	Sequence 66, Appl	225	26	89.7	42	1	US-08-179-574-1	Sequence 1, Appl
153	26	89.7	30	1	US-08-609-090-3	Sequence 3, Appl	226	26	89.7	42	1	US-08-271-162-5	Sequence 5, Appl
154	26	89.7	30	2	US-09-861-847A-1	Sequence 1, Appl	227	26	89.7	42	1	US-08-347-144-1	Sequence 1, Appl
155	26	89.7	33	1	US-08-609-090-4	Sequence 4, Appl	228	26	89.7	42	1	US-08-462-859A-19	Sequence 19, Appl
156	26	89.7	34	1	US-08-475-579A-4	Sequence 4, Appl	229	26	89.7	42	1	US-08-123-659A-19	Sequence 19, Appl
157	26	89.7	35	1	US-08-304-585-6	Sequence 6, Appl	230	26	89.7	42	1	US-08-464-247A-19	Sequence 19, Appl
158	26	89.7	35	1	US-08-612-785B-16	Sequence 16, Appl	231	26	89.7	42	1	US-08-464-248A-19	Sequence 19, Appl
159	26	89.7	35	1	US-08-612-785B-36	Sequence 36, Appl	232	26	89.7	42	1	US-08-476-464A-1	Sequence 1, Appl
160	26	89.7	35	1	US-08-612-785B-38	Sequence 38, Appl	233	26	89.7	42	1	US-08-304-585-2	Sequence 2, Appl
161	26	89.7	35	1	US-08-612-785B-40	Sequence 40, Appl	234	26	89.7	42	1	US-08-302-808-5	Sequence 5, Appl
162	26	89.7	35	1	US-08-617-267C-16	Sequence 16, Appl	235	26	89.7	42	1	US-08-268-348A-1	Sequence 1, Appl
163	26	89.7	35	2	US-09-623-548A-979	Sequence 979, App	236	26	89.7	42	1	US-08-268-348A-2	Sequence 2, Appl
164	26	89.7	35	2	US-09-623-548A-1006	Sequence 1006, Ap	237	26	89.7	42	1	US-08-268-348A-3	Sequence 3, Appl
165	26	89.7	35	2	US-09-657-276-979	Sequence 979, App	238	26	89.7	42	1	US-08-268-348A-4	Sequence 4, Appl
166	26	89.7	36	1	US-09-657-276-1006	Sequence 1006, Ap	239	26	89.7	42	1	US-08-268-348A-5	Sequence 5, Appl
167	26	89.7	36	2	US-08-609-090-6	Sequence 6, Appl	240	26	89.7	42	1	US-08-268-348A-6	Sequence 6, Appl
168	26	89.7	36	2	US-09-861-847A-6	Sequence 6, Appl	241	26	89.7	42	1	US-08-433-734-2	Sequence 2, Appl
169	26	89.7	36	2	US-09-861-847A-11	Sequence 11, Appl	242	26	89.7	42	1	US-08-609-090-9	Sequence 9, Appl
170	26	89.7	38	1	US-08-302-808-1	Sequence 1, Appl	243	26	89.7	42	1	US-07-737-371E-72	Sequence 72, Appl
171	26	89.7	38	1	US-07-737-371E-68	Sequence 68, Appl	244	26	89.7	42	1	US-08-422-333-4	Sequence 4, Appl
172	26	89.7	38	1	US-08-986-948-1	Sequence 1, Appl	245	26	89.7	42	1	US-08-682-245A-4	Sequence 4, Appl
173	26	89.7	38	2	US-09-623-548A-975	Sequence 975, App	246	26	89.7	42	1	US-08-986-948-5	Sequence 5, Appl


```
247 26 89.7 42 2 US-08-717-551A-2
248 26 89.7 42 2 US-09-388-890-1
249 26 89.7 42 2 US-09-005-215-20
250 26 89.7 42 2 US-09-242-724-23
251 26 89.7 42 2 US-08-923-930-2
252 26 89.7 42 2 US-08-660-954-1
253 26 89.7 42 2 US-08-923-055-2
254 26 89.7 42 2 US-08-922-889-2
255 26 89.7 42 2 US-09-731-460-1
256 26 89.7 42 2 US-09-133-866-2
257 26 89.7 42 2 US-09-723-384-1
258 26 89.7 42 2 US-09-724-961-42
259 26 89.7 42 2 US-09-724-552-1
260 26 89.7 42 2 US-09-580-018-42
261 26 89.7 42 2 US-10-455-218-2
262 26 89.7 42 2 US-09-723-927-1
263 26 89.7 42 2 US-09-724-489-1
264 26 89.7 42 2 US-09-724-477-1
265 26 89.7 42 2 US-09-723-762-1
266 26 89.7 42 2 US-09-201-430-1
267 26 89.7 42 2 US-09-724-551-42
268 26 89.7 42 2 US-10-815-353-1
269 26 89.7 42 2 US-10-278-181-1
270 26 89.7 42 2 US-10-816-529-1
271 26 89.7 42 2 US-09-623-548A-955
272 26 89.7 42 2 US-09-623-548A-961
273 26 89.7 42 2 US-09-623-548A-967
274 26 89.7 42 2 US-09-623-548A-988
275 26 89.7 42 2 US-09-623-548A-994
276 26 89.7 42 2 US-10-815-391-1
277 26 89.7 42 2 US-10-816-022-1
278 26 89.7 42 2 US-09-724-953-34
279 26 89.7 42 2 US-09-657-276-955
280 26 89.7 42 2 US-09-657-276-961
281 26 89.7 42 2 US-09-657-276-967
282 26 89.7 42 2 US-09-657-276-988
283 26 89.7 42 2 US-09-657-276-994
284 26 89.7 42 2 US-09-724-567-34
285 26 89.7 42 2 US-09-724-940-42
286 26 89.7 42 2 US-09-865-294A-65
287 26 89.7 42 2 US-09-979-952-34
288 26 89.7 42 2 US-09-585-817-34
289 26 89.7 42 2 US-09-962-955D-37
290 26 89.7 42 2 US-09-706-574A-20
291 26 89.7 42 2 US-10-934-609-1
292 26 89.7 42 2 US-10-884-892-1
293 26 89.7 42 4 PCT-US92-06700-2
294 26 89.7 42 4 PCT-US93-00325-1
295 26 89.7 42 4 PCT-US95-08302-5
296 26 89.7 42 6 5220013-12
297 26 89.7 42 6 5220013-14
298 26 89.7 42 6 5223482-12
299 26 89.7 43 1 US-08-235-400-1
300 26 89.7 43 1 US-08-437-067-1

ALIGNMENTS

RESULT 1
US-09-747-408-9
; Sequence 9, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-9

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 2
US-09-747-408-17
; Sequence 17, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-17

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 3
US-09-513-999C-6921
; Sequence 6921, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; Patent No. 6783961
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6921
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6921

Query Match 100.0%; Score 29; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 14;
```

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||||
Db 38 KVVFFA 43

RESULT 4

US-08-147-812-5
; Sequence 5, Application US/08147812
; Patent No. 5766909
; GENERAL INFORMATION:
; APPLICANT: Xie, Qiao-wen
; APPLICANT: Nathan, Carl F.
; APPLICANT: Mumford, Richard A.
; APPLICANT: Calaycay, Jimmy Ramos
; TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 East Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh Centris650
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,812
; FILING DATE: No. 5766909 Available
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/841,641
; FILING DATE: 02-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W III
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 186581A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1144 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

Query Match 100.0%; Score 29; DB 1; Length 1144;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||||
Db 514 KVVFFA 519

RESULT 5

US-08-319-866-12
; Sequence 12, Application US/08319866
; Patent No. 5929223
; GENERAL INFORMATION:
; APPLICANT: Tully, Timothy P.
; APPLICANT: Yin, Jerry C.
; APPLICANT: Regulski, Michael
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
; TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,866
; FILING DATE: 7-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1144 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-319-866-12

Query Match 100.0%; Score 29; DB 1; Length 1144;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||||
Db 514 KVVFFA 519

RESULT 6

US-09-123-708-2
; Sequence 2, Application US/09123708
; Patent No. 6146887
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Juergen
; APPLICANT: GOEDECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
; FILE REFERENCE: 51169-2003
; CURRENT APPLICATION NUMBER: US/09/123,708
; CURRENT FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: 08/553,503
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: P4411402.8
; EARLIER FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Cytomegalovirus
US-09-123-708-2

Query Match 100.0%; Score 29; DB 2; Length 1144;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||||


```

; LENGTH: 1144
; TYPE: PRT
; ORGANISM: mouse
US-09-419-371-12

Query Match      100.0%; Score 29; DB 2; Length 1144;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      514 KIVFFA 519

RESULT 11
US-09-747-408-1
; Sequence 1, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-1

Query Match      96.6%; Score 28; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      1 KIVFFA 6

RESULT 12
US-09-747-408-10
; Sequence 10, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-10

Query Match      96.6%; Score 28; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6

```

```

Db      1 KIVFFA 6

RESULT 13
US-09-902-540-13513
; Sequence 13513, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13513
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13513

Query Match      96.6%; Score 28; DB 2; Length 123;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      52 KIVFFA 57

RESULT 14
US-08-612-785B-9
; Sequence 9, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-785B-9

Query Match 89.7%; Score 26; DB 1; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 15
US-08-703-675C-32
; Sequence 32, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findexis, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide Aggregation Comprising D-
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996

ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-703-675C-32

Query Match 89.7%; Score 26; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 16
US-08-617-267C-9
; Sequence 9, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findexis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-617-267C-9

Query Match 89.7%; Score 26; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 17
US-09-747-408-3
; Sequence 3, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408

```
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-3

Query Match      89.7%; Score 26; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
Db      1 KLVFFA 6
|:|||||

RESULT 18
US-09-747-408-11
; Sequence 11, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NEI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-11

Query Match      89.7%; Score 26; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
Db      1 KLVFFA 6
|:|||||

RESULT 19
US-08-127-904-14
; Sequence 14, Application US/08127904
; Patent No. 5470951
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For Antagonizing
; TITLE OF INVENTION: Anesthetic Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving the
; TITLE OF INVENTION: Quality of Life in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4" diskette
; COMPUTER: Wang PC

; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,904
; FILING DATE: 29 September 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: No. 5470951e
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: No. 5470951e
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; TELEX: No. 5470951e
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown
US-08-127-904-14

Query Match      89.7%; Score 26; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
Db      1 KLVFFA 6
|:|||||

RESULT 20
US-08-612-785B-7
; Sequence 7, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
```

; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-7

Query Match 89.7%; Score 26; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 21

US-08-703-675C-30
; Sequence 30, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Fideis, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide Aggregation Comprising D-
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703.675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US98 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US98 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US98 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-703-675C-30

Query Match 89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6

Db 2 KLVFFA 7

RESULT 22

US-08-617-267C-7
; Sequence 7, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Fideis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US98 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US98 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US98 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-617-267C-7

Query Match 89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 23

US-09-264-709A-13
; Sequence 13, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
; APPLICANT: Roberts, Eugene
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
; FILE REFERENCE: 2124-310
; FILE REFERENCE: 2124-310
; CURRENT APPLICATION NUMBER: US/09/264,709A
; CURRENT FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 08/797,782
; PRIOR FILING DATE: 1997-02-07

```
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-264-709A-13

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:||||
Db      1 KLVFFA 6

RESULT 24
US-09-747-408-2
; Sequence 2, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-2

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:||||
Db      2 KLVFFA 7

RESULT 25
US-09-747-408-18
; Sequence 18, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-18

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:||||
Db      2 KLVFFA 7

RESULT 26
US-09-747-408-19
; Sequence 19, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-19

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:||||
Db      1 KLVFFA 6

RESULT 27
PCT-US94-10475-14
; Sequence 14, Application PC/TUS9410475
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For
; TITLE OF INVENTION: Antagonizing Amnestic
; TITLE OF INVENTION: Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving
; TITLE OF INVENTION: the Quality of Life
; TITLE OF INVENTION: in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4"
; MEDIUM TYPE: diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10475
; FILING DATE: 16 September 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA: U. S. Application
; PRIOR APPLICATION DATA: Serial No.
; PRIOR APPLICATION DATA: 08/127,904; filed
; PRIOR APPLICATION DATA: 29 September 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
```


REGISTRATION NUMBER: 16,541
REFERENCE/DOCKET NUMBER: None
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 626-3564 or 783-6030
TELEFAX: (202) 783-6031
TELEX: None
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7
TYPE: Amino Acid
STRANDEDNESS:
TOPOLOGY: Unknown
PCT-US94-10475-14

Query Match 89.7%; Score 26; DB 4; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 28
US-08-612-785B-5
; Sequence 5, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PFI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-785B-5

Query Match 89.7%; Score 26; DB 1; Length 8;

Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 29
US-08-630-645-1
; Sequence 1, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,645
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-630-645-1

Query Match 89.7%; Score 26; DB 1; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 30
US-08-703-675C-28
; Sequence 28, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
Aggregation Comprising D-

ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP2
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-703-675C-28

Query Match 89.7%; Score 26; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
DB 3 KLVFFA 8

RESULT 31
US-08-617-267C-5
Sequence 5, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C

FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-617-267C-5

Query Match 89.7%; Score 26; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
DB 3 KLVFFA 8

RESULT 32
US-09-095-106A-44
Sequence 44, Application US/09095106A
Patent No. 6331440
GENERAL INFORMATION:
APPLICANT: NORDSTEDT, Christer
APPLICANT: NASLUND, Jan
APPLICANT: THYBERG, Johan
APPLICANT: TJERNBERG, Lars O.
TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
FILE REFERENCE: 000500-124
CURRENT APPLICATION NUMBER: US/09/095,106A
CURRENT FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/009,386
PRIOR FILING DATE: 1995-12-29
PRIOR APPLICATION NUMBER: PCT/SE96/01621
PRIOR FILING DATE: 1996-12-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44
LENGTH: 8
TYPE: PRT
ORGANISM: Amyloidosis
US-09-095-106A-44

Query Match 89.7%; Score 26; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
DB 1 KLVFFA 6

RESULT 33
US-08-766-596A-1
Sequence 1, Application US/08766596A
Patent No. 6462171

```
;; GENERAL INFORMATION:
;; APPLICANT: SOTO-JARA, Claudio
;; APPLICANT: BAUMANN, Marc
;; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
;; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
;; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
;; TITLE OF INVENTION: DEPOSITS
;; NUMBER OF SEQUENCES: 69
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEIMARK
;; STREET: 419 Seventh Street, N.W., Suite 400
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/766,596A
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/630,645
;; FILING DATE: 10-APR-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/478,326
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: YUN, Allen C.
;; REGISTRATION NUMBER: 37,971
;; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-766-596A-1

Query Match 89.7%; Score 26; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 34
US-09-668-314C-73
;; Sequence 73, Application US/09668314C
;; Patent No. 684148
;; GENERAL INFORMATION:
;; APPLICANT: Guirney, et al
;; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;; TITLE OF INVENTION: THEREOF
;; FILE REFERENCE: 28341/6280NCP
;; CURRENT APPLICATION NUMBER: US/09/668,314C
;; CURRENT FILING DATE: 2000-09-22
;; PRIOR APPLICATION NUMBER: US 60/169,232
;; PRIOR FILING DATE: 1999-12-06
;; PRIOR APPLICATION NUMBER: US 09/416,901
;; PRIOR FILING DATE: 1999-10-13
;; PRIOR APPLICATION NUMBER: US 60/155,493
;; PRIOR FILING DATE: 1999-09-23
```

```
;; PRIOR APPLICATION NUMBER: US 09/404,133
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: PCT/US99/20881
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: US 60/101,594
;; PRIOR FILING DATE: 1998-09-24
;; NUMBER OF SEQ ID NOS: 84
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 73
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic peptide
US-09-668-314C-73

Query Match 89.7%; Score 26; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 35
PCT-US96-10220-1
;; Sequence 1, Application PC/TUS9610220
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
;; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
;; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEIMARK
;; STREET: 419 Seventh Street, N.W., Suite 400
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/10220
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/478,326
;; FILING DATE: 06-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/630,645
;; FILING DATE: 10-APR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
PCT-US96-10220-1

Query Match 89.7%; Score 26; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
```

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 36
US-08-766-596A-64
; Sequence 64, Application US/08766596A
; Patent No. 642171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-64

Query Match 89.7%; Score 26; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 37
US-09-747-408-20
; Sequence 20, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.

; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-20

Query Match 89.7%; Score 26; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 38
US-08-970-833-3
; Sequence 3, Application US/08970833
; Patent No. 6022859
; GENERAL INFORMATION:
; APPLICANT: Kiesel, Laura L.
; APPLICANT: Murphy, Regina M.
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,833
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 960296.94291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-970-833-3

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

```
RESULT 39
US-09-724-961-20
; Sequence 20, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-20
Query Match      89.7%   Score 26; DB 2; Length 10;
Best Local Similarity 83.3%   Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KVVFFA 6
    |:||||
Db  5 KLVFFA 10

RESULT 40
US-09-724-961-21
; Sequence 21, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-20
Query Match      89.7%   Score 26; DB 2; Length 10;
Best Local Similarity 83.3%   Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KVVFFA 6
    |:||||
Db  5 KLVFFA 10

RESULT 41
US-09-724-961-22
; Sequence 22, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-22
Query Match      89.7%   Score 26; DB 2; Length 10;
Best Local Similarity 83.3%   Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KVVFFA 6
    |:||||
Db  4 KLVFFA 9

RESULT 42
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
```

```
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-21
Query Match      89.7%   Score 26; DB 2; Length 10;
Best Local Similarity 83.3%   Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KVVFFA 6
    |:||||
Db  4 KLVFFA 9

RESULT 41
US-09-724-961-22
; Sequence 22, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-22
Query Match      89.7%   Score 26; DB 2; Length 10;
Best Local Similarity 83.3%   Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 KVVFFA 6
    |:||||
Db  3 KLVFFA 8

RESULT 42
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
```

```
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-724-961-23

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:|||||
Db      2 KLVFFA 7

RESULT 43
US-09-724-961-24
; Sequence 24, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-724-961-25
```

```
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-724-961-24

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:|||||
Db      1 KLVFFA 6

RESULT 44
US-09-580-018-20
; Sequence 20, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-580-018-20

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
      |:|||||
Db      5 KLVFFA 10

RESULT 45
US-09-580-018-21
; Sequence 21, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-580-018-21
```

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 46
US-09-580-018-22
; Sequence 22, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-22

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 47
US-09-580-018-23
; Sequence 23, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-23

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 48
US-09-580-018-24
; Sequence 24, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-24

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 49
US-09-724-551-20
; Sequence 20, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-20

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 50

US-09-724-551-21
; Sequence 21, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-21

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 51

US-09-724-551-22
; Sequence 22, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-22

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 52

US-09-724-551-23
; Sequence 23, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-23

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 53

US-09-724-551-24
; Sequence 24, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-24

Query Match 89.7%; Score 26; DB 2; Length 10;

Best Local Similarity 83.3%; Pred. No. 8.4; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1;

Qy 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 54

US-09-724-940-20
; Sequence 20, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-20

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 55

US-09-724-940-21
; Sequence 21, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-21

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 56

US-09-724-940-22
; Sequence 22, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-22

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 3 KLVFFA 8

```

RESULT 57
US-09-724-940-23
; Sequence 23, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-23

```

```

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KVVFFA 6
       |:|||||
DB      2 KLVFFA 7

```

```

RESULT 58
US-09-724-940-24
; Sequence 24, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1

```

```

; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-24

```

```

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KVVFFA 6
       |:|||||
DB      1 KLVFFA 6

```

```

RESULT 59
US-08-630-645-14
; Sequence 14, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,645
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-630-645-14

```

```

Query Match      89.7%; Score 26; DB 1; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KVVFFA 6
       |:|||||
DB      2 KLVFFA 7

```

RESULT 60
US-08-766-596A-14
; Sequence 14, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-14

Query Match 89.7%; Score 26; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 61
US-09-988-842-9
; Sequence 9, Application US/09988842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johanson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

Query Match 89.7%; Score 26; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 62
US-09-988-842-25
; Sequence 25, Application US/09988842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johanson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

Query Match 89.7%; Score 26; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 63
PCT-US96-10220-14
; Sequence 14, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

Query Match 89.7%; Score 26; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 62
US-09-988-842-25
; Sequence 25, Application US/09988842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johanson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

Query Match 89.7%; Score 26; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 63
PCT-US96-10220-14
; Sequence 14, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10220
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-10220-14

Query Match 89.7%; Score 26; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 64
US-09-594-366-5
Sequence 5, Application US/09594366
Patent No. 6582945
GENERAL INFORMATION:
APPLICANT: Raso, Victor
TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
FILE REFERENCE: BBRI-2004
CURRENT APPLICATION NUMBER: US/09/594,366
CURRENT FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/139,408
PRIOR FILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-594-366-5

Query Match 89.7%; Score 26; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 65
US-09-992-800-5
Sequence 5, Application US/09992800
Patent No. 6872554
GENERAL INFORMATION:

APPLICANT: Raso, Victor
TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
FILE REFERENCE: BBRI-2006
CURRENT APPLICATION NUMBER: US/09/992,800
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 09/594,366
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/139,408
PRIOR FILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-992-800-5

Query Match 89.7%; Score 26; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 66
US-08-612-785B-14
Sequence 14, Application US/08612785B
Patent No. 5854204
GENERAL INFORMATION:
APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal
US-08-612-785B-14

Query Match 89.7%; Score 26; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 67

US-08-612-785B-37
; Sequence 37, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: AD Peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-612-785B-37

Query Match 89.7%; Score 26; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 6 KLVFFA 11

RESULT 68

US-08-617-267C-14

; Sequence 14, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-617-267C-14

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 69

US-08-766-596A-56
; Sequence 56, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEROP FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.

COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-56

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 70
US-08-766-596A-57
; Sequence 57, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645

COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-57

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 71
US-08-766-596A-58
; Sequence 58, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-58

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 72

US-08-766-596A-60
; Sequence 60, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766.596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-60

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||

Db 5 KLVFFA 10

RESULT 73

US-08-766-596A-61
; Sequence 61, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766.596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-61

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 74

US-08-766-596A-62
; Sequence 62, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

```
;/ TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
;/ TITLE OF INVENTION: DEPOSITS
;/ NUMBER OF SEQUENCES: 69
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: BROWDY AND NEIMARK
;/ STREET: 419 Seventh Street, N.W., Suite 400
;/ CITY: Washington
;/ STATE: D.C.
;/ COUNTRY: USA
;/ ZIP: 20004
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/766,596A
;/ FILING DATE:
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/630,645
;/ FILING DATE: 10-APR-1996
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/478,326
;/ FILING DATE: 06-JUN-1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: YUN, Allen C.
;/ REGISTRATION NUMBER: 37,971
;/ REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-628-5197
;/ TELEFAX: 202-737-3528
;/ INFORMATION FOR SEQ ID NO: 62:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 15 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-766-596A-62

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 5 KVLFFA 10

RESULT 75
US-08-766-596A-63
; Sequence 63, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/766,596A
;/ FILING DATE:
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/630,645
;/ FILING DATE: 10-APR-1996
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/478,326
;/ FILING DATE: 06-JUN-1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: YUN, Allen C.
;/ REGISTRATION NUMBER: 37,971
;/ REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-628-5197
;/ TELEFAX: 202-737-3528
;/ INFORMATION FOR SEQ ID NO: 63:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 15 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-766-596A-63

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 5 KLVFFA 10

Search completed: December 29, 2005, 17:52:39
Job time : 21.1323 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds
(without alignments)
32.238 Million cell updates/sec

Title: US-10-009-122-17
Perfect score: 29
Sequence: 1 KVPFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : A_Geneseq_21: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *
9: Geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	4	AAB48482
2	29	100.0	6	4	AAB48490
3	29	100.0	6	4	AAB82630
4	29	100.0	6	4	AAB82638
5	29	100.0	6	5	AAB96818
6	29	100.0	6	5	AAB96826
7	29	100.0	6	5	AAU11664
8	29	100.0	6	5	AAU11656
9	29	100.0	6	6	AAE35452
10	29	100.0	6	8	ADQ37277
11	29	100.0	6	8	ADQ37321
12	29	100.0	6	8	ADQ37329
13	29	100.0	6	9	ADY37928
14	29	100.0	6	9	ADY37936
15	29	100.0	22	8	ADQ09761
16	29	100.0	23	8	ADQ09761
17	29	100.0	37	3	ABO55910
18	29	100.0	37	8	ADK34080
19	29	100.0	37	8	ADL70727
20	29	100.0	77	3	AAQ02840
21	29	100.0	175	4	AAQ11219
22	29	100.0	186	7	ADQ07962
23	29	100.0	186	7	ADQ07948
24	29	100.0	190	4	AAW83792

25	29	100.0	854	8	ADQ66704
26	29	100.0	922	8	ABM83252
27	29	100.0	925	7	ADF76335
28	29	100.0	925	7	ADF70225
29	29	100.0	925	8	ADJ75428
30	29	100.0	925	8	ADJ75495
31	29	100.0	925	8	ADN04860
32	29	100.0	925	8	ADR14233
33	29	100.0	925	8	ADP25011
34	29	100.0	925	8	ADR97294
35	29	100.0	925	9	ADY17516
36	29	100.0	925	9	AEA23525
37	29	100.0	1144	2	AAE77360
38	29	100.0	1144	2	AAW51246
39	29	100.0	1144	4	AAE64500
40	29	100.0	1144	6	ABU79138
41	29	100.0	1144	7	ADF43404
42	29	100.0	1144	7	ADP77432
43	29	100.0	1144	8	ADJ76212
44	29	100.0	1144	8	ADJ76136
45	29	100.0	1144	9	AEA03075
46	28	96.6	6	4	AAE48483
47	28	96.6	6	4	AAE48474
48	28	96.6	6	4	AAE82623
49	28	96.6	6	4	AAE82631
50	28	96.6	6	5	AAU96819
51	28	96.6	6	5	AAU96811
52	28	96.6	6	5	AAU11657
53	28	96.6	6	5	AAU11648
54	28	96.6	6	6	AAE35446
55	28	96.6	6	6	AAE35438
56	28	96.6	6	8	ADQ37322
57	28	96.6	6	8	ADQ37270
58	28	96.6	6	8	ADQ37313
59	28	96.6	6	8	ADQ37262
60	28	96.6	6	9	ADY37921
61	28	96.6	6	9	ADY37929
62	28	96.6	99	4	ABG26598
63	28	96.6	123	9	ABM94314
64	28	96.6	393	8	ADMI6726
65	28	96.6	393	8	ADMI6684
66	28	96.6	399	8	ADQ43456
67	27	93.1	564	4	ABE61977
68	27	93.1	1443	4	ABE68472
69	26	89.7	6	2	AAW02314
70	26	89.7	6	2	AAW89378
71	26	89.7	6	4	AAE48484
72	26	89.7	6	4	AAE48476
73	26	89.7	6	4	AAE82632
74	26	89.7	6	5	ABG71009
75	26	89.7	6	5	ABU05157
76	26	89.7	6	5	AAU96820
77	26	89.7	6	5	ABE83305
78	26	89.7	6	5	AAU11658
79	26	89.7	6	5	AAU11650
80	26	89.7	6	6	AAE35445
81	26	89.7	6	6	AAE35434
82	26	89.7	6	8	ADJ64060
83	26	89.7	6	8	ADQ37271
84	26	89.7	6	8	ADQ37315
85	26	89.7	6	8	ADQ37368
86	26	89.7	6	8	ADQ37269
87	26	89.7	6	8	ADQ37292
88	26	89.7	6	8	ADQ37258
89	26	89.7	6	8	ADQ37353
90	26	89.7	6	8	ADQ37323
91	26	89.7	6	9	ADY37930
92	26	89.7	6	9	ADY37948
93	26	89.7	6	9	ADY37947
94	26	89.7	6	9	AAE23039
95	26	89.7	7	2	AAE88300
96	26	89.7	7	2	AAE87921
97	26	89.7	7	2	AAW02312

Adq66704	Novel hum
Abm83252	Human dia
Adf76335	Novel hum
Adf70225	Human hea
Adj75428	Marker ge
Adj75495	Marker ge
Adn04860	Antipaori
Adr14233	Human NF-
Adp25011	PRO polyP
Adr97294	Human RIG
Ady17516	PRO polyP
Aea23525	Human PRO
Aar77360	Inducible
Aaw51246	Inducible
Aag64500	Mouse ind
Abu79138	Inducible
Adf43404	iNOS poly
Adf77432	Mouse ind
Adj76212	Marker ge
Adj76136	Marker ge
Aea03075	VEGF amin
Aab48483	Antifibri
Aab48474	Antifibri
Aab82623	Alli-D pep
Aab82631	Alli-D pep
Aau96819	Amyloid t
Aau96811	Amyloid t
Aau11657	Peptide #
Aau11648	Peptide #
Aae35446	Beta pep
Aae35438	Beta pep
Adq37322	Antifibri
Adq37270	Vaccine a
Adq37313	Antifibri
Adq37262	Vaccine a
Ady37921	Amyloid-t
Ady37929	Amyloid-t
Abg26598	Novel hum
Abm94314	M. xanthu
Admi6726	PERL-P7-G
Admi6684	PERL-P4-D6
Ado43456	Lutomyia
Abb61977	Drosophil
Abb68472	Drosophil
Aaw02314	Beta-amyl
Aaw89378	Beta-amyl
Aab48484	Antifibri
Aab48476	Antifibri
Abb82632	Alli-D pep
Abg71009	Long form
Abb05157	Beta amyl
Aau96820	Amyloid t
Abb83305	Amyloid-b
Aau11658	Peptide #
Aau11650	Peptide #
Aae35445	Abeta pep
Aae35434	Abeta pep
Adj64060	Human bet
Adq37271	Vaccine a
Adq37315	Antifibri
Adq37368	Beta-amyl
Adq37269	Vaccine a
Adq37292	Vaccine a
Adq37258	Vaccine a
Adq37353	Beta-amyl
Adq37323	Antifibri
Ady37930	Amyloid-t
Ady37948	Amyloid-t
Ady37947	Amyloid-t
Aea23039	Human bet
Aar88300	Non-amnes
Aar87921	Test pept
Aaw02312	Beta-amyl

98	26	89.7	7	2	AAW89376	Aaw89376 Beta-amyl	171	26	89.7	9	9	AEA51417	C-A 16-23
99	26	89.7	7	4	AAW67281	Aab67281 Residues	172	26	89.7	9	9	AEA62825	Immunocon
100	26	89.7	7	4	AAW48475	Aab48475 Antifibri	173	26	89.7	9	9	AEA62828	Immunocon
101	26	89.7	7	4	AAW48492	Aab48492 Antifibri	174	26	89.7	10	3	AAW79938	Beta-amyl
102	26	89.7	7	4	AAW48491	Aab48491 Antifibri	175	26	89.7	10	4	AAW46226	Human APP
103	26	89.7	7	4	AAW82624	Aab82624 All-D pep	176	26	89.7	10	4	AAW46225	Human APP
104	26	89.7	7	4	AAW82640	Aab82640 All-D pep	177	26	89.7	10	4	AAW46228	Human APP
105	26	89.7	7	4	AAW82639	Aab82639 All-D pep	178	26	89.7	10	4	AAW46224	Human APP
106	26	89.7	7	5	ABG71007	Abg71007 Long form	179	26	89.7	10	4	AAW46227	Human APP
107	26	89.7	7	5	ABW05155	Abw05155 Beta amyl	180	26	89.7	10	4	AAW82641	All-D pep
108	26	89.7	7	5	AAU96827	Aau96827 Amyloid t	181	26	89.7	10	5	AAU96829	Amyloid t
109	26	89.7	7	5	AAU96812	Aau96812 Amyloid t	182	26	89.7	10	6	ABP57511	Different
110	26	89.7	7	5	AAU96828	Aau96828 Amyloid t	183	26	89.7	10	6	AAW35455	Beta pep
111	26	89.7	7	5	ABW04920	Abw04920 Human amy	184	26	89.7	10	8	ADQ37280	Vaccine a
112	26	89.7	7	5	AAU11665	Aau11665 Peptide #	185	26	89.7	10	8	ADQ37371	Amyloid-b
113	26	89.7	7	5	AAU11649	Aau11649 Peptide #	186	26	89.7	10	8	ADQ37374	Amyloid-b
114	26	89.7	7	5	AAU11666	Aau11666 Peptide #	187	26	89.7	10	9	ADY37939	Amyloid-t
115	26	89.7	7	6	ABW82630	Abw82630 Beta fib	188	26	89.7	11	2	AAW32560	Anti-amyl
116	26	89.7	7	6	AAW35439	Aae35439 Beta pep	189	26	89.7	11	4	AAW52586	Peptide #
117	26	89.7	7	6	AAW35454	Aae35454 Beta pep	190	26	89.7	11	5	AAU99431	Human amy
118	26	89.7	7	6	AAW35453	Aae35453 Beta pep	191	26	89.7	11	5	AAE29504	Amyloid b
119	26	89.7	7	6	ADA90937	Ada90937 Solid-pha	192	26	89.7	11	6	ABU79013	Amyloidog
120	26	89.7	7	6	ADA90154	Ada90154 Anti-Abet	193	26	89.7	11	7	ABR84683	Aggrecana
121	26	89.7	7	7	ADW20746	Add20746 Human bet	194	26	89.7	11	7	ABW00147	Amyloid-b
122	26	89.7	7	7	ADF50855	Adf50855 Human cal	195	26	89.7	12	6	ABR91837	P. papata
123	26	89.7	7	8	ADW64058	Adw64058 Human bet	196	26	89.7	12	6	AAE35464	Beta pep
124	26	89.7	7	8	ADW64922	Adw64922 Beta-amyl	197	26	89.7	12	6	AAE35435	Beta pep
125	26	89.7	7	8	ADQ37278	Adq37278 Vaccine a	198	26	89.7	12	6	AAE35466	Beta pep
126	26	89.7	7	8	ADQ37314	Adq37314 Antifibri	199	26	89.7	12	7	ADW20745	Human bet
127	26	89.7	7	8	ADQ37263	Adq37263 Vaccine a	200	26	89.7	12	7	ADW20744	Human bet
128	26	89.7	7	8	ADQ37279	Adq37279 Vaccine a	201	26	89.7	12	8	ADJ71476	N-termina
129	26	89.7	7	8	ADQ37330	Adq37330 Antifibri	202	26	89.7	12	8	ADQ37407	Amyloid-b
130	26	89.7	7	8	ADQ37331	Adq37331 Antifibri	203	26	89.7	12	8	ADQ37289	Vaccine a
131	26	89.7	7	8	ADQ37351	Adq37351 Beta-amyl	204	26	89.7	12	8	ADQ37259	Vaccine a
132	26	89.7	7	9	ADY37922	Ady37922 Amyloid-t	205	26	89.7	12	9	ADZ08890	Human bet
133	26	89.7	7	9	ADY37938	Ady37938 Amyloid-t	206	26	89.7	12	9	ADZ08892	Human bet
134	26	89.7	7	9	ADY37937	Ady37937 Amyloid-t	207	26	89.7	13	6	AAE35465	Beta pep
135	26	89.7	7	9	ADZ08903	Adz08903 Human bet	208	26	89.7	13	6	AAE35467	Beta pep
136	26	89.7	8	2	AAW02310	Aaw02310 Beta-amyl	209	26	89.7	13	6	ADQ37467	Human amy
137	26	89.7	8	2	AAW45967	Aaw45967 Peptide d	210	26	89.7	13	6	ADJ71477	N-termina
138	26	89.7	8	2	AAW832551	Aaw32551 Amyloidog	211	26	89.7	13	8	ADJ71464	N-termina
139	26	89.7	8	2	AAW89374	Aaw89374 Beta-amyl	212	26	89.7	13	8	ADQ37408	Amyloid-b
140	26	89.7	8	4	AAE10663	Aae10663 Human amy	213	26	89.7	13	8	ADQ37290	Vaccine a
141	26	89.7	8	4	AAE02615	Aae02615 Human amy	214	26	89.7	14	6	ADA89887	Beta-A4 s
142	26	89.7	8	5	ABG71005	Abg71005 Long form	215	26	89.7	14	8	ADJ71452	N-termina
143	26	89.7	8	5	ABW78624	Abw78624 Human alp	216	26	89.7	14	8	ADJ71465	N-termina
144	26	89.7	8	5	ABW05153	Abw05153 Beta amyl	217	26	89.7	14	8	ADJ71478	N-termina
145	26	89.7	8	6	ABW09765	Abw09765 Amyloidog	218	26	89.7	14	9	ADZ08889	Human bet
146	26	89.7	8	6	ABW61959	Abw61959 Human amy	219	26	89.7	15	2	AAW02334	Beta-amyl
147	26	89.7	8	7	ABW00134	Abw00134 Beta-amyl	220	26	89.7	15	2	AAW89358	Beta-amyl
148	26	89.7	8	8	ADW64056	Adw64056 Human bet	221	26	89.7	15	2	AAW89354	Beta-amyl
149	26	89.7	8	8	ADQ37385	Adq37385 Antifibri	222	26	89.7	15	5	ABG71014	Long form
150	26	89.7	8	8	ADQ37349	Adq37349 Beta-amyl	223	26	89.7	15	5	ABW05162	Beta amyl
151	26	89.7	8	9	ADZ08900	Adz08900 Human bet	224	26	89.7	15	5	ABW05162	Beta amyl
152	26	89.7	8	9	AEA51423	Aea51423 C-Abeta 1	225	26	89.7	15	6	ABU79057	Human bet
153	26	89.7	8	9	AEA51420	Aea51420 A 16-22-C	226	26	89.7	15	6	ABU79057	Aggregati
154	26	89.7	8	9	AEA62831	Aea62831 Immunocon	227	26	89.7	15	6	ABU79054	Aggregati
155	26	89.7	8	9	AEA62834	Aea62834 Immunocon	228	26	89.7	15	6	ABU79056	Aggregati
156	26	89.7	8	9	AAW45239	Aaw45239 Mutant am	229	26	89.7	15	6	ABU79055	Aggregati
157	26	89.7	9	4	AAW48493	Aab48493 Antifibri	230	26	89.7	15	6	ABU79056	Aggregati
158	26	89.7	9	5	ABP57517	Aap57517 Peptide #	231	26	89.7	15	6	ABU79061	Aggregati
159	26	89.7	9	6	ABW79063	Abw79063 Aggregati	232	26	89.7	15	6	ABU79061	Aggregati
160	26	89.7	9	6	AAW79063	Aaw79063 Aggregati	233	26	89.7	15	7	ABW00190	Peptide #
161	26	89.7	9	6	AAW35436	Aae35436 Beta pep	234	26	89.7	15	7	ABW00198	Peptide #
162	26	89.7	9	7	ABW00197	Abw00197 Peptide #	235	26	89.7	15	7	ABW00189	Peptide #
163	26	89.7	9	8	ADJ36003	Adj36003 Amyloid b	236	26	89.7	15	7	ABW00193	Peptide #
164	26	89.7	9	8	ADJ35849	Adj35849 Amyloid b	237	26	89.7	15	7	ABW00191	Peptide #
165	26	89.7	9	8	ADJ35874	Adj35874 Amyloid b	238	26	89.7	15	7	ABW00196	Peptide #
166	26	89.7	9	8	ADJ35871	Adj35871 Amyloid b	239	26	89.7	15	7	ABW00195	Peptide #
167	26	89.7	9	8	ADJ35903	Adj35903 Amyloid b	240	26	89.7	15	7	ABW00194	Peptide #
168	26	89.7	9	8	ADQ37260	Adq37260 Vaccine a	241	26	89.7	15	7	ADK82695	Beta-amyl
169	26	89.7	9	8	ADQ37332	Adq37332 Antifibri	242	26	89.7	15	7	ADK82697	Beta-amyl
170	26	89.7	9	9	AEA51414	Aea51414 A 16-23-C	243	26	89.7	15	7	ADK82700	Beta-amyl

PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.

XX Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use in
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis, and
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 Db 1 KVVFFA 6

RESULT 5
 AAU96818
 ID AAU96818 standard; peptide; 6 AA.

XX AAU96818;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #8.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..6 /note= "Preferably D-form residue"

XX WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX

PR 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 PT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A t-(A l n k) z-A l a b (l) where z = 0 - 1;
 CC A t = an amyloid targeting moiety; A l n k = a linker moiety; and A l a b
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (I) to the patient, and ultrasound imaging (I) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 Db 1 KVVFFA 6

RESULT 6

AAU96826
 ID AAU96826 standard; peptide; 6 AA.

XX AAU96826;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #16.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..6

```

FT Modified-site /note= "Preferably D-form residue"
FT 6
XX /note= "Ala is amidated"
XX 6
PN WO200207781-A2.
XX
PD 31-JAN-2002.
XX
PF 25-JUL-2001; 2001WO-CA001071.
XX
PR 25-JUL-2000; 2000US-0220808P.
XX
PR 24-JUL-2001; 2001US-00915092.
XX
XX (NEUR-) NEUROCHEM INC.
PA
XX Gervais F, Kong X, Chalifour R, Migneault D;
XX WPI; 2002-371447/40.
XX
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
XX plaques and/or for the treatment of amyloidosis disorders.
XX
XX Claim 49; Page 21; 57pp; English.
XX
XX The invention relates to an amyloid-targeting imaging agent comprising an
XX amyloid targeting moiety, a linker moiety and a labelling moiety. The
XX agent is of general formula A1-L1-N1-K1-Z-A1 where z = 0 - 1;
XX A1 is an amyloid targeting moiety; L1-N1-K1 is a linker moiety; and A1-L1-N1-K1
XX is a labelling moiety. Also included are imaging amyloid deposition or
XX diagnosing an amyloid-related condition in a patient involving
XX administering (i) to the patient, and ultrasound imaging (i) in the
XX patient to determine the presence of amyloid or amyloid-related condition
XX ; and a kit for preparing a radiopharmaceutical preparation comprising
XX (i), a reducing agent, a buffering agent, a transchelating agent, and
XX instructions for the preparation and use of the radiopharmaceutical in
XX the imaging of amyloid or an amyloid-related condition. The agents are
XX used for imaging amyloid deposition and for diagnosing an amyloid related
XX condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
XX cerebral amyloidosis (transmissible virus dementias), familial CJD,
XX scrapie, transmissible mink encephalopathy, bovine spongiform
XX encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
XX prionic amyloidosis, feline spongiform encephalopathy, non-transmissible
XX cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
XX dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
XX amyloid angiopathy. The agents are capable of crossing the blood-brain
XX barrier and are capable of binding specifically to amyloid plaques. The
XX present sequence is a peptide forming the amyloid targeting moiety of the
XX agent of the invention
XX
XX Sequence 6 AA;
XX
XX Query Match 100.0%; Score 29; DB 5; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KVVFFA 6
XX |||||
XX Db 1 KVVFFA 6
XX
XX RESULT 8
XX AAU11656
XX ID AAU11656 standard; peptide; 6 AA.
XX
XX AC AAU11656;
XX
XX DT 09-APR-2002 (first entry)
XX
XX DE Peptide #9, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
XX OS Synthetic.
XX
XX PN WO200185093-A2.
XX
XX PD 15-NOV-2001.
XX
XX PF 22-DEC-2000; 2000WO-IB002078.
XX
XX PR 23-DEC-1999; 99US-0171877P.
XX
XX PA (NEUR-) NEUROCHEM INC.
XX
XX PI Green AM, Gervais F;
XX
XX DR WPI; 2002-075222/10.
XX
XX PT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
XX PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
XX PT inhibitor.
XX
XX PS Disclosure; Page 10; 68pp; English.
XX
XX CC The present invention relates to a new method of inhibiting cerebral
XX CC amyloid angiopathy. The new method of the invention involves contacting a
XX CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
XX CC can be used for treating disease states characterised by cerebral amyloid
XX CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
XX CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
XX CC The present sequence represents one of a group of peptides (AAU11648-
XX CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
XX CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
XX CC was used in the invention to treat a disease state characterised by
XX CC cerebral amyloid angiopathy (CAA)
XX
XX SQ Sequence 6 AA;
XX
XX Query Match 100.0%; Score 29; DB 5; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KVVFFA 6
XX |||||
XX Db 1 KVVFFA 6
XX
XX RESULT 8
XX AAU11656
XX ID AAU11656 standard; peptide; 6 AA.
XX
XX AC AAU11656;
XX
XX DT 09-APR-2002 (first entry)
XX
XX DE Peptide #9, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
XX OS Synthetic.
XX
XX PN WO200185093-A2.
XX
XX PD 15-NOV-2001.
XX
XX PF 22-DEC-2000; 2000WO-IB002078.
XX
XX PR 23-DEC-1999; 99US-0171877P.
XX

```

```

XX (NEUR-) NEUROCHEM INC.
XX Green AM, Gervais F;
XX WPI; 2002-075222/10.
XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
XX disease comprises contacting blood vessel wall cell with amyloid-beta 40
XX inhibitor.
XX Disclosure; Page 10; 68pp; English.
XX The present invention relates to a new method of inhibiting cerebral
XX amyloid angiopathy. The new method of the invention involves contacting a
XX blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
XX can be used for treating disease states characterised by cerebral amyloid
XX angiopathy, particularly Alzheimer's disease, hereditary cerebral
XX haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
XX The present sequence represents one of a group of peptides (AAU11648-
XX AAU11669, AAU11910 & AAU11911) that were used in the invention as a
XX carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
XX was used in the invention to treat a disease state characterised by
XX cerebral amyloid angiopathy (CAA)
XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVVFFFA 6
Db 1 KVVFFFA 6
|||||
1 KVVFFFA 6

RESULT 9
AAE35452
ID AAE35452 standard; peptide; 6 AA.
AC AAE35452;
DT 17-JUN-2003 (first entry)
DE Abeta peptide #23.
KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
XX Unidentified.
OS
FH Key Location/Qualifiers
FT Misc-difference 1. .6 /note= "D-form residues"
FT Modified-site 6 /note= "C-terminal amide"
FT WO200296937-A2.
PN
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-CA000763.
XX
PR 29-MAY-2001; 2001US-00867847.
XX
PA (NEUR-) NEUROCHEM INC.
XX
PI Gervais F, Hebert L, Chalifour RJ, Kong X;

```

```

XX WPI; 2003-201269/19.
XX Prevention and/or treatment of an amyloid-related disease e.g.
XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
XX Claim 1; Page 59; 44pp; English.
XX The invention relates to a method for prevention and/or treatment of an
XX amyloid-related disease which comprises administration of an all-D -
XX amyloid-beta peptide. The method is used for preventing and/or treating
XX Alzheimer's and other amyloid related disease e.g. cerebral amyloid
XX angiopathy; for altering serum levels of amyloid-beta in a mammal and
XX favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
XX the mammal; and reducing or inhibiting the formation of plaques. It is
XX also used for treating AA (reactive) amyloid diseases including
XX inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
XX arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
XX Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
XX disease. AA deposits are also produced as a result of chronic microbial
XX infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
XX ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
XX Certain malignant neoplasms can also result in AA fibril amyloid deposits
XX including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
XX and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
XX present sequence is an Abeta peptide used to illustrate the method of the
XX invention
XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 29; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVVFFFA 6
Db 1 KVVFFFA 6
|||||
1 KVVFFFA 6

RESULT 10
ADQ37277
ID ADQ37277 standard; peptide; 6 AA.
AC ADQ37277;
XX
DT 07-OCT-2004 (first entry)
DE Vaccine antigen amyloid-beta related amino acid sequence.
DE amyloid-beta; amyloid-beta related disease;
KW amyloid-beta fibril formation; immune response; nontropic;
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
KW antichryoid; vasotropic; cardiovascular; tranquilliser; uropathic;
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
KW cardiant; antidepressant; endocrine; hypnotic;
KW amyloid-beta fibril formation modulator; immune system modulator;
KW Alzheimer's disease; mild cognitive impairment;
KW mild-to-moderate cognitive impairment; vascular dementia;
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
KW senile dementia; Down's syndrome; inclusion body myositis;
KW age-related macular degeneration; hypothyroidism;
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
KW behavioural dysfunction; neurological condition; psychological condition;
KW vaccine antigen.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 1. .6 /note= "D-form residues"
FT Modified-site 6 /note= "amidated"
FT
XX

```

PN	WO2004058239-A1.	ID	ADQ37321 standard; peptide; 6 AA.
XX	15-JUL-2004.	XX	ADQ37321;
XX		XX	
XX	24-DEC-2003; 2003WO-CA002021.	DT	07-OCT-2004 (first entry)
XX		XX	
PR	24-DEC-2002; 2002US-0436379P.	DE	Antifibrillogenic amyloidosis inhibiting peptide.
PR	23-JUN-2003; 2003US-0482214P.	XX	
XX	(NEUR-) NEUROCHEM INT LTD.	XX	
PA		XX	amyloid-beta; amyloid-beta related disease;
XX	Gervais F, Bellini F;	KW	amyloid-beta fibril formation; immune response; nootropic;
XX		KW	neuroprotective; cerebroprotective; haemostatic; ophthalmological;
XX		KW	antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
XX		KW	anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
XX		KW	cardiant; antidepressant; endocrine; hypnotic;
XX		KW	amyloid-beta fibril formation modulator; immune system modulator;
XX		KW	Alzheimer's disease; mild cognitive impairment;
XX		KW	mild-to-moderate cognitive impairment; vascular dementia;
XX		KW	cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
XX		KW	senile dementia; Down's syndrome; inclusion body myositis;
XX		KW	age-related macular degeneration; hypothyroidism;
XX		KW	cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
XX		KW	behavioural dysfunction; neurological condition; psychological condition;
XX		KW	vaccine antigen.
XX		OS	Synthetic.
XX		PN	WO2004058239-A1.
XX		XX	15-JUL-2004.
XX		XX	
XX		XX	24-DEC-2003; 2003WO-CA002021.
XX		XX	
XX		XX	24-DEC-2002; 2002US-0436379P.
XX		XX	23-JUN-2003; 2003US-0482214P.
XX		XX	(NEUR-) NEUROCHEM INT LTD.
XX		XX	Gervais F, Bellini F;
XX		XX	WPI; 2004-543342/52.
XX		XX	
XX		XX	Composition for treating e.g. Alzheimer's disease comprises first agent
XX		XX	that prevents or treats amyloid-beta related disease and second agent
XX		XX	that is either a peptide or peptidomimetic or an immune system modulator.
XX		XX	Disclosure; Page 67; 143pp; English.
XX		XX	The present invention describes compositions (C) comprising: (a) a first
XX		XX	agent (a1) that prevents or treats amyloid-beta related disease; and (b)
XX		XX	a second agent (a2) that is: (i) a peptide or peptidomimetic that
XX		XX	modulates amyloid-beta fibril formation or induces a prophylactic or
XX		XX	therapeutic immune response against amyloid-beta fibril formation; or
XX		XX	(ii) an immune system modulator that prevents or inhibits amyloid-beta
XX		XX	fibril formation. Also described is a kit comprising (C). (C) have
XX		XX	nootropic, neuroprotective, cerebroprotective, haemostatic,
XX		XX	ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
XX		XX	uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
XX		XX	neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
XX		XX	and can be used as amyloid-beta fibril formation modulators, and as
XX		XX	immune system modulators. (C) can be used for preventing or treating an
XX		XX	amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
XX		XX	(non-hereditary) or familial (hereditary)), mild cognitive impairment,
XX		XX	mild-to-moderate cognitive impairment, vascular dementia, cerebral
XX		XX	Down's syndrome, inclusion body myositis, age-related macular
XX		XX	degeneration, or a condition associated with Alzheimer's disease
XX		XX	(including hypothyroidism, cerebrovascular disease, cardiovascular
XX		XX	disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
XX		XX	aggression, or incontinence), a neurological condition (e.g. Huntington's
XX		XX	disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
XX		XX	Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
XX		XX	with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
XX		XX	field deficits, incoordination, gait disturbance, transient ischaemic
XX		XX	attack or stroke, transient alertness, attention deficit, frequent falls,
XX		XX	syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
XX		XX	haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
XX		XX	damage), or a psychological condition (e.g. depression, delusions,
XX		XX	illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
XX		XX	disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
XX		XX	ideation, depressed mood, irritability, anhedonia, social withdrawal, or
XX		XX	excessive guilt)) in a subject e.g. human having a genomic mutation in an
XX		XX	amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
XX		XX	having amyloid-beta deposits. The present sequence represents a peptide
XX		XX	that can be used as a vaccine antigen in the exemplification of the
XX		XX	present invention.
XX		XX	
SQ	Sequence 6 AA;		
	Query Match 100.0%; Score 29; DB 8; Length 6;		
	Best Local Similarity 100.0%; Pred. No. 2e+06;		
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1 KVVFFA 6		
Db	1 KVVFFA 6		
RESULT 11			
ADQ37321			

CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |||||
 Db 1 KVVFFA 6

RESULT 12

ADQ37329
 ID ADQ37329 standard; peptide; 6 AA.

AC ADQ37329;

DT 07-OCT-2004 (first entry)

DE Antifibrillogenic amyloidosis inhibiting peptide.

XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW antiprotective; cerebroprotective; haemostatic; ophthalmological;
 KW neurotrophic; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiac; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.

OS Synthetic.

FT Key Location/Qualifiers
 FT Modified-site 6 /note= "amidated"

PN WO2004058239-A1.

PD 15-JUL-2004.

PF 24-DEC-2003; 2003WO-CA002021.

PR 24-DEC-2002; 2002US-0436379P.

PR 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

PA Gervais F, Bellini F;

PI WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent
 FT that prevents or treats amyloid-beta related disease and second agent

PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 PS Disclosure; Page 70; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiac, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |||||
 Db 1 KVVFFA 6

RESULT 13

ADY37928

ID ADY37928 standard; peptide; 6 AA.

AC ADY37928;

XX 19-MAY-2005 (first entry)

DT Amyloid-targeting peptide, SEQ ID NO:8, for use in imaging agent.

DE Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;

XX transmissible spongiform encephalopathy; scrapie; BSE;

XX Alzheimer's disease; neurological disease; amyloidosis;

XX non-insulin dependent diabetes; metabolic disorder.

OS Synthetic.

PN US2005048000-A1.

XX

PD 03-MAR-2005.
 XX
 PF 03-DEC-2003; 2003US-00728028.
 XX
 PR 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.
 PR 29-JAN-2003; 2003US-0443291P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 XX
 XX Gervais F, Kong X, Chalifour R, Migneault D;
 XX WPI; 2005-212201/22.
 XX
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
 PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.
 XX
 XX Disclosure; SEQ ID NO 8; 34pp; English.
 XX
 CC The invention relates to an amyloid-targeting imaging agent. The imaging
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
 CC a labeling moiety via a linking moiety, and is preferably able to cross
 CC the blood-brain barrier. The invention also relates to a kit for
 CC preparing a radiopharmaceutical preparation from the imaging agent of the
 CC invention, a method for imaging amyloid deposition in a patient and a
 CC method for diagnosing an amyloid-related condition in a patient. The
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
 CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
 CC transmissible cerebral amyloidoses (also known as transmissible virus
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
 CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
 CC mediated diseases, dialysis-related amyloidosis, light chain-related
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
 CC patient. The agent does not exhibit excessive toxicity or irritation,
 CC does not induce an allergic response, and permits an earlier diagnosis of
 CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 1 KVVFFA 6
 RESULT 14
 ID ADY37936
 XX
 AC ADY37936;
 XX
 DT 19-MAY-2005 (first entry)
 XX
 DE Amyloid-targeting peptide, SEQ ID NO:16, for use in imaging agent.
 XX
 KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
 KW transmissible spongiform encephalopathy; scrapie; BSE;
 KW Alzheimers disease; neurological disease; amyloidosis;
 KW non-insulin dependent diabetes; metabolic disorder.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 6
 FT

FT
 XX
 PN US2005048000-A1.
 XX
 PD 03-MAR-2005.
 XX
 PF 03-DEC-2003; 2003US-00728028.
 XX
 PR 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.
 PR 29-JAN-2003; 2003US-0443291P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 XX
 XX Gervais F, Kong X, Chalifour R, Migneault D;
 XX WPI; 2005-212201/22.
 XX
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
 PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.
 XX
 XX Disclosure; SEQ ID NO 16; 34pp; English.
 XX
 CC The invention relates to an amyloid-targeting imaging agent. The imaging
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
 CC a labeling moiety via a linking moiety, and is preferably able to cross
 CC the blood-brain barrier. The invention also relates to a kit for
 CC preparing a radiopharmaceutical preparation from the imaging agent of the
 CC invention, a method for imaging amyloid deposition in a patient and a
 CC method for diagnosing an amyloid-related condition in a patient. The
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
 CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
 CC transmissible cerebral amyloidoses (also known as transmissible virus
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
 CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
 CC mediated diseases, dialysis-related amyloidosis, light chain-related
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
 CC patient. The agent does not exhibit excessive toxicity or irritation,
 CC does not induce an allergic response, and permits an earlier diagnosis of
 CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 1 KVVFFA 6
 RESULT 15
 ID ADQ09761
 XX
 AC ADQ09761;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Rice 26kDa globulin signal sequence SEQ ID NO:117.
 XX
 KW prolamine; rice; plant; seed; transgenic plant; signal.
 XX
 OS Oryza sativa.
 XX
 FN WO2004056993-A1.

/note= "C-terminal amide"

XX PD 08-JUL-2004.
 XX PF 09-DEC-2003; 2003WO-JP015753.
 XX PR 20-DEC-2002; 2002JP-00369700.
 XX PA (NAG-) NAT AGRIC & BIO-ORIENTED RES ORG.
 XX PI Kuroda M;
 XX DR WPI; 2004-525439/50.
 XX DR N-ESDB; ADQ09760.
 XX
 PT Novel nucleic acid molecule antisense to nucleic acid sequence encoding
 PT prolamine, useful for reducing expression dose of protein in seed, and
 PT for producing transgenic plant, preferably rice plant having reduced
 PT storage protein.
 XX
 FS Example 13; SEQ ID NO 117; 272pp; Japanese.
 XX
 CC The present invention describes a nucleic acid molecule (I) comprising a
 CC consecutive nucleic acid sequence (S1) of at least 15 bp in length and
 CC complementary with a nucleic acid sequence encoding a prolamine
 CC polypeptide or a nucleic acid sequence having a homology of at least
 CC about 70% to (S1). Also described: (1) a nucleic acid molecule (N1)
 CC comprising a nucleic acid sequence (A) having about 70% homology to a
 CC nucleic acid sequence encoding a prolamine polypeptide and a nucleic acid
 CC sequence (B) having about 70% homology to the complement of the nucleic
 CC acid sequence encoding a prolamine polypeptide; (2) a factor (II) capable
 CC of causing RNA interference of the gene sequence encoding a prolamine
 CC polypeptide; (3) a nucleic acid cassette (III) containing (1); (4)
 CC producing (III); (5) a vector (IV) comprising (1); (6) a plant cell (V)
 CC containing (1); (7) a plant tissue (VI) comprising (V); (8) a plant (VII)
 CC comprising (1) or (V); (9) a seed (VIII) produced by (VII); (10) starch
 CC preparation produced from (VII) or (VIII); and (11) a composition
 CC containing gene product of foreign gene produced from (VII) or (VIII).
 CC (I) is useful for decreasing the expression level of a protein in the
 CC seed of a plant, for expressing a foreign gene in the seed of a plant and
 CC for decreasing the expression of a natural protein in the seed of a
 CC plant. The method of decreasing the amount of expression level of a
 CC protein in the seed of a plant involves providing (I), introducing (I)
 CC into the cell of the plant, redifferentiating the cell, producing a
 CC transgenic plant, and obtaining the seed from the transgenic plant. The
 CC method after the step of introduction, further involves selecting the
 CC cell introduced with (I), by determining resistance with respect to
 CC antibiotics. The method of expressing a foreign gene in the seed of a
 CC plant, involves providing (I) and the nucleic acid molecule encoding a
 CC foreign gene product, introducing (I) and the nucleic acid molecule
 CC encoding a foreign gene product into cell of the plant, re-
 CC differentiating the cell, producing a transgenic plant, and obtaining the
 CC seed from the transgenic plant. The method further involves isolating the
 CC gene product of the foreign gene from the seed. (I) is useful for
 CC producing transgenic plants having reduced expression of storage proteins
 CC and for reducing the expression dose of a protein in a seed of a plant.
 CC The present sequence represents a rice 26kDa globulin signal sequence,
 XX which is used in the exemplification of the present invention.

Sequence 22 AA;

Query Match 100.0%; Score 29; DB 8; Length 22;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |||||
 Db 4 KVVFFA 9

RESULT 16

ADT93984

ID ADT93984 standard; peptide; 23 AA.

XX

AC ADT93984;
 XX 27-JAN-2005 (first entry)
 XX Rice 26 kDa peptide.
 XX
 KW Storage protein; allergen specific T cell epitope;
 KW vesicle anchoring signal; transgenic plant; rice albumen;
 KW T cell epitope-attached peptide; 7crp; seed; glutenin; edible vaccine;
 KW Japanese cedar pollen antigen; Cry11; Cry12; allergic disease; hay fever;
 KW antiallergic; plant; 26 kDa.
 XX
 OS Oryza sativa.
 XX
 XX WO2004094637-A1.
 XX
 XX 04-NOV-2004.
 XX
 XX 23-APR-2004; 2004WO-JP005938.
 XX
 XX 24-APR-2003; 2003JP-00120639.
 XX
 XX (NORQ) NAT INST AGROBIOLOGICAL SCI.
 XX
 XX Takaiwa F, Takagi H;
 XX
 XX WPI; 2004-784905/77.
 XX
 PT Novel DNA having sequence encoding allergen specific T-cell epitope
 PT peptide, useful for accumulating T-cell epitope peptide in plants and for
 PT treating allergic diseases such as pollinosis.
 XX
 XX Disclosure; SEQ ID NO 5; 79pp; Japanese.
 XX
 CC This invention relates to a DNA (I) having a sequence under the control
 CC of a storage protein promoter, chosen from a sequence encoding storage
 CC protein signal sequence at the 5' end of a sequence encoding allergen
 CC specific T cell epitope peptide and/or a sequence encoding vesicle
 CC anchoring signal sequence at the 3' end, and a DNA sequence encoding a
 CC polypeptide having allergen specific T-cell epitope peptide inserted in
 CC the variable region of a storage protein. Also disclosed is a vector (II)
 CC for T-cell epitope accumulated plant preparation, and a method of
 CC accumulating allergen specific T-cell epitope in a plant. The method
 CC involves introducing (I) or (II) to a plant, obtaining DNA encoding
 CC allergen specific T-cell epitope peptide, adding a DNA encoding a storage
 CC protein signal sequence to the 5' end and/or a vesicle anchoring signal
 CC sequence to the 3' end of the obtained DNA, and expressing the DNA in a
 CC plant under the control of a storage protein promoter, or obtaining DNA
 CC encoding allergen specific T-cell epitope peptide, inserting a DNA into
 CC the variable region of storage protein of the plant and expressing the
 CC peptide in the transgenic plant. The invention describes the accumulation
 CC of human T cell epitope in rice albumen, a method of accumulating T cell
 CC epitope-attached peptide (7crp) in seeds, a method of inserting the 7crp
 CC into the variable region of glutenin (the major storage protein of rice),
 CC and expressing and accumulating 7crp as part of the glutenin. The rice
 CC capable of producing the 7crp is useful as an edible vaccine against
 CC Japanese (Cryptomeria japonica) cedar pollen antigen. The pollen allergen
 CC is Cry11 or Cry12. The T-cell epitope is integrated on an edible region
 CC such as the seed of a plant. The method of the invention is useful for
 CC producing a plant accumulated with allergen specific T-cell epitope, and
 CC manufacturing a transgenic plant, preferably rice, integrated with T-cell
 CC epitope. The method is useful for preventing or treating allergic disease
 CC such as hay fever. The method enables the production of allergen specific
 CC T-cell epitope at a low cost and also reduces the amount for
 CC administration. The allergen specific T-cell epitope accumulated in a
 CC seed is stable for storage. This sequence represents rice 26 kDa peptide.
 XX
 SQ Sequence 23 AA;

Query Match

100.0%; Score 29; DB 8; Length 23;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 Db 4 KVVFFA 9

RESULT 17
 AAB05910
 ID AAB05910 standard; peptide; 37 AA.
 XX
 AC AAB05910;
 XX
 DT 16-OCT-2000 (first entry)
 XX
 DE Mouse inducible nitric oxide synthase calmodulin-binding region.
 XX
 KW Mouse; inducible nitric oxide synthase; iNOS;
 KW endothelial nitric oxide synthase; eNOS; vasotropic; hypertensive;
 KW AMP-activated protein kinase; AMPK; calmodulin; CaM;
 KW eNOS phosphorylation; ischaemic heart disease; pulmonary hypertension;
 KW obstructive airways disease.
 XX
 OS Mus sp.
 XX
 PN WO200028076-A1.
 XX
 PD 18-MAY-2000.
 XX
 PF 05-NOV-1999; 99WO-AU000968.
 XX
 PR 06-NOV-1998; 98AU-00006976.
 XX
 PA (SVIN-) ST VINCENTS INST MEDICAL RES.
 XX
 PI Stapleton DJ, Chen Z, Michell BJ, Kemp BE, Mitchellhill KI;
 XX
 DR WPI; 2000-376583/32.
 XX
 PT Identifying modulators of AMP-activated protein kinase-mediated
 PT activation of a nitric oxide synthase (NOS), for use in ischemic heart
 PT disease, comprises testing for the increase or decrease in
 PT phosphorylation of NOS.
 XX
 PS Example 4; Fig 5; 4lpp; English.
 XX
 CC The present sequence is the calmodulin (CaM)-binding region of mouse
 CC inducible nitric oxide synthase (iNOS). iNOS is one of three isoforms of
 CC the enzyme NOS, which synthesises nitric oxide from the amino acid L-
 CC arginine. The sequence is provided for comparison with endothelial nitric
 CC oxide synthase (eNOS). The threonine residue at position 495 of eNOS is
 CC phosphorylated by AMP-activated protein kinase (AMPK) in the absence of
 CC Ca2+-CaM. Phosphorylation results in inhibition of eNOS. In the presence
 CC of Ca2+-CaM, phosphorylation by AMPK occurs predominantly at Ser-1177 and
 CC eNOS is activated. Modulators which activate AMPK may be used in the
 CC treatment of ischaemic heart disease by promoting glucose and fatty acid
 CC metabolism, and improving nutrient and oxygen supply to the myocytes.
 CC They may also be used for the treatment of pulmonary hypertension and
 CC obstructive airways disease
 XX
 SQ Sequence 37 AA;
 Query Match 100.0%; Score 29; DB 3; Length 37;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 Db 18 KVVFFA 23

RESULT 18
 ADK34080
 ID ADK34080 standard; peptide; 37 AA.
 XX

AC ADK34080;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human nNOS calmodulin binding domain peptide seqid 7.
 XX
 KW vasotropic; antiangiogenic; gene therapy; critical limb ischaemia; CLI;
 KW eNOS; endothelial nitric oxide synthase; angiogenesis;
 KW microvascular dysfunction; human; calmodulin binding domain;
 KW neuronal nitric oxide; nNOS.
 XX
 OS Homo sapiens.
 XX
 PN WO2004016761-A2.
 XX
 PD 26-FEB-2004.
 XX
 PF 15-AUG-2003; 2003WO-US025626.
 PP
 PR 16-AUG-2002; 2002US-0403637P.
 XX
 PA (SCHD) SCHERING AG.
 XX
 PI Dole WP, Kauser K, Qian HS, Rubanyi G;
 XX
 DR WPI; 2004-203789/19.
 XX
 PT Treating critical limb ischemia (CLI), or angiogenesis comprises
 PT administering to a patient a polynucleotide encoding a mammalian
 PT endothelial nitric oxide synthase (eNOS) polypeptide.
 XX
 PS Example 1; SEQ ID NO 7; 82pp; English.
 XX
 CC The invention describes a method of creating critical limb ischaemia
 CC (CLI) comprising administering to a patient a polynucleotide encoding a
 CC mammalian eNOS (endothelial nitric oxide synthase) polypeptide. Also
 CC described are: a method for treating angiogenesis by administering to a
 CC patient a polynucleotide encoding eNOS; and ameliorating microvascular
 CC dysfunction by administering to the patient the polynucleotide encoding
 CC the eNOS polypeptide. The method is useful for treating critical limb
 CC ischaemia or angiogenesis, or ameliorating a microvascular dysfunction.
 CC This is the amino acid sequence of a human neuronal nitric synthase
 CC (nNOS) calmodulin binding domain peptide.
 XX
 SQ Sequence 37 AA;
 Query Match 100.0%; Score 29; DB 8; Length 37;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 Db 18 KVVFFA 23

RESULT 19
 ADL70727
 ID ADL70727 standard; peptide; 37 AA.
 XX
 AC ADL70727;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Mouse iNOS calmodulin-binding site amino acid sequence SEQ ID NO:7.
 XX
 KW mouse; endothelial nitric oxide synthase; eNOS; enzyme; mutant;
 KW calmodulin-binding domain; vasotropic; antiarteriosclerotic; hypotensive;
 KW antidiabetic; vulnerary; antilipaeamic; anorectic;
 KW reduced calcium dependence; ischaemia; atherosclerosis; hypertension;
 KW diabetes; Raynaud's phenomenon; poor wound healing; hyperlipidaemia;
 KW obesity; iNOS.
 XX
 OS Mus musculus.

XX PN WO2004016764-A2.
 XX XX
 XX PD 26-FEB-2004.
 XX XX
 XX PP 15-AUG-2003; 2003WO-US025745.
 XX XX
 XX PR 16-AUG-2002; 2002US-0403638P.
 XX XX
 XX PA (SCHD) SCHERING AG.
 XX XX
 XX PI Blasko E, Kauser K, Parkinson J;
 XX XX
 XX DR WPI; 2004-203792/19.
 XX XX
 XX PT New isolated endothelial nitric oxide synthase polypeptide mutant, useful
 XX PT for diagnosing or treating ischemia, atherosclerosis, hypertension,
 XX PT diabetes, Raynaud's phenomenon, poor wound healing, hyperlipidemia or
 XX PT obesity.
 XX XX
 XX PS Example 1; SEQ ID NO 7; 57pp; English.
 XX XX
 XX CC The present sequence represents the calmodulin-binding site of mouse iNOS
 XX CC amino acid sequence. The present invention describes endothelial nitric
 XX CC oxide synthase (eNOS) mutants having one or more mutations in an amino
 XX CC acid sequence corresponding to a functional domain of a mammalian eNOS.
 XX CC At least one of the mutations is at a position corresponding to an amino
 XX CC acid residue in a calmodulin-binding domain that is phosphorylated in
 XX CC mammalian cells, and not an amino acid substitution to Ala or Asp. Also
 XX CC described: (1) an isolated eNOS polypeptide mutant that is substantially
 XX CC homologous, or has a 95-99% sequence identity to the amino acid sequence
 XX CC of the novel eNOS polypeptide mutant; (2) an isolated polynucleotide
 XX CC encoding the polypeptide mutant; (3) a recombinant vector comprising the
 XX CC polynucleotide operably linked to at least one regulatory sequence; (4) a
 XX CC pharmaceutical composition comprising the polypeptide mutant or the
 XX CC polynucleotide; (5) a binding partner of the polypeptide mutant; (6)
 XX CC modulating eNOS activity in a cell by administering to the cell the
 XX CC polypeptide mutant; (7) modulating eNOS activity in a cell by
 XX CC administering the polypeptide mutant or the polynucleotide to the cell,
 XX CC such that the polypeptide mutant is expressed in the cell; (8) diagnosing
 XX CC a condition associated with aberrant eNOS activity by contacting a cell
 XX CC of a patient with the polynucleotide, and detecting a level of eNOS
 XX CC activity indicative of the medical condition; and (9) prophylactic and
 XX CC therapeutic methods of treating a condition associated with aberrant eNOS
 XX CC activity by administering the polypeptide mutant or polynucleotide to the
 XX CC patient. The eNOS mutant has vasotropic, antiarteriosclerotic,
 XX CC hypotensive, antidiabetic, vulnary, antilipaseic and anorectic
 XX CC activities, and has reduced calcium dependence and increased activity.
 XX CC The polypeptide mutant, polynucleotide and methods are useful for
 XX CC diagnosing or treating a condition associated with aberrant eNOS
 XX CC activity, e.g. ischaemia, atherosclerosis, hypertension, diabetes,
 XX CC Raynaud's phenomenon, poor wound healing, hyperlipidaemia or obesity.
 XX XX
 XX SQ Sequence 37 AA;
 Query Match 100.0%; Score 29; DB 8; Length 37;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVVFFA 6
 Db 18 KVVFFA 23
 RESULT 20
 AAG02840
 ID AAG02840 standard; protein; 77 AA.
 XX AC AAG02840;
 XX XX
 XX DT 06-OCT-2000 (first entry)
 XX XX
 XX DB Human secreted protein, SEQ ID NO: 6921.

XX XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX XX
 XX OS Homo sapiens.
 XX XX
 XX PN EP1033401-A2.
 XX XX
 XX PD 06-SEP-2000.
 XX XX
 XX PF 21-FEB-2000; 2000EP-00200610.
 XX XX
 XX PR 26-FEB-1999; 99US-0122487P.
 XX XX
 XX PA (GEST) GENSET.
 XX XX
 XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX XX
 XX DR WPI; 2000-500381/45.
 XX DR N-PSDB; AAC02846.
 XX XX
 XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX PS Claim 13; SEQ ID NO 6921; 71pp + Sequence Listing; English.
 XX XX
 XX CC The present sequence is a polypeptide encoded by one of a large number of
 XX CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 XX CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 XX CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 XX CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 XX CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 XX CC sequences derived from the 5' ends of mRNAs and even in those cases where
 XX CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 XX CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 XX CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 XX CC are also used in diagnostic, forensic, gene therapy and chromosome
 XX CC mapping procedures. They are used to obtain upstream regulatory sequences
 XX CC and to design expression and secretion vectors
 XX XX
 XX SQ Sequence 77 AA;
 Query Match 100.0%; Score 29; DB 3; Length 77;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVVFFA 6
 Db 38 KVVFFA 43
 RESULT 21
 AAO11219
 ID AAO11219 standard; protein; 175 AA.
 XX XX
 XX AC AAO11219;
 XX XX
 XX DT 06-NOV-2001 (first entry)
 XX XX
 XX DE Human polypeptide SEQ ID NO 25111.
 XX XX
 XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX XX
 XX OS Homo sapiens.
 XX XX
 XX PN WO200164835-A2.
 XX XX
 XX PD 07-SEP-2001.
 XX XX

PF 26-FEB-2001; 2001WO-US004927.
 XX
 PR 28-FEB-2000; 2000US-00515126.
 PR 18-MAY-2000; 2000US-00577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 PI
 DR WPI: 2001-514838/56.
 DR N-PSDB; AAI91150.
 XX
 XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 PT
 XX Claim 20; SEQ ID NO 25111; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 175 AA;
 Query Match 100.0%; Score 29; DB 4; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 128 KVVFFA 133
 |||||
 RESULT 22
 ADC07962
 ID ADC07962 standard; protein; 186 AA.
 XX
 AC ADC07962;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Rice protein sequence Seq ID228 related to grain filling.
 XX
 KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW gene; ds; plant.
 XX
 OS Oryza sativa.
 XX
 PN WO2003000905-A2.
 XX
 PD 03-JAN-2003.
 XX
 PF 21-JUN-2002; 2002WO-IB002450.
 XX
 PR 22-JUN-2001; 2001US-0300112P.
 PR 26-SEP-2001; 2001US-0325277P.
 XX
 PF 21-JUN-2002; 2002WO-IB002450.
 XX
 PR 22-JUN-2001; 2001US-0300112P.
 PR 26-SEP-2001; 2001US-0325277P.
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA
 XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
 DR WPI: 2003-229341/22.
 DR N-PSDB; ADC07947.

PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
 XX
 DR WPI: 2003-229341/22.
 DR N-PSDB; ADC07961.
 XX
 PT New plant genes encoding polypeptides having an activity involved in or
 PT associated with the synthesis, metabolism or degradation of carbohydrates
 PT in the plant grain useful in generating plants having improved
 PT nutritional properties.
 XX
 XX Claim 15; SEQ ID NO 228; 130pp; English.
 XX
 CC This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarbeet, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is the
 CC amino acid sequence of a rice protein of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences.
 XX
 SQ Sequence 186 AA;
 Query Match 100.0%; Score 29; DB 7; Length 186;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 4 KVVFFA 9
 |||||
 RESULT 23
 ADC07948
 ID ADC07948 standard; protein; 186 AA.
 XX
 AC ADC07948;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Rice protein sequence Seq ID214 related to grain filling.
 XX
 KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW gene; ds; plant.
 XX
 OS Oryza sativa.
 XX
 PN WO2003000905-A2.
 XX
 PD 03-JAN-2003.
 XX
 PF 21-JUN-2002; 2002WO-IB002450.
 XX
 PR 22-JUN-2001; 2001US-0300112P.
 PR 26-SEP-2001; 2001US-0325277P.
 XX
 PF 20-DEC-2001; 2001US-0342327P.
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA
 XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
 DR WPI: 2003-229341/22.
 DR N-PSDB; ADC07947.

PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
DR N-PSDB; AAK56573.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Claim 11; SEQ ID NO 11385; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic

CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 190 AA;
Query Match 100.0%; Score 29; DB 4; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
Db 14 KVVFFA 19
RESULT 25	
ADQ66704	
ID ADQ66704 standard; protein; 854 AA.	
XX	
AC ADQ66704;	
XX	
DT 07-OCT-2004 (first entry)	
XX	
XX Novel human protein sequence #1677.	
XX	
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;	
KW gene therapy; diagnostic marker; morbid state; osteoporosis;	
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;	
XX cancer.	
XX	
XX Homo sapiens.	
XX	
XX EP1440981-A2.	
XX	
XX 28-JUL-2004.	
XX	
XX 21-JAN-2004; 2004EP-00001196.	
XX	
XX 21-JAN-2003; 2003JP-00102206.	
XX 09-MAY-2003; 2003JP-00131392.	
XX	
XX (REAS-) RES ASSOC BIOTECHNOLOGY.	
XX	
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;	
PI Yamamoto J, Isono Y, Nagai K, Irie R;	
XX	
XX WPI; 2004-535376/52.	
XX N-PSDB; ADQ64516.	
XX	
XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,	
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.	
XX	
XX Claim 1; SEQ ID NO 3865; 2449pp; English.	
XX	
XX The invention relates to 2495 novel polynucleotides (I) and their encoded	
CC polypeptides, sequences hybridizing to these nucleotides, sequences	
CC encoding partial polypeptides and sequences having 70% or 90% identity to	
CC the nucleotide and protein sequences. The nucleotides and polypeptides	
CC are useful as diagnostic markers or therapeutic target for the diseases	
CC or morbid states. They are also useful for treating osteoporosis,	
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,	
CC dementia and various cancers. This sequence corresponds to a protein	
CC sequence of the invention.	
XX	
SQ Sequence 854 AA;	
Query Match 100.0%; Score 29; DB 8; Length 854;	
Best Local Similarity 100.0%; Pred. No. 5.2e+02;	
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 KVVFFA 6	
Db 221 KVVFFA 226	

RESULT 27
AD76335
ID ADF76335 standard; protein; 925 AA.
XX AC
XX AC ADF76335;
XX AC
XX AC
XX DT 26-FEB-2004 (first entry)
XX AC
XX AC Novel human secreted and transmembrane protein SeqID 8.
XX AC
XX AC human; PRO; membrane bound protein; membrane bound receptor;
KW KW cell proliferation; cell migration; cell differentiation;
KW KW mitogenic factor; survival factor; cytotoxic factor;
KW KW differentiation factor; neurotrophic factor; hormone; cell receptor;
KW KW receptor-ligand interaction; cytoskeletal; chondrocyte; tumour.
XX KW
XX OS Homo sapiens.
XX OS
XX PN W02003072035-A2.
XX PN
XX PD 04-SEP-2003.
XX PD
XX XX 21-FEB-2003; 2003WO-US005241.
XX PF
XX PR 22-FEB-2002; 2002US-0359461P.
XX PR
XX PA (GETH) GENENTECH INC.
XX PA
XX PI Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
PI PI Williams FM, Wood WI, Wu TD;
XX DR
XX DR WPI; 2003-721702/68.
XX DR N-PSDB; ADF76334.
XX PT
XX PT New PRO polypeptides, useful for diagnosing and treating an immune
XX PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
XX PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
XX PT diabetes mellitus.
XX PS Claim 10; SEQ ID NO 8; 918pp; English.
XX PS
XX CC This invention relates to novel nucleic acids encoding human PRO secreted
XX CC and transmembrane proteins. Extracellular proteins play important roles
XX CC in the formation, differentiation and maintenance of multicellular
XX CC organisms. The fate of many individual cells (for example proliferation,
XX CC migration or differentiation) is typically governed by information
XX CC received from other cells and the immediate environment. The information
XX CC is often transmitted by secreted polypeptides (for example mitogenic
XX CC factors, survival factors, cytotoxic factors, differentiation factors,
XX CC neuropeptides and hormones) which are received and interpreted by diverse
XX CC cell receptors or membrane bound proteins. These membrane bound proteins
XX CC and receptors may be of use as pharmaceutical and diagnostic agents, such
XX CC as in the blocking of receptor-ligand interactions. The current invention
XX CC provides the amino acid sequences of novel human membrane bound receptors
XX CC and proteins, along with the cDNA sequences encoding them. The novel
XX CC proteins of the invention may have cytostatic activities through the
XX CC stimulation of chondrocytes. The nucleic acids of the invention may be
XX CC useful for the manufacture of a medicament for diagnosing or treating a
XX CC tumour in a mammal. In addition, they may be useful for measuring or
XX CC detecting the expression of a tumour associated gene. The present
XX CC sequence is the amino acid sequence of a human PRO protein of the
XX CC invention.
XX CC
XX CC Sequence 925 AA;
XX SQ

XX	RESULT 26
XX	ABM83252
XX	ABM83252 standard; protein; 922 AA.
XX	AC
XX	ABM83252;
XX	18-NOV-2004 (first entry)
XX	Human diagnostic and therapeutic pprotein SEQ ID NO:3501.
XX	gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX	Homo sapiens.
XX	WO2004023973-A2.
XX	25-MAR-2004.
XX	12-SEP-2003; 2003WO-US028227.
XX	12-SEP-2002; 2002US-0410259P.
XX	12-SEP-2002; 2002US-0410260P.
XX	(INCY-) INCYTE CORP.
XX	Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
XX	Harthshorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;
XX	Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
XX	Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
XX	Peralta CH, Anderson SB, Rioux P, Shen BJ, Wu MC, Stuve LL;
XX	Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtan BS;
XX	Xu Y, Kwong M, Policky JL, Hurwitz BU, Ma Y, Jackson JL, Gietzen D;
XX	Fatury S, Shi X, Suarez CU;
XX	WPI; 2004-329368/30.
XX	N-PSDB; ACN41904.
XX	New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX	in diagnosing a condition, disease or disorder associated with human
XX	molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX	in gene mapping.
XX	Claim 27; Page: 190pp; English.
XX	The invention relates to novel diagnostic and therapeutic polynucleotides
XX	selected from one of the 2722 sequences defined in the specification. A
XX	polynucleotide of the invention may have a use in gene therapy. The human
XX	diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
XX	used to diagnose a particular condition, disease or disorder associated
XX	with human molecules, e.g. cell proliferative disorders,
XX	autoimmune/inflammatory disorder, developmental disorder, endocrine
XX	disorder, neurological disorders, gastrointestinal disorders, or
XX	infections caused by virus, bacteria, fungi or parasite. The dithp
XX	molecules may also be used in genetic mapping, in identifying individuals
XX	from minute biological samples, in detecting single nucleotide
XX	polymorphisms, as molecular weight markers, and for somatic or germline
XX	gene therapy. The present sequence represents a dithp protein of the
XX	invention. Note: The sequence data for this patent is not represented in
XX	the printed specification, but was obtained in electronic format directly
XX	from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX	Sequence 922 AA;
XX	XX
XX	SQ

RESULT 28
ADJ70225
ID ADJ70225 standard; protein; 925 AA.
XX
XX
AC ADJ70225;
XX
XX
DT 06-MAY-2004 (first entry)
XX
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID2031.
XX
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
XX WO2003087768-A2.
PN
XX
PD 23-OCT-2003.
XX
XX
PF 04-APR-2003; 2003WO-US010870.
XX
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
XX WPI; 2003-845369/78.
XX
XX
XX Identifying a mitochondrial target for drug screening assays and for
XX treating diseases associated with altered mitochondrial function,
XX PT comprises detecting a modified polypeptide in a sample and correlating
XX PT with the disease.
XX
XX
XX Claim 1; SEQ ID NO 2031; 180pp; English.
XX
XX
XX This invention relates to novel mitochondrial targets that can be used
XX for therapeutic intervention in treating a disease associated with
XX altered mitochondrial function. Specifically, it refers to a method for
XX identifying proteins of the human heart mitochondrial proteome that are
XX useful for drug screening assays, as well as therapeutic targets. The
XX present invention describes a method for identifying such proteins that
XX can be used in the treatment of various diseases associated with altered
XX mitochondrial function including diabetes mellitus, Huntington's disease,
XX osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
XX encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
XX ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
XX compositions have neuroprotective, neurotropic, antidiabetic,
XX anticonvulsant, antiarthritic, osteopathic, ophthalmological and
XX cytostatic activities. This polypeptide sequence is a human heart
XX mitochondrial protein of the invention.
XX
SQ Sequence 925 AA;

Query Match 100.0%; Score 29; DB 7; Length 925;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||||
Db 292 KVVFFA 297

RESULT 29
ADJ75428
ID ADJ75428 standard; protein; 925 AA.
XX
XX
AC ADJ75428;
XX
XX
DT 20-MAY-2004 (first entry)
XX
XX
DE Marker gene related amino acid sequence SEQ ID NO:680.
XX
XX
KW bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker.
XX
OS Homo sapiens.
XX
XX EPI394274-A2.
PN
XX
PD 03-MAR-2004.
XX
XX
PF 04-AUG-2003; 2003EP-00254857.
XX
XX
PR 06-AUG-2002; 2002JP-00229312.
PR 20-MAR-2003; 2003JP-00077212.
XX
XX (GENO-) GENOX RES INC.
XX
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
XX WPI; 2004-193155/19.
XX
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
XX comparing the expression level of a marker gene in a biological sample
XX from a subject with the expression level of the gene in a sample from a
XX healthy subject.
XX
XX Example 11; SEQ ID NO 680; 241pp; English.
XX
XX The present invention describes a method of testing for bronchial asthma
XX or chronic obstructive pulmonary disease. The method comprises
XX determining the expression level of a marker gene in a biological sample
XX from a subject, comparing the expression level determined with the
XX expression level of the marker gene in a biological sample from a healthy
XX subject, and judging whether the subject has bronchial asthma or chronic
XX obstructive pulmonary disease. The marker gene comprises: (a) a group of
XX genes (S1) whose expression levels increase when respiratory epithelial
XX cells are stimulated with interleukin-13; or (b) a group of genes (S2)
XX whose expression levels decrease when respiratory epithelial cells are
XX stimulated with interleukin-13. Also described: (1) a reagent (1) for
XX testing for bronchial asthma or chronic obstructive pulmonary disease;
XX (2) a kit for screening for a candidate compound for a therapeutic agent
XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
XX an animal model for bronchial asthma or chronic obstructive pulmonary
XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
XX method for producing an animal model for bronchial asthma or chronic
XX obstructive pulmonary disease; (6) a therapeutic agent for bronchial
XX asthma or chronic obstructive pulmonary disease, comprising the compound,
XX a marker gene or an antisense nucleic acid corresponding to a portion of
XX the marker gene, a ribozyme, a polynucleotide that suppresses the
XX expression of the gene through an RNAi effect or an antibody recognising
XX a protein encoded by a marker gene; and (7) a DNA chip for testing for
XX bronchial asthma or a chronic obstructive pulmonary disease, on which a
XX probe has been immobilised to assay a marker gene. (1) has respiratory
XX and antiasthmatic activities, and can be used in gene therapy. The method
XX is useful for testing for or screening for a therapeutic agent for
XX bronchial asthma or chronic obstructive pulmonary disease. The present
XX sequence is used in the exemplification of the present invention.
XX
SQ Sequence 925 AA;

Query Match 100.0%; Score 29; DB 8; Length 925;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 292 KVVFFA 297

RESULT 30
ADJ75495
ID ADJ75495 standard; protein; 925 AA.
AC ADJ75495;
XX
XX
XX 20-MAY-2004 (first entry)
XX
XX Marker gene related amino acid sequence SEQ ID NO:747.
XX
XX bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker.
XX
XX Homo sapiens.
XX
XX EPI394274-A2.
XX
XX 03-MAR-2004.
XX
XX 04-AUG-2003; 2003EP-00254857.
XX
XX 06-AUG-2002; 2002JP-00229312.
XX
XX 20-MAR-2003; 2003JP-00077212.
XX
XX (GENO-) GENOX RES INC.
XX
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;
XX WPI; 2004-193155/19.
XX
XX
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.
XX
XX Example 11; SEQ ID NO 747; 241pp; English.

The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (I) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (I) has respiratory and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 925 AA;
Query Match 100.0%; Score 29; DB 8; Length 925;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVVFFA 6
Db 292 KVVFFA 297

RESULT 31
ADN04860
ID ADN04860 standard; protein; 925 AA.
XX
XX ADN04860;
XX
XX 01-JUL-2004 (first entry)
XX
XX Antipsoriatic protein sequence #610.
XX
XX antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
XX Homo sapiens.
XX
XX WO2004028479-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030907.
XX
XX 25-SEP-2002; 2002US-0414006P.
XX
XX (GETH) GENENTECH INC.
XX
XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
XX Wu TD;
XX
XX WPI; 2004-305105/28.
XX
XX N-PSDB; ADN04859.
XX
XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX
XX Claim 9; SEQ ID NO 1254; 3069pp; English.
XX
XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.
XX
XX SQ Sequence 925 AA;
Query Match 100.0%; Score 29; DB 8; Length 925;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVVFFA 6
Db 292 KVVFFA 297

RESULT 32
ADR14233
ID ADR14233 standard; protein; 925 AA.
XX
XX ADR14233;
XX
XX 21-OCT-2004 (first entry)
XX

DE Human NF-kappaB pathway-associated protein SeqID234.

XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;

KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;

KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;

KW immunosuppressive; vulnary; gene therapy; immune disorder;

KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;

KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;

KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;

KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;

KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;

KW viral replication; host cell survival; evasion of immune response;

KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;

KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;

KW autoimmune disorder; hyper immune activity;

KW aberrant acute phase response; hypercongenital condition; birth defect;

KW necrotic lesion; wound; organ transplant rejection;

KW aberrant signal transduction; proliferating disorder; cancer;

KW HIV propagation; human.

XX

OS Homo sapiens.

XX

XX WO2004065577-A2.

XX

XX 05-AUG-2004.

XX

XX 13-JAN-2004; 2004WO-US000798.

XX

XX 14-JAN-2003; 2003US-0440068P.

PR 12-MAY-2003; 2003US-0469757P.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

XX Nadler SG, Neubauer MG, Feder JN, Carman J;

PI WPI; 2004-562168/54.

DR N-PSDB; ADRI4232.

XX

XX New isolated polynucleotides and polypeptides associated with NF-kappaB

PT pathway, useful for diagnosing, treating, or preventing disorders or

PT diseases associated with NF-kappaB pathway.

XX

XX Claim 6; SEQ ID NO 234; 237pp; English.

XX

XX This invention relates to the novel association of protein sequences (and

CC the genes which encode them) to the NF-kappaB pathway. The invention may

CC be useful for the production of compounds with an antiinflammatory,

CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,

CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,

CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or

CC vulnary activity or for gene therapy. The proteins and nucleotides are

CC useful for diagnosing, preventing, treating, or ameliorating conditions

CC or diseases associated with the NF-kappaB pathway. The condition is an

CC immune disorder, an inflammatory disorder, an inflammatory disorder

CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,

CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM

CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic

CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,

CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell

CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory

CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick

CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper

CC immune activity, disorders related to aberrant acute phase responses,

CC hypercongenital conditions, birth defects, necrotic lesions, wounds,

CC organ transplant rejection, conditions related to organ transplant

CC rejection, disorders related to aberrant signal transduction,

CC proliferating disorders, cancers and HIV propagation in cells infected

CC with other viruses. The present sequence is that of a human protein which

CC is subject to the novel association with the NF-kappaB pathway of the

CC invention. Note: This sequence does not appear in the specification but

CC was obtained by the indexer from Genbank.

XX

XX Sequence 925 AA;

Query Match 100.0%; Score 29; DB 8; Length 925;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 292 KVVFFA 297

|||||

RESULT 33

ADP25011

ID ADP25011 standard; protein; 925 AA.

XX

AC ADP25011;

XX

DT 18-NOV-2004 (first entry)

XX

DE PRO polypeptide SEQ ID NO:2189.

XX

KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;

KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;

KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

XX

OS Unidentified.

XX

XX WO2004041170-A2.

XX

PD 21-MAY-2004.

XX

PF 30-OCT-2003; 2003WO-US034312.

XX

PR 01-NOV-2002; 2002US-0423394P.

XX

XX (GETH) GENENTECH INC.

XX

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;

PI Wu TD;

XX

XX WPI; 2004-419628/39.

DR N-PSDB; ADP25010.

XX

XX New PRO polypeptides and polynucleotides, useful for treating e.g.

PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated

PT renal disease, or demyelinating diseases of the central or peripheral

PT nervous system.

XX

PS Claim 7; SEQ ID NO 2189; 2940pp; English.

XX

CC The invention relates to a novel isolated nucleic acid and the PRO

CC polypeptide encoded by it. A protein of the invention has

CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,

CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,

CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide

CC of the invention may have a use in gene therapy. The PRO polypeptide, its

CC agonist, antagonist, or antibody that specifically binds to the

CC polypeptide is useful for treating an immune related disorder such as

CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an

CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic

CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune

CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal

CC disease, a demyelinating disease of the central or peripheral nervous

CC system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome,

CC a chronic inflammatory demyelinating polynuropathy, a hepatobiliary

CC disease, infectious or autoimmune chronic active hepatitis, primary

CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,

CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's

CC disease, an autoimmune or immune-mediated skin disease, a bullous skin

CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic

CC disease, asthma, allergic rhinitis, atopic dermatitis, food

CC hypersensitivity, urticaria, an immunologic disease of the lung,

CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity

CC pneumonia, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.

SQ Sequence 925 AA;

Query Match 100.0%; Score 29; DB 8; Length 925;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |||||
 Db 292 KVVFFA 297

RESULT 34

ID ADR97294 standard; protein; 925 AA.

XX ADR97294;

DT 02-DEC-2004 (first entry)

DE Human RIG-I-DEAD/H box protein, an apoptosis related target Seq 2.

XX human; enzyme; apoptosis; cancer; inflammation; autoimmune;
 KW neurodegenerative disorder; cytostatic; antiinflammatory;
 KW immunosuppressive; neuroprotective; gene therapy; RIG-I-DEAD/H box.

XX Homo sapiens.

XX WO2004078783-A2.

XX 16-SEP-2004.

XX 05-MAR-2004; 2004WO-GB000957.

XX 07-MAR-2003; 2003GB-00005267.

XX (EIRX-) EIRX THERAPEUTICS LTD.

XX Murphy FJ, Sheehan DE, Keating KE, Hayes I, Seera L;

XX WPI; 2004-662402/64.

DR N-PSDB; ADR97293.

PT Identifying an agent that modulates the function of an apoptosis-
 PT associated polypeptide, useful for diagnosing or treating e.g. cancer,
 PT comprises comparing the binding of the polypeptide to the candidate agent
 PT and to a control agent.

PS Claim 1; SEQ ID NO 2; 304pp; English.

XX This invention relates to novel agents that modulates the function of
 CC human apoptosis-associated proteins specified within the specification.
 CC Specifically, it refers to a method for the identification of target
 CC genes whose expression is correlated with an early stage in the
 CC regulation of apoptosis. The present invention describes a method of
 CC contacting either candidate agents or control agents to the target genes
 CC and assessing the difference of binding and inhibitory activity, where
 CC the candidate agent is selected from a low molecular weight organic
 CC molecule, an antibody or fragment thereof, an antisense oligonucleotide,
 CC a small inhibitory dsRNA, or a ribozyme. As such, the compositions and
 CC methods are useful for diagnosing and treating diseases or conditions
 CC associated with abnormal apoptosis in mammalian tissue, such as cancer,
 CC inflammation, autoimmune or neurodegenerative disorders. Accordingly,
 CC they exhibit cytostatic, antiinflammatory, immunosuppressive and
 CC neuroprotective activities. These may also be used for drug screening
 CC purposes and in gene therapy. This polypeptide sequence is a human target
 CC protein, an enzyme associated with the regulation of apoptosis whose
 CC expression is modulated by novel agents of the invention.

XX Sequence 925 AA;

Query Match 100.0%; Score 29; DB 8; Length 925;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |||||
 Db 292 KVVFFA 297

RESULT 35

ID ADY17516 standard; protein; 925 AA.

XX ADY17516;

DT 05-MAY-2005 (first entry)

DE PRO polypeptide SEQ ID NO 3322.

XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
 KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
 KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
 KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
 KW Antiallergic; diagnosis.

XX Homo sapiens.

XX WO2005016962-A2.

XX 24-FEB-2005.

XX 11-AUG-2004; 2004WO-US026249.

XX 11-AUG-2003; 2003US-0493546P.

XX (GETH) GENENTECH INC.

XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX WPI; 2005-182330/19.

PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

PS Claim 8; SEQ ID NO 3322; 158pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
 CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
 CC composition, and method are useful for diagnosing and treating an immune
 CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
 CC arthritis. The present sequence represents a PRO polypeptide.

XX Sequence 925 AA;

Query Match 100.0%; Score 29; DB 9; Length 925;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |||||
 Db 292 KVVFFA 297

RESULT 36

ID AEA23525 standard; protein; 925 AA.

XX AEA23525;

DT 11-AUG-2005 (first entry)

XX

```

DE Human PRO polypeptide SEQ ID NO 67.
XX
KW Immune disorder; PRO; Antiinflammatory; Dermatological;
KW Immunosuppressive; Antirheumatic; Antiarthritic; Osteopathic;
KW Muscular-Gen.; Vasotropic; Antianemic; Antipsoriatic; Immunostimulant.
XX
OS Homo sapiens.
XX
PN WO2005051988-A2.
XX
PD 09-JUN-2005.
XX
PF 02-MAR-2004; 2004WO-US006460.
XX
PR 03-MAR-2003; 2003US-0451884P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Abbas A, Bodary S, Clark H, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX
DR WPI; 2005-417958/42.
DR N-PSDB; AEA23524.
XX
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, autoimmune hemolytic anemia, or
PT psoriasis.
XX
PS Disclosure; SEQ ID NO 67; 966pp; English.
XX
XX The invention relates to an isolated nucleic acid. The polypeptide,
CC compound or composition, and methods are useful for diagnosing and
CC treating an immune related disorder, e.g. systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis,
CC spondyloarthritides, systemic sclerosis, idiopathic inflammatory
CC myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
CC autoimmune hemolytic anemia, autoimmune or immune-mediated skin diseases
CC including bullous skin diseases, erythema multiforme and contact
CC dermatitis, psoriasis, lymphadenopathy, splenomegaly and leukopenia. The
CC present sequence represents the amino acid sequence of a human PRO
CC polypeptide.
XX
SQ Sequence 925 AA;
Query Match 100.0%; Score 29; DB 9; Length 925;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 292 KVVFFA 297
|||||

RESULT 37
AAR77360
ID AAR77360 standard; protein; 1144 AA.
XX
AC AAR77360;
XX
XX 10-MAY-1996 (first entry)
XX
XX Inducible nitrogen monoxide synthase.
XX
XX nitrogen monoxide synthase; inducible; treatment; prevention;
XX vascular disease; restenosis.
XX
OS Mus musculus.
XX
PN DE4411402-A1.
XX
PD 05-OCT-1995.
XX
XX

```

```

PF 31-MAR-1994; 94DE-04411402.
XX
PR 31-MAR-1994; 94DE-04411402.
XX
PA (SCHR/) SCHRADER J.
XX
PI Schrader J, Goedecke A;
XX
DR WPI; 1995-345550/45.
DR N-PSDB; AAQ94252.
XX
XX Eukaryotic expression vector for nitrogen-mon:oxide synthase gene -
PT useful in the treatment and prevention of diseases of blood vessels by
PT gene therapy.
XX
PS Claim 5; Fig 1; 28pp; German.
XX
XX Inducible nitrogen monoxide synthase (iNOS) was isolated from mice, and
CC is encoded by AAQ94252. iNOS is homodimer with a mol. wt. of 130 kDa per
CC subunit. The activity of iNOS is independent of calmodulin and cellular
CC calcium levels. Vectors contg. the DNA are used in the treatment or
CC prevention of vascular diseases, high blood pressure, arteriosclerosis,
CC stenosis or restenosis of blood vessels, esp. coronary vessels after
CC percutane transluminal coronary angioplasty. See AAR77363 and AAR77362
CC for endothelial and brain-derived NOS
XX
SQ Sequence 1144 AA;
Query Match 100.0%; Score 29; DB 2; Length 1144;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 514 KVVFFA 519
|||||

RESULT 38
AAW51246
ID AAW51246 standard; protein; 1144 AA.
XX
AC AAW51246;
XX
XX 25-MAR-2003 (revised)
DT 12-AUG-1998 (first entry)
XX
XX Inducible nitric oxide synthase, long isoform.
XX
XX Inducible nitric oxide synthase; iNOS; recombinant protein; cDNA library;
KW isoform.
XX
XX Mus sp.
XX
XX US5766909-A.
XX
XX 16-JUN-1998.
XX
XX 05-NOV-1993; 93US-00147812.
XX
XX 04-FEB-1992; 92US-00841641.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Mumford RA, Calaycay JR, Xie Q, Nathan CF;
XX
XX WPI; 1998-361696/31.
DR N-PSDB; AAV07247.
XX
XX DNA encoding inducible nitric oxide synthase proteins - useful for
PT producing recombinant proteins.
XX
PS Claim 1; Col 25-32; 39pp; English.
XX

```

CC The invention relates to two DNA molecules encoding inducible nitric
 CC oxide synthase (iNOS) proteins, where the DNA molecules comprise defined
 CC sequences of 4041 and 4165 base pairs given in the specification and the
 CC proteins have 1144 amino acids. Also claimed are expression vectors
 CC containing the DNA molecules, and recombinant host cells containing the
 CC vectors. The DNA molecules are useful for producing the recombinant
 CC proteins. The present sequence represents inducible nitric oxide, long
 CC isoform. (Updated on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 2; Length 1144;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |||||
 Db 514 KVVFFA 519

RESULT 39
 AAG64500
 ID AAG64500 standard; protein; 1144 AA.

XX AAG64500;

DT 02-OCT-2001 (first entry)

DE Mouse inducible nitric oxide synthase 2.

KW Antisense oligonucleotide; inducible nitric oxide synthase;
 KW modulate expression; immunomodulator; antidiabetic; cardiovascular;
 KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;
 KW 2'-O-methoxyethyl; phosphorothioate; mouse.

XX Mus sp.

XX WO200152902-A1.

XX 26-JUL-2001.

XX 15-JAN-2001; 2001WO-US001381.

XX 24-JAN-2000; 2000US-00490208.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dean NM, Cowbert LM;

XX WPI; 2001-465340/50.

XX N-PSDB; AAH47974.

PT New antisense oligonucleotides for modulating the expression of inducible
 PT nitric oxide synthase in cells or tissues, particularly useful for
 PT treating e.g. immunological, cardiovascular or neurological disorders, or
 PT ischemia.

XX Example 17; Page 110-114; 144pp; English.

XX The invention relates to antisense compounds, especially
 CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
 CC nitric oxide synthase and which specifically hybridize to and modulate
 CC expression of inducible nitric oxide synthase. The antisense compounds
 CC have immunomodulator, antidiabetic, cardiovascular, cardiant,
 CC neuroprotective, disorder and vasotropic activity. The antisense
 CC oligonucleotides are useful for inhibiting the expression of inducible
 CC nitric oxide synthase in cells or tissues. In particular, the antisense
 CC oligonucleotides are useful for treating diseases or disorders associated
 CC with inducible nitric oxide synthase, e.g. diabetes, immunological
 CC disorder, cardiovascular disorder, neurological disorder or
 CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
 CC useful for research and diagnostics. The present sequence is that of
 CC mouse inducible nitric oxide synthase

XX SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 4; Length 1144;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |||||
 Db 514 KVVFFA 519

RESULT 40
 ABU79138
 ID ABU79138 standard; protein; 1144 AA.

XX ABU79138;

DT 18-JUN-2003 (first entry)

DE Inducible nitric oxide synthase protein.

KW Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 KW gene therapy; mammalian cell receptor; cytostatic;
 KW tumour associated lipid; energy; T cell; antigen presenting cell; APC;
 KW tumouricidal immunocyte; antitumour.

XX Unidentified.

XX US2002177551-A1.

XX 28-NOV-2002.

XX 30-MAY-2001; 2001US-00870759.

XX 31-MAY-2000; 2000US-0208128P.

XX (TERM/) TERMAN D S.

XX Terman DS;

XX WPI; 2003-361759/34.

XX N-PSDB; ACA64740.

XX A mammalian cell receptor, useful in the treatment of cancer by binding
 PT to tumor associated lipids where the binding induces energy or apoptosis
 PT in T cells and antigen presenting cells.

XX Example 2; Page; 167pp; English.

XX The invention relates to a mammalian cell receptor, useful in the
 CC treatment of cancer, which binds to tumour associated lipids and induces
 CC energy or apoptosis in the T cells and antigen presenting cells (APCs).
 CC Also included are a mammalian cell useful in the treatment of cancer
 CC where the receptor which binds tumour associated lipids and induces
 CC cellular inactivation or death is deleted or functionally deactivated,
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 CC (by allowing tumour associated lipids to contact immunocytes in which
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 CC deleted), a construct useful in the treatment of cancer comprising a
 CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 CC useful in the treatment of cancer (where an adaptor protein which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidal
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to

CC contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidally activated population,
 CC and administering APCs to the host), producing a tumouricidal T cell
 CC population ex vivo in a mammal) by allowing a tumour associated lipids to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC administering the tumouricidally activated T cells to the host, or
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidally activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC receptors, methods and compositions are useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents an anti-tumour protein which is co-administered with
 CC or incorporated into a fusion construct with a superantigen. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from the US patent
 CC office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"
 XX
 SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 6; Length 1144;
 Best Local Similarity 100.0%; Pred. No. 76+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 Db 514 KVVFFA 519

RESULT 41
 ADF43404
 ID ADF43404 standard; protein; 1144 AA.

AC ADF43404;

DT 12-FEB-2004 (first entry)

DE INOS polypeptide seqid 124.

XX receptor; lipid-based tumour associated antigen; cytostatic;
 KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
 KW infectious disease; iNOS.

XX Unidentified.

XX US2003157113-A1.

XX 21-AUG-2003.

XX 28-DEC-2000; 2000US-00751708.

XX 28-DEC-1999; 99US-0173371P.

XX (TERM/) TERMAN D S.

XX Terman DS;

XX WPI; 2003-787326/74.

XX N-PSDB; ADF43403.

XX New receptor in a mammalian cell that inhibits regular activation by
 PT receptors specific for lipid-based tumor associated antigens, useful for
 PT treating a neoplastic disease or tumor, and infectious diseases.

PS Example 3; SEQ ID NO 124; 151pp; English.
 XX The invention describes a receptor in a mammalian cell that inhibits
 CC regular activation by receptors specific for lipid-based tumour
 CC associated antigen. The receptor has cytostatic and antimicrobial
 CC properties and is suitable for use in gene therapy. The receptors,
 CC methods and compositions are useful for treating a neoplastic disease or
 CC tumour (cancer), and infectious diseases. This sequence represents iNOS
 CC polypeptide, a cell surface moiety, the DNA of which can be transfected
 CC into a cell with superantigen DNA to generate antitumour immunity.

XX Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 7; Length 1144;
 Best Local Similarity 100.0%; Pred. No. 76+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 Db 514 KVVFFA 519

RESULT 42

ADP77432
 ID ADF77432 standard; protein; 1144 AA.

XX ADF77432;

XX 26-FEB-2004 (first entry)

XX Mouse inducible nitric oxide synthase, iNOS.

KW Mouse; inducible nitric oxide synthase; iNOS; cardiant; vasodilator;
 KW cytostatic; gynaecological; restenotic response; angioplasty;

KW vasodilation; angina; cancer; cell death; premature labour; tumour;

KW nervous system; brain; erectile dysfunction; uterus; lung; vascular tone;

KW regional blood flow.

XX Mus musculus.

XX US6620616-B1.

XX 16-SEP-2003.

XX 13-SEP-2000; 2000US-00661258.

XX 13-SEP-2000; 2000US-00661258.

XX (CLEV-) CLEVELAND CLINIC FOUND.

XX Stuehr DJ, Adak S;

XX WPI; 2003-895427/82.

XX New isolated polynucleotide encoding a variant of a corresponding wild-
 PT type nitric oxide synthase, useful for reducing the restenotic response
 PT after angioplasty, or for inhibiting the development or onset of
 PT premature labor.

XX Disclosure; SEQ ID NO 5; 35pp; English.

XX The invention relates to an isolated polynucleotide encoding a variant of
 CC a corresponding wild-type nitric oxide synthase (NOS). The variant has
 CC the tryptophan in the alpha 3 helix substituted by tyrosine or
 CC phenylalanine. Also included are a nucleic acid construct comprising the
 CC nucleotide sequence that encodes a variant of a corresponding wild-type
 CC nitric oxide synthase and a promoter operably linked to the encoding
 CC sequence of the variant and a transformed cell comprising the construct,
 CC where the cell expresses the nitric oxide synthase variant. The variant
 CC has an in vitro enzymatic activity that is greater than the in vitro
 CC enzymatic activity of the corresponding wild-type nitric oxide synthase.
 CC The variant can preferably be of a corresponding wild-type endothelial
 CC nitric oxide synthase (eNOS), neuronal nitric oxide synthase (nNOS), or

CC inducible nitric oxide synthase (iNOS). The polynucleotides are useful
 CC for reducing the restenotic response after angioplasty, or related
 CC interventional procedures, or to enhance the vasodilation response in
 CC treating angina, for anticancer therapy to promote cell death, and for
 CC inhibiting the development or onset of premature labour. The
 CC polynucleotides are useful to achieve or augment expression of NOS
 CC variant proteins or polypeptides in vivo to increase NOS production in
 CC target tissue, tumour tissue, tissue of the nervous system, including
 CC brain, penis (e.g. in erectile dysfunction) and uterine tissue, and lung
 CC tissue. NOS is useful for maintaining vascular tone and regulating
 CC regional blood flow. The present sequence is wild-type mouse iNOS.

XX
 XX Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 7; Length 1144;

Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

|||||

Db 514 KVVFFA 519

RESULT 43

ADJ76212
 ID ADJ76212 standard; protein; 1144 AA.

XX AC

XX ADJ76212;

XX DT 20-MAY-2004 (first entry)

XX DE Marker gene related amino acid sequence SEQ ID NO:1464.

XX DE bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.

XX OS Mus musculus.

XX PN EPI394274-A2.

XX PD 03-MAR-2004.

XX PF 04-AUG-2003; 2003EP-00254857.

XX PR 06-AUG-2002; 2002JP-00229312.

XX PR 20-MAR-2003; 2003JP-00077212.

XX PA (GENO-) GENOX RES INC.

XX PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuohara K;

XX DR WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.

XX PS Claim 16; SEQ ID NO 1464; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (1) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;

CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (1) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 8; Length 1144;

Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

|||||

Db 514 KVVFFA 519

RESULT 44

ADJ76136
 ID ADJ76136 standard; protein; 1144 AA.

XX AC ADJ76136;

XX DT 20-MAY-2004 (first entry)

XX DE Marker gene related amino acid sequence SEQ ID NO:1388.

XX DE bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.

XX OS Mus musculus.

XX PN EPI394274-A2.

XX PD 03-MAR-2004.

XX PF 04-AUG-2003; 2003EP-00254857.

XX PR 06-AUG-2002; 2002JP-00229312.

XX PR 20-MAR-2003; 2003JP-00077212.

XX PA (GENO-) GENOX RES INC.

XX PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuohara K;

XX DR WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.

XX PS Claim 16; SEQ ID NO 1388; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic

CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (I) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 8; Length 1144;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 DB 514 KVVFFA 519

RESULT 45

AEA03075
 ID AEA03075 standard; protein; 1144 AA.

XX AC AEA03075;

XX DT 28-JUL-2005 (first entry)

XX VEGF amino acid sequence SEQ ID NO:101.

XX tumor; neoplasm; gene therapy; immunotherapy; cytostatic;
 KW vascular endothelial cell growth factor.

XX Unidentified.

XX US2005112141-A1.

XX PD 26-MAY-2005.

XX PF 08-SEP-2004; 2004US-00937758.

XX PR 30-AUG-2000; 2000US-00650884.

XX PA (TERM/) TERMAN D S.

XX PI Terman DS;

XX DR WPI; 2005-394926/40.

XX DR N-PSDB; AEA03074.

XX PT New composition for treating a tumor or neoplastic disease in a subject
 PT comprises conjugates comprising superantigen polypeptides or nucleic
 PT acids with other molecules that produce a tumoricidal response.

XX Example 3; SEQ ID NO 101; 125pp; English.

XX The invention relates to a composition for treating a tumor or neoplastic
 CC disease in a subject. Also described: (1) a mammalian cell comprising an

CC exogenous nucleic acid encoding a superantigen expressed in the cell,
 CC which cell also produces or expresses all alpha-anomers of
 CC monoglycosylceramide or diglycosylceramide, where expression of the
 CC superantigen and the mono- or diglycosylceramide is capable of eliciting
 CC an antitumor immune response in a mammal into which the cell is
 CC introduced; (2) treating a tumor or neoplastic disease in a subject; (3)
 CC preparing a population of immunotherapeutic T or natural killer T (NKT)
 CC cells useful to treat a tumor or neoplastic disease in a subject; (4) an
 CC apoptotic cell preparation or lysate useful for treating a tumor or
 CC neoplastic disease in a subject, comprising a cell population that has
 CC been transfected with naked DNA encoding a superantigen, and treated to
 CC undergo apoptosis or lysis; and (5) a cell that has ingested or been
 CC transfected with the above apoptotic preparation or lysate, thus,
 CC rendering the cell effective in presenting material expressed from
 CC transfecting nucleic acid or material ingested to the immune system of a
 CC mammal to elicit an anti-tumor immune response. The composition and
 CC methods are useful for treating tumors or neoplastic diseases. The
 CC present sequence represents a VEGF protein sequence, which is used in an
 CC example from the present invention. Note - The sequence data for this
 CC patent is not represented in the printed specification, but was obtained
 CC in electronic format directly from the USPTO web site.

XX SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 9; Length 1144;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 DB 514 KVVFFA 519

RESULT 46

ABB48483
 ID AAB48483 standard; peptide; 6 AA.

XX AC AAB48483;

XX DT 02-MAR-2001 (first entry)

XX DE Antifibrillogenic peptide #10.

XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Modified-site 6 /note= "C-terminal amide"

XX PN WO200068263-A2.

XX PD 16-NOV-2000.

XX PF 04-MAY-2000; 2000WO-CA0000515.

XX PR 05-MAY-1999; 99US-0132592P.

XX PA (NEUR-) NEUROCHEM INC.

XX PI Chalifour R, Gervais F, Gupta A;

XX WPI; 2001-031852/04.

XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.

XX Claim 7; Page 25; 46pp; English.

CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 Db 1 KIVFFA 6

RESULT 47

AAB48474
 ID AAB48474 standard; peptide; 6 AA.

AC AAB48474;

XX 02-MAR-2001 (first entry)

XX Antifibrillogenic peptide #1.

XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.

XX Homo sapiens.

XX WO200068263-A2.

XX 16-NOV-2000.

XX 04-MAY-2000; 2000WO-CA000515.

XX 05-MAY-1999; 99US-0132592P.

XX (NEUR-) NEUROCHEM INC.

XX Chalifour R, Gervais F, Gupta A;

XX WPI; 2001-031852/04.

XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.

XX Claim 7; Page 25; 46pp; English.

XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 Db 1 KIVFFA 6

RESULT 48

AAB82623

ID AAB82623 standard; peptide; 6 AA.

XX AAB82623;

XX 02-OCT-2001 (first entry)

XX All-D peptide used in Alzheimer's disease vaccine.

XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 1..6 /note= "all D-form residues"

XX WO200139796-A2.

XX 07-JUN-2001.

XX 29-NOV-2000; 2000WO-CA001413.

XX 29-NOV-1999; 99US-0168594P.

XX 28-NOV-2000; 2000US-00724842.

XX (NEUR-) NEUROCHEM INC.

XX Chalifour R, Hebert L, Kong X, Gervais F;

XX WPI; 2001-441458/47.

XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.

XX Disclosure; Page 10; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
XX |:|||||
SQ 1 KIVFFA 6

RESULT 49
ID AAB82631 standard; peptide; 6 AA.
XX AAB82631;
AC AAB82631;
XX 02-OCT-2001 (first entry)
DT
DE All-D peptide used in Alzheimer's disease vaccine.
XX
KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
KW therapy; antigen.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1.6 /note= "all D-form residues"
FT Modified-site 6 /note= "C-terminal amide"
FT
FT
XX WO200139796-A2.
XX
XX 07-JUN-2001.
XX
XX 29-NOV-2000; 2000WO-CA001413.
XX
XX 29-NOV-1999; 99US-0168594P.
PR
XX 28-NOV-2000; 2000US-00724842.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Chalifour R, Hebert L, Kong X, Gervais F;
XX WPI; 2001-441458/47.
XX
XX Preventing/treating amyloid-related disease, especially Alzheimer's
XX disease, comprises administering antigenic all-D peptide, eg. as vaccine,
XX which elicits production of antibodies to prevent fibrillogenesis and
XX associated cellular toxicity.
XX
XX Disclosure; Page 11; 31pp; English.

The present sequence is that of an all-D peptide suitable for use for
preparing vaccines for preventing or treating Alzheimer's disease and
other amyloid related disorders in humans. It is based on a portion of
amyloid-beta peptide (see AAB82622), and may be modified by removing or
inserting 1 or more amino acid residues, or by substituting 1 or more
amino acid residues with other amino acid residues or non-amino acid
fragments. Vaccines of the invention are produced using 'non-self'
peptides synthesised from the unnatural D-configuration amino acids to
avoid the drawbacks of 'self' proteins. The all-D peptides need not be
aggregated to be operative or immunogenic. They preferably interact with
at least 1 region of an amyloid protein, e.g. the beta-sheet region or
CAG-binding site region, the amyloid-beta peptide, or their immunogenic
fragments, protein conjugates, immunogenic derivative peptides and
immunogenic peptidomimetics. Examples include all-D peptides
corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
36-42 of the amyloid-beta peptide and the all-D derivative peptides given
in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
preventing fibrillogenesis and associated cellular toxicity. The amyloid
related diseases may be localised amyloidosis, e.g. diabetes type II,
neurodegenerative diseases, e.g. bovine spongiform encephalitis,
Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
prion protein related disorders, or systemic amyloidosis associated with
chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic

CC amyloidosis found in long-term haemodialysis patients
XX
SQ Sequence 6 AA;
Query Match 96.6%; Score 28; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
Db |:|||||
1 KIVFFA 6

RESULT 50
AAU96819
ID AAU96819 standard; peptide; 6 AA.
XX
AC AAU96819;
XX
DT 30-JUL-2002 (first entry)
XX
DE Amyloid targeting peptide #9.
XX
KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
KW transmissible cerebral amyloidosis; transmissible virus dementia;
KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
KW bovine spongiform encephalopathy; inflammation associated amyloid;
KW primary amyloidosis; feline spongiform encephalopathy;
KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
KW dialysis-related amyloidosis; light chain-related amyloidosis;
KW cerebral amyloid angiopathy.
XX
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
FT Misc-difference 1.6 /note= "Preferably D-form residue"
FT Modified-site 6 /note= "Ala is amidated"
FT
FT
XX WO200207781-A2.
XX
XX 31-JAN-2002.
XX
XX 25-JUL-2001; 2001WO-CA001071.
XX
XX 25-JUL-2000; 2000US-0220808P.
PR
XX 24-JUL-2001; 2001US-00915092.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Gervais F, Kong X, Chalifour R, Migneault D;
XX
XX WPI; 2002-371447/40.
XX
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
XX plaques and/or for the treatment of amyloidosis disorders.
XX
XX Claim 49; Page 21; 57pp; English.

The invention relates to an amyloid-targeting imaging agent comprising an
amyloid targeting moiety, a linker moiety and a labelling moiety. The
agent is of general formula A-t-(A₁n₁k) z-A₁l₁a₁b₁(t) where z = 0 - 1;
A-t = an amyloid targeting moiety; A₁n₁k = a linker moiety; and A₁l₁a₁b₁
= a labelling moiety. Also included are imaging amyloid deposition or
diagnosing an amyloid-related condition in a patient involving
administering (i) to the patient, and ultrasound imaging (ii) in the
patient to determine the presence of amyloid or amyloid-related condition
; and a kit for preparing a radiopharmaceutical preparation comprising
(i), a reducing agent, a buffering agent, a transchelating agent, and
instructions for the preparation and use of the radiopharmaceutical in
the imaging of amyloid or an amyloid-related condition. The agents are
used for imaging amyloid deposition and for diagnosing an amyloid related

CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |:||||
 Db 1 KVVFFA 6

RESULT 51

ID AAU96811 standard; peptide; 6 AA.

XX AC AAU96811;

XX DT 30-JUL-2002 (first entry)

XX DE Amyloid targeting peptide #1.

XX KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 1. 6 /note= "preferably D-form residue"

XX PN WO200207781-A2.

XX PD 31-JAN-2002.

XX PF 25-JUL-2001; 2001WO-CA001071.

XX PR 25-JUL-2000; 2000US-0220808P.

XX PR 24-JUL-2001; 2001US-00915092.

XX PA (NEUR-) NEUROCHEM INC.

XX PI Gervais F, Kong X, Chalifour R, Migneault D;

XX DR WPI; 2002-371447/40.

XX PT New amyloid-targeting imaging agents useful for in vivo imaging amyloid

XX PT plaques and/or for the treatment of amyloidosis disorders.

XX PS Claim 49; Page 21; 57pp; English.

XX CC The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A₁-A₂-A₃-A₄-A₅-A₆-A₇-A₈-A₉-A₁₀-A₁₁-A₁₂-A₁₃-A₁₄-A₁₅-A₁₆-A₁₇-A₁₈-A₁₉-A₂₀-A₂₁-A₂₂-A₂₃-A₂₄-A₂₅-A₂₆-A₂₇-A₂₈-A₂₉-A₃₀-A₃₁-A₃₂-A₃₃-A₃₄-A₃₅-A₃₆-A₃₇-A₃₈-A₃₉-A₄₀-A₄₁-A₄₂-A₄₃-A₄₄-A₄₅-A₄₆-A₄₇-A₄₈-A₄₉-A₅₀-A₅₁-A₅₂-A₅₃-A₅₄-A₅₅-A₅₆-A₅₇-A₅₈-A₅₉-A₆₀-A₆₁-A₆₂-A₆₃-A₆₄-A₆₅-A₆₆-A₆₇-A₆₈-A₆₉-A₇₀-A₇₁-A₇₂-A₇₃-A₇₄-A₇₅-A₇₆-A₇₇-A₇₈-A₇₉-A₈₀-A₈₁-A₈₂-A₈₃-A₈₄-A₈₅-A₈₆-A₈₇-A₈₈-A₈₉-A₉₀-A₉₁-A₉₂-A₉₃-A₉₄-A₉₅-A₉₆-A₉₇-A₉₈-A₉₉-A₁₀₀-A₁₀₁-A₁₀₂-A₁₀₃-A₁₀₄-A₁₀₅-A₁₀₆-A₁₀₇-A₁₀₈-A₁₀₉-A₁₁₀-A₁₁₁-A₁₁₂-A₁₁₃-A₁₁₄-A₁₁₅-A₁₁₆-A₁₁₇-A₁₁₈-A₁₁₉-A₁₂₀-A₁₂₁-A₁₂₂-A₁₂₃-A₁₂₄-A₁₂₅-A₁₂₆-A₁₂₇-A₁₂₈-A₁₂₉-A₁₃₀-A₁₃₁-A₁₃₂-A₁₃₃-A₁₃₄-A₁₃₅-A₁₃₆-A₁₃₇-A₁₃₈-A₁₃₉-A₁₄₀-A₁₄₁-A₁₄₂-A₁₄₃-A₁₄₄-A₁₄₅-A₁₄₆-A₁₄₇-A₁₄₈-A₁₄₉-A₁₅₀-A₁₅₁-A₁₅₂-A₁₅₃-A₁₅₄-A₁₅₅-A₁₅₆-A₁₅₇-A₁₅₈-A₁₅₉-A₁₆₀-A₁₆₁-A₁₆₂-A₁₆₃-A₁₆₄-A₁₆₅-A₁₆₆-A₁₆₇-A₁₆₈-A₁₆₉-A₁₇₀-A₁₇₁-A₁₇₂-A₁₇₃-A₁₇₄-A₁₇₅-A₁₇₆-A₁₇₇-A₁₇₈-A₁₇₉-A₁₈₀-A₁₈₁-A₁₈₂-A₁₈₃-A₁₈₄-A₁₈₅-A₁₈₆-A₁₈₇-A₁₈₈-A₁₈₉-A₁₉₀-A₁₉₁-A₁₉₂-A₁₉₃-A₁₉₄-A₁₉₅-A₁₉₆-A₁₉₇-A₁₉₈-A₁₉₉-A₂₀₀-A₂₀₁-A₂₀₂-A₂₀₃-A₂₀₄-A₂₀₅-A₂₀₆-A₂₀₇-A₂₀₈-A₂₀₉-A₂₁₀-A₂₁₁-A₂₁₂-A₂₁₃-A₂₁₄-A₂₁₅-A₂₁₆-A₂₁₇-A₂₁₈-A₂₁₉-A₂₂₀-A₂₂₁-A₂₂₂-A₂₂₃-A₂₂₄-A₂₂₅-A₂₂₆-A₂₂₇-A₂₂₈-A₂₂₉-A₂₃₀-A₂₃₁-A₂₃₂-A₂₃₃-A₂₃₄-A₂₃₅-A₂₃₆-A₂₃₇-A₂₃₈-A₂₃₉-A₂₄₀-A₂₄₁-A₂₄₂-A₂₄₃-A₂₄₄-A₂₄₅-A₂₄₆-A₂₄₇-A₂₄₈-A₂₄₉-A₂₅₀-A₂₅₁-A₂₅₂-A₂₅₃-A₂₅₄-A₂₅₅-A₂₅₆-A₂₅₇-A₂₅₈-A₂₅₉-A₂₆₀-A₂₆₁-A₂₆₂-A₂₆₃-A₂₆₄-A₂₆₅-A₂₆₆-A₂₆₇-A₂₆₈-A₂₆₉-A₂₇₀-A₂₇₁-A₂₇₂-A₂₇₃-A₂₇₄-A₂₇₅-A₂₇₆-A₂₇₇-A₂₇₈-A₂₇₉-A₂₈₀-A₂₈₁-A₂₈₂-A₂₈₃-A₂₈₄-A₂₈₅-A₂₈₆-A₂₈₇-A₂₈₈-A₂₈₉-A₂₉₀-A₂₉₁-A₂₉₂-A₂₉₃-A₂₉₄-A₂₉₅-A₂₉₆-A₂₉₇-A₂₉₈-A₂₉₉-A₃₀₀-A₃₀₁-A₃₀₂-A₃₀₃-A₃₀₄-A₃₀₅-A₃₀₆-A₃₀₇-A₃₀₈-A₃₀₉-A₃₁₀-A₃₁₁-A₃₁₂-A₃₁₃-A₃₁₄-A₃₁₅-A₃₁₆-A₃₁₇-A₃₁₈-A₃₁₉-A₃₂₀-A₃₂₁-A₃₂₂-A₃₂₃-A₃₂₄-A₃₂₅-A₃₂₆-A₃₂₇-A₃₂₈-A₃₂₉-A₃₃₀-A₃₃₁-A₃₃₂-A₃₃₃-A₃₃₄-A₃₃₅-A₃₃₆-A₃₃₇-A₃₃₈-A₃₃₉-A₃₄₀-A₃₄₁-A₃₄₂-A₃₄₃-A₃₄₄-A₃₄₅-A₃₄₆-A₃₄₇-A₃₄₈-A₃₄₉-A₃₅₀-A₃₅₁-A₃₅₂-A₃₅₃-A₃₅₄-A₃₅₅-A₃₅₆-A₃₅₇-A₃₅₈-A₃₅₉-A₃₆₀-A₃₆₁-A₃₆₂-A₃₆₃-A₃₆₄-A₃₆₅-A₃₆₆-A₃₆₇-A₃₆₈-A₃₆₉-A₃₇₀-A₃₇₁-A₃₇₂-A₃₇₃-A₃₇₄-A₃₇₅-A₃₇₆-A₃₇₇-A₃₇₈-A₃₇₉-A₃₈₀-A₃₈₁-A₃₈₂-A₃₈₃-A₃₈₄-A₃₈₅-A₃₈₆-A₃₈₇-A₃₈₈-A₃₈₉-A₃₉₀-A₃₉₁-A₃₉₂-A₃₉₃-A₃₉₄-A₃₉₅-A₃₉₆-A₃₉₇-A₃₉₈-A₃₉₉-A₄₀₀-A₄₀₁-A₄₀₂-A₄₀₃-A₄₀₄-A₄₀₅-A₄₀₆-A₄₀₇-A₄₀₈-A₄₀₉-A₄₁₀-A₄₁₁-A₄₁₂-A₄₁₃-A₄₁₄-A₄₁₅-A₄₁₆-A₄₁₇-A₄₁₈-A₄₁₉-A₄₂₀-A₄₂₁-A₄₂₂-A₄₂₃-A₄₂₄-A₄₂₅-A₄₂₆-A₄₂₇-A₄₂₈-A₄₂₉-A₄₃₀-A₄₃₁-A₄₃₂-A₄₃₃-A₄₃₄-A₄₃₅-A₄₃₆-A₄₃₇-A₄₃₈-A₄₃₉-A₄₄₀-A₄₄₁-A₄₄₂-A₄₄₃-A₄₄₄-A₄₄₅-A₄₄₆-A₄₄₇-A₄₄₈-A₄₄₉-A₄₅₀-A₄₅₁-A₄₅₂-A₄₅₃-A₄₅₄-A₄₅₅-A₄₅₆-A₄₅₇-A₄₅₈-A₄₅₉-A₄₆₀-A₄₆₁-A₄₆₂-A₄₆₃-A₄₆₄-A₄₆₅-A₄₆₆-A₄₆₇-A₄₆₈-A₄₆₉-A₄₇₀-A₄₇₁-A₄₇₂-A₄₇₃-A₄₇₄-A₄₇₅-A₄₇₆-A₄₇₇-A₄₇₈-A₄₇₉-A₄₈₀-A₄₈₁-A₄₈₂-A₄₈₃-A₄₈₄-A₄₈₅-A₄₈₆-A₄₈₇-A₄₈₈-A₄₈₉-A₄₉₀-A₄₉₁-A₄₉₂-A₄₉₃-A₄₉₄-A₄₉₅-A₄₉₆-A₄₉₇-A₄₉₈-A₄₉₉-A₅₀₀-A₅₀₁-A₅₀₂-A₅₀₃-A₅₀₄-A₅₀₅-A₅₀₆-A₅₀₇-A₅₀₈-A₅₀₉-A₅₁₀-A₅₁₁-A₅₁₂-A₅₁₃-A₅₁₄-A₅₁₅-A₅₁₆-A₅₁₇-A₅₁₈-A₅₁₉-A₅₂₀-A₅₂₁-A₅₂₂-A₅₂₃-A₅₂₄-A₅₂₅-A₅₂₆-A₅₂₇-A₅₂₈-A₅₂₉-A₅₃₀-A₅₃₁-A₅₃₂-A₅₃₃-A₅₃₄-A₅₃₅-A₅₃₆-A₅₃₇-A₅₃₈-A₅₃₉-A₅₄₀-A₅₄₁-A₅₄₂-A₅₄₃-A₅₄₄-A₅₄₅-A₅₄₆-A₅₄₇-A₅₄₈-A₅₄₉-A₅₅₀-A₅₅₁-A₅₅₂-A₅₅₃-A₅₅₄-A₅₅₅-A₅₅₆-A₅₅₇-A₅₅₈-A₅₅₉-A₅₆₀-A₅₆₁-A₅₆₂-A₅₆₃-A₅₆₄-A₅₆₅-A₅₆₆-A₅₆₇-A₅₆₈-A₅₆₉-A₅₇₀-A₅₇₁-A₅₇₂-A₅₇₃-A₅₇₄-A₅₇₅-A₅₇₆-A₅₇₇-A₅₇₈-A₅₇₉-A₅₈₀-A₅₈₁-A₅₈₂-A₅₈₃-A₅₈₄-A₅₈₅-A₅₈₆-A₅₈₇-A₅₈₈-A₅₈₉-A₅₉₀-A₅₉₁-A₅₉₂-A₅₉₃-A₅₉₄-A₅₉₅-A₅₉₆-A₅₉₇-A₅₉₈-A₅₉₉-A₆₀₀-A₆₀₁-A₆₀₂-A₆₀₃-A₆₀₄-A₆₀₅-A₆₀₆-A₆₀₇-A₆₀₈-A₆₀₉-A₆₁₀-A₆₁₁-A₆₁₂-A₆₁₃-A₆₁₄-A₆₁₅-A₆₁₆-A₆₁₇-A₆₁₈-A₆₁₉-A₆₂₀-A₆₂₁-A₆₂₂-A₆₂₃-A₆₂₄-A₆₂₅-A₆₂₆-A₆₂₇-A₆₂₈-A₆₂₉-A₆₃₀-A₆₃₁-A₆₃₂-A₆₃₃-A₆₃₄-A₆₃₅-A₆₃₆-A₆₃₇-A₆₃₈-A₆₃₉-A₆₄₀-A₆₄₁-A₆₄₂-A₆₄₃-A₆₄₄-A₆₄₅-A₆₄₆-A₆₄₇-A₆₄₈-A₆₄₉-A₆₅₀-A₆₅₁-A₆₅₂-A₆₅₃-A₆₅₄-A₆₅₅-A₆₅₆-A₆₅₇-A₆₅₈-A₆₅₉-A₆₆₀-A₆₆₁-A₆₆₂-A₆₆₃-A₆₆₄-A₆₆₅-A₆₆₆-A₆₆₇-A₆₆₈-A₆₆₉-A₆₇₀-A₆₇₁-A₆₇₂-A₆₇₃-A₆₇₄-A₆₇₅-A₆₇₆-A₆₇₇-A₆₇₈-A₆₇₉-A₆₈₀-A₆₈₁-A₆₈₂-A₆₈₃-A₆₈₄-A₆₈₅-A₆₈₆-A₆₈₇-A₆₈₈-A₆₈₉-A₆₉₀-A₆₉₁-A₆₉₂-A₆₉₃-A₆₉₄-A₆₉₅-A₆₉₆-A₆₉₇-A₆₉₈-A₆₉₉-A₇₀₀-A₇₀₁-A₇₀₂-A₇₀₃-A₇₀₄-A₇₀₅-A₇₀₆-A₇₀₇-A₇₀₈-A₇₀₉-A₇₁₀-A₇₁₁-A₇₁₂-A₇₁₃-A₇₁₄-A₇₁₅-A₇₁₆-A₇₁₇-A₇₁₈-A₇₁₉-A₇₂₀-A₇₂₁-A₇₂₂-A₇₂₃-A₇₂₄-A₇₂₅-A₇₂₆-A₇₂₇-A₇₂₈-A₇₂₉-A₇₃₀-A₇₃₁-A₇₃₂-A₇₃₃-A₇₃₄-A₇₃₅-A₇₃₆-A₇₃₇-A₇₃₈-A₇₃₉-A₇₄₀-A₇₄₁-A₇₄₂-A₇₄₃-A₇₄₄-A₇₄₅-A₇₄₆-A₇₄₇-A₇₄₈-A₇₄₉-A₇₅₀-A₇₅₁-A₇₅₂-A₇₅₃-A₇₅₄-A₇₅₅-A₇₅₆-A₇₅₇-A₇₅₈-A₇₅₉-A₇₆₀-A₇₆₁-A₇₆₂-A₇₆₃-A₇₆₄-A₇₆₅-A₇₆₆-A₇₆₇-A₇₆₈-A₇₆₉-A₇₇₀-A₇₇₁-A₇₇₂-A₇₇₃-A₇₇₄-A₇₇₅-A₇₇₆-A₇₇₇-A₇₇₈-A₇₇₉-A₇₈₀-A₇₈₁-A₇₈₂-A₇₈₃-A₇₈₄-A₇₈₅-A₇₈₆-A₇₈₇-A₇₈₈-A₇₈₉-A₇₉₀-A₇₉₁-A₇₉₂-A₇₉₃-A₇₉₄-A₇₉₅-A₇₉₆-A₇₉₇-A₇₉₈-A₇₉₉-A₈₀₀-A₈₀₁-A₈₀₂-A₈₀₃-A₈₀₄-A₈₀₅-A₈₀₆-A₈₀₇-A₈₀₈-A₈₀₉-A₈₁₀-A₈₁₁-A₈₁₂-A₈₁₃-A₈₁₄-A₈₁₅-A₈₁₆-A₈₁₇-A₈₁₈-A₈₁₉-A₈₂₀-A₈₂₁-A₈₂₂-A₈₂₃-A₈₂₄-A₈₂₅-A₈₂₆-A₈₂₇-A₈₂₈-A₈₂₉-A₈₃₀-A₈₃₁-A₈₃₂-A₈₃₃-A₈₃₄-A₈₃₅-A₈₃₆-A₈₃₇-A₈₃₈-A₈₃₉-A₈₄₀-A₈₄₁-A₈₄₂-A₈₄₃-A₈₄₄-A₈₄₅-A₈₄₆-A₈₄₇-A₈₄₈-A₈₄₉-A₈₅₀-A₈₅₁-A₈₅₂-A₈₅₃-A₈₅₄-A₈₅₅-A₈₅₆-A₈₅₇-A₈₅₈-A₈₅₉-A₈₆₀-A₈₆₁-A₈₆₂-A₈₆₃-A₈₆₄-A₈₆₅-A₈₆₆-A₈₆₇-A₈₆₈-A₈₆₉-A₈₇₀-A₈₇₁-A₈₇₂-A₈₇₃-A₈₇₄-A₈₇₅-A₈₇₆-A₈₇₇-A₈₇₈-A₈₇₉-A₈₈₀-A₈₈₁-A₈₈₂-A₈₈₃-A₈₈₄-A₈₈₅-A₈₈₆-A₈₈₇-A₈₈₈-A₈₈₉-A₈₉₀-A₈₉₁-A₈₉₂-A₈₉₃-A₈₉₄-A₈₉₅-A₈₉₆-A₈₉₇-A₈₉₈-A₈₉₉-A₉₀₀-A₉₀₁-A₉₀₂-A₉₀₃-A₉₀₄-A₉₀₅-A₉₀₆-A₉₀₇-A₉₀₈-A₉₀₉-A₉₁₀-A₉₁₁-A₉₁₂-A₉₁₃-A₉₁₄-A₉₁₅-A₉₁₆-A₉₁₇-A₉₁₈-A₉₁₉-A₉₂₀-A₉₂₁-A₉₂₂-A₉₂₃-A₉₂₄-A₉₂₅-A₉₂₆-A₉₂₇-A₉₂₈-A₉₂₉-A₉₃₀-A₉₃₁-A₉₃₂-A₉₃₃-A₉₃₄-A₉₃₅-A₉₃₆-A₉₃₇-A₉₃₈-A₉₃₉-A₉₄₀-A₉₄₁-A₉₄₂-A₉₄₃-A₉₄₄-A₉₄₅-A₉₄₆-A₉₄₇-A₉₄₈-A₉₄₉-A₉₅₀-A₉₅₁-A₉₅₂-A₉₅₃-A₉₅₄-A₉₅₅-A₉₅₆-A₉₅₇-A₉₅₈-A₉₅₉-A₉₆₀-A₉₆₁-A₉₆₂-A₉₆₃-A₉₆₄-A₉₆₅-A₉₆₆-A₉₆₇-A₉₆₈-A₉₆₉-A₉₇₀-A₉₇₁-A₉₇₂-A₉₇₃-A₉₇₄-A₉₇₅-A₉₇₆-A₉₇₇-A₉₇₈-A₉₇₉-A₉₈₀-A₉₈₁-A₉₈₂-A₉₈₃-A₉₈₄-A₉₈₅-A₉₈₆-A₉₈₇-A₉₈₈-A₉₈₉-A₉₉₀-A₉₉₁-A₉₉₂-A₉₉₃-A₉₉₄-A₉₉₅-A₉₉₆-A₉₉₇-A₉₉₈-A₉₉₉-A₁₀₀₀-A₁₀₀₁-A₁₀₀₂-A₁₀₀₃-A₁₀₀₄-A₁₀₀₅-A₁₀₀₆-A₁₀₀₇-A₁₀₀₈-A₁₀₀₉-A₁₀₁₀-A₁₀₁₁-A₁₀₁₂-A₁₀₁₃-A₁₀₁₄-A₁₀₁₅-A₁₀₁₆-A₁₀₁₇-A₁₀₁₈-A₁₀₁₉-A₁₀₂₀-A₁₀₂₁-A₁₀₂₂-A₁₀₂₃-A₁₀₂₄-A₁₀₂₅-A₁₀₂₆-A₁₀₂₇-A₁₀₂₈-A₁₀₂₉-A₁₀₃₀-A₁₀₃₁-A₁₀₃₂-A₁₀₃₃-A₁₀₃₄-A₁₀₃₅-A₁₀₃₆-A₁₀₃₇-A₁₀₃₈-A₁₀₃₉-A₁₀₄₀-A₁₀₄₁-A₁₀₄₂-A₁₀₄₃-A₁₀₄₄-A₁₀₄₅-A₁₀₄₆-A₁₀₄₇-A₁₀₄₈-A₁₀₄₉-A₁₀₅₀-A₁₀₅₁-A₁₀₅₂-A₁₀₅₃-A₁₀₅₄-A₁₀₅₅-A₁₀₅₆-A₁₀₅₇-A₁₀

CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 XX
 SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 Db |:||||
 1 KIVFFA 6

RESULT 53

AAU11648
 ID AAU11648 standard; peptide; 6 AA.
 XX

AC AAU11648;

XX 09-APR-2002 (first entry)

DE Peptide #1, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.

XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
 XX

OS Synthetic.

XX WO200185093-A2.

PN 15-NOV-2001.

PD 22-DEC-2000; 2000WO-18002078.

XX 23-DEC-1999; 99US-0171877P.

XX (NEUR-) NEUROCHEM INC.

XX Green AM, Gervais F;

XX WPI; 2002-075222/10.

XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.

XX Disclosure; Page 10; 68pp; English.

XX The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 XX

SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db |:||||
 1 KIVFFA 6
 RESULT 54
 AAE35446
 ID AAE35446 standard; peptide; 6 AA.
 XX
 AC AAE35446;
 XX
 DT 17-JUN-2003 (first entry)
 XX
 DE Abeta peptide #17.
 XX
 KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT
 XX WO200296937-A2.
 PN
 XX 05-DEC-2002.
 XX
 PF 29-MAY-2002; 2002WO-CA000763.
 XX
 PR 29-MAY-2001; 2001US-00867847.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 PI Gervais F, Hebert L, Chalifour RJ, Kong X;
 XX WPI; 2003-201269/19.
 XX
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX
 PS Claim 1; Page 59; 44pp; English.
 XX
 CC The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX
 SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 1 KIVFFA 6

RESULT 55

AAE35438
ID AAE35438 standard; peptide; 6 AA.

XX AC AAE35438;

XX DT 17-JUN-2003 (first entry)

XX DE Abeta peptide #9.

XX KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotic;
chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
ulcer; antiinflammatory; cytostatic; uropathic; therapy.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT Misc-difference 1..6 /note= "D-form residues"

XX PN WO200296937-A2.

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-CA000763.

XX PR 29-MAY-2001; 2001US-00867847.

XX PA (NEUR-) NEUROCHEM INC.

XX PI Gervais F, Hebert L, Chalfour RJ, Kong X;

XX DR WPI; 2003-201269/19.

XX PS Prevention and/or treatment of an amyloid-related disease e.g.

XX PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.

XX TS Claim 1; Page 58; 4pp; English.

XX CC The invention relates to a method for prevention and/or treatment of an
XX CC amyloid-related disease which comprises administration of an all-D -
XX CC amyloid-beta peptide. The method is used for preventing and/or treating
XX CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
XX CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
XX CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
XX CC the mammal; and reducing or inhibiting the formation of plaques. It is
XX CC also used for treating AA (reactive) amyloid diseases including
XX CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
XX CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
XX CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
XX CC disease. AA deposits are also produced as a result of chronic microbial
XX CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
XX CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
XX CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
XX CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
XX CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
XX CC present sequence is an Abeta peptide used to illustrate the method of the
XX CC invention

SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 1 KIVFFA 6

RESULT 56

ADQ37322
ID ADQ37322 standard; peptide; 6 AA.

XX AC ADQ37322;

XX DT 07-OCT-2004 (first entry)

XX DE Antifibrillogenic amyloidosis inhibiting peptide.

XX KW amyloid-beta; amyloid-beta related disease;
amyloid-beta fibril formation; immune response; neurotic;
neuroprotective; cerebroprotective; haemostatic; ophthalmological;
antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;
anticongulans; anti-HIV; antiparkinsonian; muscular; neuroleptic;
cardiant; antidepressant; endocrine; hypnotic;
amyloid-beta fibril formation modulator; immune system modulator;
Alzheimer's disease; mild cognitive impairment;
mild-to-moderate cognitive impairment; vascular dementia;
cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
senile dementia; Down's syndrome; inclusion body myositis;
age-related macular degeneration; hypothyroidism;
cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
behavioural dysfunction; neurological condition; psychological condition;
vaccine antigen.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-eite 6 /note= "amidated"

XX PN WO2004058239-A1.

XX PD 15-JUL-2004.

XX PF 24-DEC-2003; 2003WO-CA002021.

XX PR 24-DEC-2002; 2002US-0436379P.

XX PR 23-JUN-2003; 2003US-0482214P.

XX PA (NEUR-) NEUROCHEM INT LTD.

XX PI Gervais F, Bellini F;

XX DR WPI; 2004-543342/52.

XX PT Composition for treating e.g. Alzheimer's disease comprises first agent
XX PT that prevents or treats amyloid-beta related disease and second agent
XX PT that is either a peptide or peptidomimetic or an immune system modulator.
XX PS Disclosure; Page 69; 143pp; English.

XX CC The present invention describes compositions (C) comprising: (a) a first
XX CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
XX CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
XX CC modulates amyloid-beta fibril formation or induces a prophylactic or
XX CC therapeutic immune response against amyloid-beta fibril formation; or
XX CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
XX CC fibril formation. Also described is a kit comprising (C). (C) have
XX CC neurotropic, neuroprotective, cerebroprotective, haemostatic, tranquiliser,
XX CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,

CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 1 KIVFFA 6

RESULT 57

ADQ37270

ID ADQ37270 standard; peptide; 6 AA.

XX AC ADQ37270;

XX XT 07-OCT-2004 (first entry)

XX DE Vaccine antigen amyloid-beta related amino acid sequence.

XX KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 XX KW vaccine antigen.

OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 1..6

FT /note= "D-form residues"

FT Modified-site 6

/note= "amidated"

XX PN WO2004058239-A1.

XX PD 15-JUL-2004.

XX PF 24-DEC-2003; 2003WO-CA002021.

XX PR 24-DEC-2002; 2002US-0436379P.

XX PR 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent
 FT that prevents or treats amyloid-beta related disease and second agent
 FT that is either a peptide or peptidomimetic or an immune system modulator.

XX Disclosure; Page 67; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, muscular,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.

XX SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;

Best Local Similarity 83.3%; Pred. No. 2e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 1 KIVFFA 6

RESULT 58
ADQ37313
ID ADQ37313 standard; peptide; 6 AA.
XX
AC ADQ37313;
XX
DT 07-OCT-2004 (first entry)
XX
DE Antifibrillogenic amyloidosis inhibiting peptide.
XX
KW amyloid-beta; amyloid-beta related disease;
KW amyloid-beta fibril formation; immune response; neurotropic;
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
KW cardiant; antidepressant; endocrine; hypnotic;
KW amyloid-beta fibril formation modulator; immune system modulator;
KW Alzheimer's disease; mild cognitive impairment;
KW mild-to-moderate cognitive impairment; vascular dementia;
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
KW senile dementia; Down's syndrome; inclusion body myositis;
KW age-related macular degeneration; hypothyroidism;
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
KW behavioural dysfunction; neurological condition; psychological condition;
KW vaccine antigen.
XX
OS Synthetic.
XX
FN WO2004058239-A1.
XX
PD 15-JUL-2004.
XX
PP 24-DEC-2003; 2003WO-CA002021.
XX
PR 24-DEC-2002; 2002US-0436379P.
PR 23-JUN-2003; 2003US-0482214P.
XX
XX (NEUR-) NEUROCHEM INT LTD.
XX
PI Gervais F, Bellini F;
XX
XX WPI; 2004-543342/52.
XX
DR Composition for treating e.g. Alzheimer's disease comprises first agent
PT that prevents or treats amyloid-beta related disease and second agent
PT that is either a peptide or peptidomimetic or an immune system modulator.
XX
PS Disclosure; Page 69; 143pp; English.
XX
CC The present invention describes compositions (C) comprising: (a) a first
CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
CC modulates amyloid-beta fibril formation or induces a prophylactic or
CC therapeutic immune response against amyloid-beta fibril formation; or
CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
CC fibril formation. Also described is a kit comprising (C). (C) have
CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
CC and can be used as amyloid-beta fibril formation modulators, and as
CC immune system modulators. (C) can be used for preventing or treating an
CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
CC Down's syndrome, inclusion body myositis, age-related macular
CC degeneration, or a condition associated with Alzheimer's disease
CC (including hypothyroidism, cerebrovascular disease, cardiovascular
CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
CC aggression, or incontinence), a neurological condition (e.g. Huntington's
CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia

CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
CC field deficits, incoordination, gait disturbance, transient ischaemic
CC attack or stroke, transient alertness, attention deficit, frequent falls,
CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
CC damage), or a psychological condition (e.g. depression, delusions,
CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
CC having amyloid-beta deposits. The present sequence represents a peptide
CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
CC in the exemplification of the present invention.
XX
SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 1 KIVFFA 6

RESULT 59
ADQ37262
ID ADQ37262 standard; peptide; 6 AA.
XX
AC ADQ37262;
XX
DT 07-OCT-2004 (first entry)
XX
DE Vaccine antigen amyloid-beta related amino acid sequence.
XX
KW amyloid-beta; amyloid-beta related disease;
KW amyloid-beta fibril formation; immune response; neurotropic;
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
KW cardiant; antidepressant; endocrine; hypnotic;
KW amyloid-beta fibril formation modulator; immune system modulator;
KW Alzheimer's disease; mild cognitive impairment;
KW mild-to-moderate cognitive impairment; vascular dementia;
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
KW senile dementia; Down's syndrome; inclusion body myositis;
KW age-related macular degeneration; hypothyroidism;
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
KW behavioural dysfunction; neurological condition; psychological condition;
KW vaccine antigen.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..6 /note= "D-form residues"
XX
XX WO2004058239-A1.
XX
PD 15-JUL-2004.
XX
PP 24-DEC-2003; 2003WO-CA002021.
XX
PR 24-DEC-2002; 2002US-0436379P.
PR 23-JUN-2003; 2003US-0482214P.
XX
XX (NEUR-) NEUROCHEM INT LTD.
XX
PI Gervais F, Bellini F;
XX
XX WPI; 2004-543342/52.
XX

PT Composition for treating e.g. Alzheimer's disease comprises first agent
PT that prevents or treats amyloid-beta related disease and second agent
PT that is either a peptide or peptidomimetic or an immune system modulator.
XX
XX
PS Disclosure; Page 67; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
CC modulates amyloid-beta fibril formation or induces a prophylactic or
CC therapeutic immune response against amyloid-beta fibril formation; or
CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
CC fibril formation. Also described is a kit comprising (C). (C) have
CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
CC ophthalmological, antithyroid, vasotropic, cardiovascular, muscular,
CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
CC and can be used as amyloid-beta fibril formation modulators, and as
CC immune system modulators. (C) can be used for preventing or treating an
CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
CC Down's syndrome, inclusion body myositis, age-related macular
CC degeneration, or a condition associated with Alzheimer's disease
CC (including hypothyroidism, cerebrovascular disease, cardiovascular
CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
CC aggression, or incontinence), a neurological condition (e.g. Huntington's
CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
CC field deficits, incoordination, gait disturbance, transient ischaemic
CC attack or stroke, transient alertness, attention deficit, frequent falls,
CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
CC damage), or a psychological condition (e.g. depression, delusions,
CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
CC excessive guilt) in a subject e.g. human having a genomic mutation in an
CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
CC having amyloid-beta deposits. The present sequence represents a peptide
CC that can be used as a vaccine antigen in the exemplification of the
XX present invention.

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 1 KIVFFA 6

RESULT 60

ADV37921
ID ADY37921 standard; peptide; 6 AA.

XX
AC ADY37921;

XX 19-MAY-2005 (first entry)

XX Amyloid-targeting peptide, SEQ ID NO:1, for use in imaging agent.

XX Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimer's disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.

XX Synthetic.

XX

PN US2005048000-A1.
XX
PD 03-MAR-2005.

XX 03-DEC-2003; 2003US-00728028.

XX 25-JUL-2000; 2000US-0220808P.

PR 24-JUL-2001; 2001US-00915092.

PR 29-JAN-2003; 2003US-0443291P.

XX (NEUR-) NEUROCHEM INT LTD.

PI Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2005-212201/22.

XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
encephalopathy, primary amyloidosis or Alzheimer's disease.

PS Disclosure; SEQ ID NO 1; 34pp; English.

XX The invention relates to an amyloid-targeting imaging agent. The imaging
agent comprises an amyloid targeting moiety (such as a peptide) joined to
a labeling moiety via a linking moiety, and is preferably able to cross
the blood-brain barrier. The invention also relates to a kit for
preparing a radiopharmaceutical preparation from the imaging agent of the
invention, a method for imaging amyloid deposition in a patient and a
method for diagnosing an amyloid-related condition in a patient. The
amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
transmissible cerebral amyloidosis (also known as transmissible virus
dementias), familial CJD, scrapie, transmissible mink encephalopathy,
bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
mediated diseases, dialysis-related amyloidosis, light chain-related
amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
patient. The agent does not exhibit excessive toxicity or irritation,
does not induce an allergic response, and permits an earlier diagnosis of
amyloid-related conditions, thereby allowing earlier treatment and hence
prevention of the undesirable effects of such disorders. Sequences
ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
the amyloid-targeting moiety in an imaging agent of the invention.

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 1 KIVFFA 6

RESULT 61

ADV37929
ID ADY37929 standard; peptide; 6 AA.

XX
AC ADY37929;

XX 19-MAY-2005 (first entry)

XX Amyloid-targeting peptide, SEQ ID NO:9, for use in imaging agent.

XX Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimer's disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.

XX Synthetic.

XX

FH Key Location/Qualifiers
 FT Modified-site 6
 XX /note= "C-terminal amide"
 XX US2005048000-A1.
 XX 03-MAR-2005.
 XX 03-DEC-2003; 2003US-00728028.
 XX 25-JUL-2000; 2000US-0220808P.
 XX 24-JUL-2001; 2001US-00915092.
 XX 29-JAN-2003; 2003US-0443281P.
 XX (NEUR-) NEUROCHEM INT LTD.
 XX Gervais F, Kong X, Chalifour R, Migneault D;
 XX WPI; 2005-212201/22.
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
 XX related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
 XX encephalopathy, primary amyloidosis or Alzheimer's disease.
 XX Disclosure; SEQ ID NO 9; 34pp; English.
 XX The invention relates to an amyloid-targeting imaging agent. The imaging
 XX agent comprises an amyloid targeting moiety (such as a peptide) joined to
 XX a labeling moiety via a linking moiety, and is preferably able to cross
 XX the blood-brain barrier. The invention also relates to a kit for
 XX preparing a radiopharmaceutical preparation from the imaging agent of the
 XX invention, a method for imaging amyloid deposition in a patient and a
 XX method for diagnosing an amyloid-related condition in a patient. The
 XX amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
 XX related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
 XX transmissible cerebral amyloidosis (also known as transmissible virus
 XX dementia), familial CJD, scrapie, transmissible mink encephalopathy,
 XX bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
 XX type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
 XX non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
 XX mediated diseases, dialysis-related amyloidosis, light chain-related
 XX amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
 XX patient. The agent does not exhibit excessive toxicity or irritation,
 XX does not induce an allergic response, and permits an earlier diagnosis of
 XX amyloid-related conditions, thereby allowing earlier treatment and hence
 XX prevention of the undesirable effects of such disorders. Sequences
 XX ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 XX the amyloid-targeting moiety in an imaging agent of the invention.
 XX Sequence 6 AA;
 SQ Query Match 96.6%; Score 28; DB 9; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFFA 6
 Db 1 KIVFFFA 6
 RESULT 62
 ABG26598
 ID ABG26598 standard; protein; 99 AA.
 XX AC ABG26598;
 XX 18-FEB-2002 (first entry)
 XX Novel human diagnostic protein #26589.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.
 XX WO200175067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US008631.
 XX 31-MAR-2000; 2000US-00540217.
 XX 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 XX Dmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX N-PSDB; AAS90785.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits and to assess
 XX biodiversity.
 XX Claim 20; SEQ ID NO 56957; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 XX sequences. (I) is useful as hybridisation probes, polymerase chain
 XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 XX and in recombinant production of (II). The polynucleotides are also used
 XX in diagnostics as expressed sequence tags for identifying expressed
 XX genes. (I) is useful in gene therapy techniques to restore normal
 XX activity of (II) or to treat disease states involving (II). (II) is
 XX useful for generating antibodies against it, detecting or quantitating a
 XX polypeptide in tissue, as molecular weight markers and as a food
 XX supplement. (II) and its binding partners are useful in medical imaging
 XX of sites expressing (II). (I) and (II) are useful for treating disorders
 XX involving aberrant protein expression or biological activity. The
 XX polypeptide and polynucleotide sequences have applications in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits to assess biodiversity
 XX and to produce other types of data and products dependent on DNA and
 XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 XX amino acid sequences of the invention. Note: The sequence data for this
 XX patent did not appear in the printed specification, but was obtained in
 XX electronic format directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 99 AA;
 SQ Query Match 96.6%; Score 28; DB 4; Length 99;
 Best Local Similarity 83.3%; Pred. No. 1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFFA 6
 Db 63 KIVFFFA 68
 RESULT 63
 ABM94314
 ID ABM94314 standard; protein; 123 AA.
 XX AC ABM94314;
 XX 02-JUN-2005 (first entry)
 XX M. xanthus protein sequence, seq id 13513.
 XX Transgenic plant; DNA replication; gene regulation; gene expression.
 XX Myxococcus xanthus.
 XX US6833447-B1.

XX PD 21-DEC-2004.
 XX XX
 XX PF 10-JUL-2001; 2001US-00902540.
 XX XX
 XX PR 10-JUL-2000; 2000US-0217883P.
 XX XX
 XX PA (MONS) MONSANTO TECHNOLOGY LLC.
 XX XX
 XX PI Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
 XX XX
 XX DR WPI; 2005-028716/03.
 XX XX
 XX PT New substantially purified Myxococcus xanthus nucleic acid molecule
 XX PT encoding a nitrite reductase, useful for determining gene expression,
 XX PT identifying mutations in a gene of interest, and for constructing
 XX PT mutations in a gene of interest.
 XX XX
 XX PS Example 2; SEQ ID NO 13513; 25pp; English.
 XX XX
 XX CC The invention relates to a substantially purified nucleic acid molecule
 XX CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
 XX CC recombinant DNA construct for expression of a nitrite reductase gene in a
 XX CC plant cell, and a plant cell comprising the recombinant DNA construct.
 XX CC The nucleic acid is useful for determining gene expression, identifying
 XX CC mutations in a gene of interest, and for constructing mutations in a gene
 XX CC of interest. Sequences given in records for SEQ IDs 9692-16825 represent
 XX CC a group of 7134 Myxococcus xanthus proteins and peptides. Note: The
 XX CC sequence data for this patent did not form part of the printed
 XX CC specification, but was obtained in electronic format directly from USPTO
 XX XX
 XX SQ Sequence 123 AA;
 Query Match 96.6%; Score 28; DB 9; Length 123;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 52 KVIFFA 57
 ||:||||
 RESULT 64
 ADM16726
 ID ADM16726 standard; protein; 393 AA.
 XX AC
 XX AD M16726;
 XX XX
 XX DT 17-JUN-2004 (first entry)
 XX DE PERL-P7-G8 protein.
 XX DE Phlebotomus ariasi; Phlebotomus perniciosus; Vaccine;
 XX KW Leishmania infection.
 XX KW Phlebotomus perniciosus.
 XX OS
 XX XX WO2004027041-A2.
 XX PN
 XX PD 01-APR-2004.
 XX PF 18-SEP-2003; 2003WO-US029833.
 XX PR 19-SEP-2002; 2002US-0412327P.
 XX PR 12-NOV-2002; 2002US-0425852P.
 XX XX
 XX PA (MERI-) Merial LTD.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Valenzuela JG, Ribiero JMC, Kamhawi S, Belkaid Y, Fischer L;
 XX PI Audonnet J, Milward F;
 XX XX WPI; 2004-295410/27.
 XX DR N-PSDB; ADM16685.
 XX XX
 XX PT New substantially purified salivary Phlebotomus ariasi or Phlebotomus
 XX PT perniciosus polypeptide, useful for inhibiting, treating or preventing
 XX PT Leishmania infection in a subject.
 XX XX
 XX PS Claim 1; SEQ ID NO 7; 200pp; English.
 XX XX
 XX CC The present invention relates to a substantially purified salivary
 XX CC Phlebotomus ariasi or Phlebotomus perniciosus polypeptide. The
 XX CC composition comprising the polypeptide or the nucleic acid encoding the
 XX CC polypeptide is useful for inducing an immune response to a P.
 XX CC and nucleic acids are useful for inducing an immune response to a P.
 XX CC ariasi or P. perniciosus polypeptide. It is also useful for inhibiting a
 XX CC symptom of a Leishmania infection or preventing a Leishmania infection in
 XX CC a subject. The present sequence represents a purified Phlebotomus ariasi
 XX CC protein.

DR N-PSDB; ADM16727.
 XX XX
 XX PT New substantially purified salivary Phlebotomus ariasi or Phlebotomus
 XX PT perniciosus polypeptide, useful for inhibiting, treating or preventing
 XX PT Leishmania infection in a subject.
 XX XX
 XX PS Claim 40; SEQ ID NO 49; 200pp; English.
 XX XX
 XX CC The present invention relates to a substantially purified salivary
 XX CC Phlebotomus ariasi or Phlebotomus perniciosus polypeptide. The
 XX CC composition comprising the polypeptide or the nucleic acid encoding the
 XX CC polypeptide is useful for inducing an immune response to a P.
 XX CC and nucleic acids are useful for inducing an immune response to a P.
 XX CC ariasi or P. perniciosus polypeptide. It is also useful for inhibiting a
 XX CC symptom of a Leishmania infection or preventing a Leishmania infection in
 XX CC a subject. The present sequence represents a purified Phlebotomus ariasi
 XX CC protein.
 XX XX
 XX SQ Sequence 393 AA;
 Query Match 96.6%; Score 28; DB 8; Length 393;
 Best Local Similarity 83.3%; Pred. No. 4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 299 KVIFFA 304
 ||:||||
 RESULT 65
 ADM16684
 ID ADM16684 standard; protein; 393 AA.
 XX AC
 XX AD M16684;
 XX XX
 XX DT 17-JUN-2004 (first entry)
 XX DE PRL-P4-D6 protein.
 XX DE Phlebotomus ariasi; Phlebotomus perniciosus; Vaccine;
 XX KW Leishmania infection.
 XX KW Phlebotomus ariasi.
 XX OS
 XX XX WO2004027041-A2.
 XX PN
 XX PD 01-APR-2004.
 XX PF 18-SEP-2003; 2003WO-US029833.
 XX PR 19-SEP-2002; 2002US-0412327P.
 XX PR 12-NOV-2002; 2002US-0425852P.
 XX XX
 XX PA (MERI-) Merial LTD.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Valenzuela JG, Ribiero JMC, Kamhawi S, Belkaid Y, Fischer L;
 XX PI Audonnet J, Milward F;
 XX XX WPI; 2004-295410/27.
 XX DR N-PSDB; ADM16685.
 XX XX
 XX PT New substantially purified salivary Phlebotomus ariasi or Phlebotomus
 XX PT perniciosus polypeptide, useful for inhibiting, treating or preventing
 XX PT Leishmania infection in a subject.
 XX XX
 XX PS Claim 1; SEQ ID NO 7; 200pp; English.
 XX XX
 XX CC The present invention relates to a substantially purified salivary
 XX CC Phlebotomus ariasi or Phlebotomus perniciosus polypeptide. The
 XX CC composition comprising the polypeptide or the nucleic acid encoding the
 XX CC polypeptide is useful for inducing an immune response to a P.
 XX CC and nucleic acids are useful for inducing an immune response to a P.

CC ariasi or P. perniciosus polypeptide. It is also useful for inhibiting a
 CC symptom of a Leishmania infection or preventing a Leishmania infection in
 CC a subject. The present sequence represents a purified Phlebotomus ariasi
 CC protein.

XX SQ Sequence 393 AA;

Query Match 96.6%; Score 28; DB 8; Length 393;
 Best Local Similarity 83.3%; Pred. No. 4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 ||:||||
 Db 298 KVIFFA 303

RESULT 66

ADO43456
 ID ADO43456 standard; protein; 399 AA.

XX AC ADO43456;

XX DT 29-JUL-2004 (first entry)

XX DE Lutzomyia longipalpis (sand fly) salivary protein LJM11.

XX KW LJM11; sand fly; leishmaniasis; diagnosis; vaccine; genetic immunisation.
 XX OS Lutzomyia longipalpis.

XX FH Key Location/Qualifiers
 FT Peptide 1..24
 FT Protein /label= Signal_peptide
 FT /label= Mature_protein

XX PN WO2004039958-A2.

XX PD 13-MAY-2004.

XX PF 29-OCT-2003; 2003WO-US034453.

XX PR 29-OCT-2002; 2002US-0422303P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PA (PESQ-) CENT PESQUISAS GONCALO MONIZ.

XX PI Valenzuela JG, Ribeiro JMC, Barral A, Netto M, Brodskyn C;
 XX PI Gomes R;

XX DR WPI; 2004-376184/35.
 XX DR N-PSDB; ADO43457.

XX PT Novel salivary Lutzomyia longipalpis polypeptide, useful for inhibiting
 XX PT symptom of Leishmania infection or preventing Leishmania infection in
 XX PT subjects.

XX PS Claim 2; SEQ ID NO 63; 145pp; English.

XX CC The present sequence is the protein sequence of LJM11, a Lutzomyia
 XX CC longipalpis (New World sand fly) salivary polypeptide. The invention
 XX CC provides substantially purified L. longipalpis polypeptides and the
 XX CC polynucleotides encoding them, as well as vectors, host cells, antibodies
 XX CC and pharmaceutical compositions comprising the polypeptides or
 XX CC polynucleotides. A claimed method for inducing an immune response to L
 XX CC longipalpis in a subject involves administering a L. longipalpis salivary
 XX CC polypeptide (or its variant or immunogenic fragment) or a polynucleotide
 XX CC encoding it. The immune response is a T-cell or B-cell response, and the
 XX CC subject is preferably a dog or a human. A claimed method for inhibiting a
 XX CC symptom of a Leishmania infection or preventing a Leishmania infection in
 XX CC a subject comprises administering a L. longipalpis salivary protein or
 XX CC polynucleotide. A claimed method of diagnosing Leishmania infection
 XX CC comprises contacting a solid substrate comprising at least 3, 6 or 10 L.

CC longipalpis salivary polypeptides with a sample from the subject and
 CC detecting binding of a component of the sample to at least one of the
 CC polypeptides.

XX SQ Sequence 399 AA;

Query Match 96.6%; Score 28; DB 8; Length 399;
 Best Local Similarity 83.3%; Pred. No. 4.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 ||:||||
 Db 305 KVIFFA 310

RESULT 67

ABB61977
 ID ABB61977 standard; protein; 564 AA.

XX AC ABB61977;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 12723.

XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE) PE CORP NY.
 XX PA Venter JC, Adams M, Li PWD, Myers EW;

XX PI WPI; 2001-656860/75.
 XX DR N-PSDB; ABL06080.

XX FT New isolated nucleic acid detection reagent for detecting 1000 or more
 XX FT genes from Drosophila and for elucidating cell signaling and cell-cell
 XX FT interactions.

XX PS Disclosure; SEQ ID NO 12723; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent
 XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
 XX CC useful in developmental biology and in elucidating cell signalling and
 XX CC cell-cell interactions in higher eukaryotes for the development of
 XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
 XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 XX CC ABB72072). The sequence data for this patent did not form part of the
 XX CC printed specification, but was obtained in electronic format directly
 XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 564 AA;

Query Match 93.1%; Score 27; DB 4; Length 564;
 Best Local Similarity 66.7%; Pred. No. 9.9e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 ||:||||
 Db 53 KVIFFA 58

RESULT 68
 ABB68472
 ID ABB68472 standard; protein; 1443 AA.
 XX
 AC ABB68472;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 32208.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 pharmacological.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 XX
 PS 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 XX
 DR N-PSDB; ABL12575.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 genes from Drosophila and for elucidating cell signaling and cell-cell
 interactions.
 XX
 PS Disclosure; SEQ ID NO 32208; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 capable of detecting 1000 or more genes from Drosophila. The invention is
 useful in developmental biology and in elucidating cell signalling and
 cell-cell interactions in higher eukaryotes for the development of
 insecticides, therapeutics and pharmaceutical drugs. The invention
 discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 ABB72072). The sequence data for this patent did not form part of the
 printed specification, but was obtained in electronic format directly
 from WIPO at filp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1443 AA;
 Query Match 93.1%; Score 27; DB 4; Length 1443;
 Best Local Similarity 66.7%; Pred. No. 2.5e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 1204 KLIFFA 1209
 XX
 RESULT 69
 AAW02314
 ID AAW02314 standard; peptide; 6 AA.
 XX
 AC AAW02314;
 XX
 DT 02-MAY-1997 (first entry)
 XX
 DE Beta-amyloid modulator peptide #5.
 XX
 KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
 cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
 familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
 KW

KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
 bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
 adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
 scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
 XX
 OS Synthetic.
 XX
 PN WO9628471-A1.
 XX
 PD 19-SEP-1996.
 XX
 PF 14-MAR-1996; 96WO-US003492.
 XX
 PR 14-MAR-1995; 95US-00404831.
 XX
 PR 07-JUN-1995; 95US-00475579.
 XX
 PR 27-OCT-1995; 95US-00548998.
 XX
 PA (PHAR-) PHARM PEPTIDES INC.
 XX
 PI Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ, Molineaux S;
 PI Kubasek W, Chin J, Lee J, Kelley M;
 XX
 DR WPI; 1996-433762/43.
 XX
 PT Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
 protein coupled (in)directly to at least 1 modifying gp., useful in
 treatment of Alzheimer's disease.
 XX
 PS Claim 16; Page 91; 106pp; English.
 XX
 CC AAW02310-W02332 represent the peptide portions of the beta-amyloid
 modulator compounds of the invention. Beta-amyloid peptide is a 4
 kilodalton peptide that is the major protein component of amyloid
 plaques. Amyloid plaques are present both in the brain lesions, and in
 the walls of cerebral blood vessels in Alzheimer's disease patients. The
 amyloid modulators of the invention comprise an amyloidogenic protein or
 peptide (such as this sequence) coupled directly or indirectly to at
 least one modifying group. The modifying group is preferably a cyclic,
 heterocyclic, or polycyclic group, such as decaalin, a cholanyl group, a
 biotin containing group, or a fluorescein containing group. These
 compounds then modulate the aggregation of these sequences to natural
 amyloid proteins or peptides when contacted with the natural
 amyloidogenic proteins or peptides. The modulator compounds can be used
 in the treatment of disorders associated with amyloidosis, such as
 familial amyloid polyneuropathy, familial amyloid cardiomyopathy,
 isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
 bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
 diabetes, insulinoma, familial Mediterranean fever, familial amyloid
 nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
 and other types of amyloidosis. The modulators are also useful for the
 treatment of disorders associated with beta-amyloidosis, especially
 Alzheimer's disease
 XX
 SQ Sequence 6 AA;
 Query Match 89.7%; Score 26; DB 2; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 1 KLVFFA 6
 XX
 RESULT 70
 AAW89378
 ID AAW89378 standard; peptide; 6 AA.
 XX
 AC AAW89378;
 XX
 DT 02-MAR-1999 (first entry)
 XX
 XX

DE Beta-amyloid peptide derivative A-beta-16-21.
 XX Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
 KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
 KW familial amyloid polynuropathy; bovine spongiform encephalopathy;
 KW Creutzfeldt-Jakob disease; BAP.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX US5854204-A.
 XX
 PD 29-DEC-1998.
 XX
 XX 14-MAR-1996; 96US-00612785.
 XX
 PR 14-MAR-1995; 95US-00404831.
 PR 07-JUN-1995; 95US-00475579.
 PR 27-OCT-1995; 95US-00548998.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 XX Hundal A, Gafter ML, Kasman L, Musso G, Molineaux S, Benjamin H;
 PI Findeis MA, Chin J, Lee J, Kelley M, Reed M, Wakefield J;
 PI Garnick MB, Kubasek W, Signer ER;
 XX
 DR WPI; 1999-094964/08.
 XX
 PT New peptide(s) derived from beta-amyloid peptide that inhibit amyloid
 PT aggregation, and neurotoxicity, specifically for treatment and
 PT prevention of Alzheimer's disease.
 XX
 XX Example 12; Col 64; 52pp; English.
 XX
 CC The present invention describes beta-amyloid peptide (BAP) derivatives.
 CC The BAP derivatives inhibit aggregation of amyloidogenic proteins and
 CC peptides, specifically BAP, and their neurotoxicity, so are useful for
 CC treating and preventing any disease involving amyloidosis, specifically
 CC Alzheimer's disease but also Down's syndrome, familial amyloid
 CC polynuropathy or cardiomyopathy, bovine spongiform encephalopathy and
 CC Creutzfeldt-Jakob disease. The BAP derivatives are also used to diagnose
 CC these diseases, in vitro or in vivo, by detecting binding of BAP to
 CC labelled BAP derivatives. Some BAP derivatives inhibit BAP aggregation
 CC even when BAP is present in molar excess. The present sequence represents
 CC a BAP derivative
 XX
 SQ Sequence 6 AA;
 Query Match 89.7%; Score 26; DB 2; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVVFFA 6
 Db 1 KLVFFA 6
 RESULT 71
 AAB48484
 ID AAB48484 standard; peptide; 6 AA.
 XX
 AC AAB48484;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Antifibrillogenic peptide #11.
 XX
 KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX

PH Key Location/Qualifiers
 FT Modified-site 6 /note= "C-terminal amide"
 XX
 PN WO200068263-A2.
 XX
 PD 16-NOV-2000.
 XX
 XX 04-MAY-2000; 2000WO-CA000515.
 XX
 PR 05-MAY-1999; 99US-0132592P.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 PI Chalifour R, Gervais F, Gupta A;
 XX
 DR WPI; 2001-031852/04.
 XX
 PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 XX
 PS Claim 7; Page 25; 46pp; English.
 XX
 CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 XX
 SQ Sequence 6 AA;
 Query Match 89.7%; Score 26; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVVFFA 6
 Db 1 KLVFFA 6
 RESULT 72
 AAB48476
 ID AAB48476 standard; peptide; 6 AA.
 XX
 AC AAB48476;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Antifibrillogenic peptide #3.
 XX
 KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200068263-A2.
 XX
 PD 16-NOV-2000.
 XX
 PR 04-MAY-2000; 2000WO-CA000515.
 XX
 PR 05-MAY-1999; 99US-0132592P.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 PI Chalifour R, Gervais F, Gupta A;
 XX
 DR WPI; 2001-031852/04.
 XX

PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
PT its isomer or peptidomimetic.
XX
XX
PS Claim 7; Page 25; 46pp; English.
XX
CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
CC useful for treating amyloidosis disorders such as Alzheimer's disease.
CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
CC binding region and the prot-prot interaction region of the human amyloid
CC protein
XX
XX Sequence 6 AA;
SQ

Query Match 89.7%; Score 26; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 73
AAB82632
ID AAB82632 standard; peptide; 6 AA.
XX
AC AAB82632;
XX
DT 02-OCT-2001 (first entry)
XX
DE All-D peptide used in Alzheimer's disease vaccine.
XX
KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
KW therapy; antigen.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..6 /note= "all D-form residues"
FT Modified-site 6 /note= "C-terminal amide"
FT
XX WO200139796-A2.
XX
PD 07-JUN-2001.
XX
XX 29-NOV-2000; 2000WO-CA001413.
XX
XX 29-NOV-1999; 99US-0168594P.
XX
XX 28-NOV-2000; 2000US-00724842.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Chalifour R, Hebert L, Kong X, Gervais F;
XX
XX WPI; 2001-441458/47.
XX
XX Preventing/treating amyloid-related disease, especially Alzheimer's
PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
PT which elicits production of antibodies to prevent fibrillogenesis and
PT associated cellular toxicity.
XX
XX Disclosure; Page 11; 31pp; English.
XX
XX The present sequence is that of an all-D peptide suitable for use for
XX preparing vaccines for preventing or treating Alzheimer's disease and
XX other amyloid related disorders in humans. It is based on a portion of
CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
XX inserting 1 or more amino acid residues, or by substituting 1 or more

CC amino acid residues with other amino acid residues or non-amino acid
CC fragments. Vaccines of the invention are produced using 'non-self'
CC peptides synthesised from the unnatural D-configuration amino acids to
CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
CC aggregated to be operative or immunogenic. They preferably interact with
CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
CC fragments, protein conjugates, immunogenic derivative peptides and
CC immunogenic peptidomimetics. Examples include all-D peptides
CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
CC related diseases may be localised amyloidosis, e.g. diabetes type II,
CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
CC prion protein related disorders, or systemic amyloidosis associated with
CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
CC amyloidosis found in long-term haemodialysis patients. The present all-D
CC peptide was demonstrated to elicit antibody production in rabbits, and
CC provided greater anti-fibrillogenic activity than its all-L equivalent
XX
XX Sequence 6 AA;
SQ

Query Match 89.7%; Score 26; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 74
ABG71009
ID ABG71009 standard; peptide; 6 AA.
XX
AC ABG71009;
XX
DT 05-DEC-2002 (first entry)
XX
DE Long form beta-amyloid protein fragment #6.
XX
KW Beta-amyloid; amyloid modulator; amyloidogenic protein; amyloidosis;
KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
KW isolated cardiac amyloid; systemic senile amyloidosis; scrapie; myeloma;
KW bovine spongiform encephalopathy; BSE; Creutzfeldt-Jakob disease;
KW adult onset diabetes; Gerstmann-Strausler-Scheinker syndrome;
KW insulinoma; atrial amyloidosis; idiopathic amyloidosis; haemodialysis;
KW macroglobulinaemia-associated amyloidosis; reactive amyloidosis;
KW primary localised cutaneous nodular amyloidosis; Sjogren's syndrome;
KW hereditary cerebral haemorrhage with amyloidosis; Muckle-Wells syndrome;
KW hereditary non-neuropathic systemic amyloidosis;
KW familial Mediterranean Fever.
XX
XX Homo sapiens.
XX
XX US2002098173-A1.
XX
XX 25-JUL-2002.
XX
XX 04-OCT-2001; 2001US-00972475.
XX
XX 14-MAR-1995; 95US-00404831.
XX
XX 07-JUN-1995; 95US-00475579.
XX
XX 27-OCT-1995; 95US-00548998.
XX
XX 14-MAR-1996; 96US-00617267.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX
XX Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;

XX WPI; 2002-697709/75.
 XX
 DR Amyloid modulator useful for treating a disorder associated with
 PT amyloidosis, comprises an amyloidogenic protein and/or a peptide fragment
 PT coupled to a modifying group.
 XX
 PS Example 12; Page 35; 41pp; English.
 XX
 CC The invention describes an amyloid modulator comprising an amyloidogenic
 CC protein and/or peptide fragment coupled to a modifying group so that the
 CC compound modulates the aggregation of natural amyloid proteins or
 CC peptides. The modulator is used for treating a disorder associated with
 CC amyloidosis e.g. familial amyloid polyneuropathy (Portuguese, Japanese
 CC and Swedish types), familial amyloid cardiomyopathy (Danish type),
 CC isolated cardiac amyloid, systemic senile amyloidosis, scrapie, bovine
 CC spongiform encephalopathy, Creutzfeldt-Jakob disease, adult onset
 CC diabetes, Gerstmann-Strausler-Scheinker syndrome, insulinoma, isolated
 CC atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or
 CC macroglobulinaemia-associated amyloidosis, primary localised cutaneous
 CC nodular amyloidosis associated with Sjogren's syndrome, reactive
 CC (secondary) amyloidosis, familial Mediterranean Fever and familial
 CC amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome),
 CC hereditary cerebral haemorrhage with amyloidosis of Icelandic type,
 CC amyloidosis associated with long term haemodialysis, hereditary non-
 CC neuropathic systemic amyloidosis (familial amyloid polyneuropathy III),
 CC familial amyloidosis of Finnish type, amyloidosis associated with
 CC medullary carcinoma of the thyroid, fibrinogen-associated hereditary
 CC renal amyloidosis and lysosome-associated hereditary systemic
 CC amyloidosis. The compound is capable of altering and inhibiting beta-
 CC amyloid protein (beta-AP) aggregation of natural amyloidogenic proteins
 CC or peptides when contacted with a molar excess amount of natural beta-APs
 CC relative to the modulator. This sequence represents a fragment of the
 CC long form of beta-amyloid used in the creation of an amyloid modulator
 XX
 SQ Sequence 6 AA;
 Query Match 89.7%; Score 26; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVVFFA 6
 Db 1 KLVFFA 6
 |:|||||
 |:|||||

RESULT 75
 ABB05157
 ID ABB05157 standard, peptide; 6 AA.
 XX
 AC ABB05157;
 XX
 XX 02-APR-2002 (first entry)
 DT
 XX Beta amyloid peptide (16-21) SEQ ID NO:9.
 DE
 XX Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta;
 KW APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease;
 KW neurotropic; neuroprotective; immunosuppressive; antimicrobial; auditory;
 KW antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic;
 KW amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;
 KW amyloidogenic disease; beta amyloid deposition; amyloidosis;
 KW hereditary cerebral haemorrhage; familial amyloid polyneuropathy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX US6319498-B1.
 PN
 XX 20-NOV-2001.
 PD
 XX 14-MAR-1996; 96US-00617267.
 PF
 XX

PR 14-MAR-1995; 95US-00404831.
 PR 07-JUN-1995; 95US-00475579.
 PR 27-OCT-1995; 95US-00548998.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 PI Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A;
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;
 XX
 DR WPI; 2002-146668/19.
 XX
 CC Amyloid modulator compound useful for treatment of an amyloidogenic
 CC disease such as Alzheimer's disease comprises an aggregation core domain
 CC and a modifying group attached to it.
 PT
 XX Disclosure; Col 18; 54pp; English.
 PS
 CC The present invention describes an amyloid modulator compound (I)
 CC comprising an aggregation core domain and a modifying group attached to
 CC it. (I) has neurotropic, neuroprotective, immunosuppressive, antimicrobial,
 CC antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic
 CC and auditory activities, and can be used as a natural amyloid aggregation
 CC inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide
 CC (beta-AP). (I) are used in the manufacture of a medicament for the
 CC diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's
 CC disease and other clinical occurrences of beta amyloid deposition such as
 CC Down's syndrome individuals and in patients with hereditary cerebral
 CC haemorrhage with amyloidosis, and for treating a disorder associated with
 CC amyloidosis such as familial amyloid polyneuropathy. (I) reduces the
 CC toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)
 CC not only reduces the formation of neurotoxic aggregates but also have the
 CC ability to reduce the neurotoxicity of performed A-beta fibrils. The
 CC present sequence represents a beta-AP peptide, which is used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 6 AA;
 Query Match 89.7%; Score 26; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVVFFA 6
 Db 1 KLVFFA 6
 |:|||||
 |:|||||

Search completed: December 29, 2005, 17:33:41
 Job time : 82.7742 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78,1936 Seconds
(without alignments)
54.137 Million cell updates/sec

Title: US-10-009-122-15

Perfect score: 29

Sequence: 1 KAVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	143	Q91V69	MESAU
2	29	100.0	162	Q9N284	BOVIN
3	29	100.0	248	Q9BGL4	SHEEP
4	29	100.0	261	Y1086	HAEIN
5	29	100.0	261	Q4QLK2	HAEI8
6	29	100.0	277	Q73KX6	TREDE
7	29	100.0	314	Q9WY6	ARATH
8	29	100.0	381	Q5L1A8	GEOKA
9	29	100.0	389	Q8KHB6	CLODI
10	29	100.0	469	Q888Q7	ARATH
11	29	100.0	632	Q9N1P6	CANFA
12	29	100.0	654	Q6U7G9	MEIGA
13	29	100.0	660	Q9N1P6	MEIGA
14	29	100.0	660	Q9N1P6	MEIGA
15	29	100.0	661	Q9N1P6	MEIGA
16	29	100.0	661	Q9N1P6	MEIGA
17	29	100.0	661	Q9N1P6	MEIGA
18	29	100.0	661	Q9N1P6	MEIGA
19	29	100.0	661	Q9N1P6	MEIGA
20	29	100.0	661	Q9N1P6	MEIGA
21	29	100.0	661	Q9N1P6	MEIGA
22	29	100.0	661	Q9N1P6	MEIGA
23	29	100.0	661	Q9N1P6	MEIGA
24	29	100.0	661	Q9N1P6	MEIGA
25	29	100.0	661	Q9N1P6	MEIGA
26	29	100.0	661	Q9N1P6	MEIGA
27	29	100.0	661	Q9N1P6	MEIGA
28	29	100.0	661	Q9N1P6	MEIGA
29	29	100.0	661	Q9N1P6	MEIGA
30	29	100.0	661	Q9N1P6	MEIGA
31	29	100.0	661	Q9N1P6	MEIGA

Q8YL62 ralstonia s
Q8U159 agrobacteri
Q19334 caenorhabdi
Q8EM92 oceaobacil
Q6LJY6 photobacter
Q8XIN5 clostridium
Q19641 caenorhabdi
Q731J0 wolbachia p
Q8XQ19 ralstonia s
Q6G347 bartonella
Q6C1M8 yarrowia li
Q6G346 bartonella
Q5SKK3 thermus the
Q4JC95 sulfolobus
Q5WU01 legionella
Q5X274 legionella
Q5ZSR4 legionella
Q51314 nostoc sp.
Q54598 bacillus au
Q5WBB0 bacillus cl
Q59317 pyrococcus
Q67590 aquifex aeo
P67966 gallus gall
P67967 coturnix co
Q9XR88 deinococcus
Q67911 symbiobacte
Q52718 magnaporth
Q30760 rhodobacter
Q9N2Y5 caenorhabdi
Q5UEW2 uncultured
Q5GU79 xanthomonas
Q7G835 giardia lam
Q48777 arabisopsia
Q5A5P9 candida alb
Q751V7 oryza sativ
Q00165 ictalurid h
Q8GX90 arabidopsis
Q6AEC1 desulfotale
Q9E299 zymomonas m
Q609Q1 methylococc
Q83MJ3 shigella fl
Q73M3 desulfovibri
Q6MI90 bdellovibri
Q4HML6 campylobact
Q4WJL6 aspergillus
P32135 escherichia
Q8EBG3 escherichia
Q8X8F3 escherichia
Q895U4 clostridium
Q84QAB oryza sativ
Q616X4 rock bream
Q616X5 sea bass ir
Q75PQ4 turbot irid
Q5YF80 rock bream
Q68Y86 olive floun
Q6GVF2 korean flou
Q6GVF3 korean flou
Q6GVF4 korean flou
Q6GVF5 korean flou
Q6GVF6 korean flou
Q6GVF7 korean flou
Q6GVF8 korean flou
Q6GVF9 korean flou
Q6GVG0 korean flou
Q6GVG1 korean flou
Q6GVG2 korean flou
Q6GVG3 korean flou
Q6PNE1 turbot redd
Q6QNG1 rock bream
Q6QNG4 rock bream
Q6QNG5 rock bream
Q6QNG6 rock bream

105	26	89.7	453	2	Q6QNG7_9VIRU	Q6qng7 rock bream	178	25	86.2	46	2	Q81W20_BACAN	Q81w20 bacillus an
106	26	89.7	453	2	Q6QNG8_9VIRU	Q6qng8 rock bream	179	25	86.2	54	2	Q421B9_PLABE	Q421b9 plasmodium
107	26	89.7	453	2	Q6QNH0_9VIRU	Q6qnh0 rock bream	180	25	86.2	61	2	Q72A11_DESVH	Q72a11 desulfovibr
108	26	89.7	453	2	Q6QNH1_9VIRU	Q6qnh1 rock bream	181	25	86.2	72	2	Q7Y541_BPR69	Q7y541 bacterioph
109	26	89.7	453	2	Q7T3Y6_9VIRU	Q7t3y6 dwarf goura	182	25	86.2	75	2	Q4KA43_PSEF5	Q4ka43 pseudomonas
110	26	89.7	453	2	Q7T3Y7_9VIRU	Q7t3y7 african lam	183	25	86.2	76	2	Q6MKJ3_BDEBA	Q6mkj3 bdellovibri
111	26	89.7	453	2	Q7T321_RSIV	Q7t321 red sea bre	184	25	86.2	76	2	Q72DT7_DESVH	Q72dt7 desulfovibr
112	26	89.7	453	2	Q80M45_RSIV	Q80m45 red sea bre	185	25	86.2	76	2	Q5LDJ7_BACFN	Q5ldj7 bacteroides
113	26	89.7	453	2	Q8VSD9_9VIRU	Q8vsd9 infectious	186	25	86.2	95	2	Q64UL9_BACFR	Q64ul9 bacteroides
114	26	89.7	453	2	Q516L1_9VIRU	Q5i6l1 rock bream	187	25	86.2	95	2	Q8YMO6_ANASP	Q8ym06 anabaena sp
115	26	89.7	453	2	Q516L2_9VIRU	Q5i6l2 rock bream	188	25	86.2	100	2	Q4U9W4_THEAN	Q4u9w4 thelleria a
116	26	89.7	453	2	Q77ZP6_9VIRU	Q77zp6 sea bass ir	189	25	86.2	107	2	Q650T2_ORYZA	Q650t2 oryza sativ
117	26	89.7	453	2	Q7T3Y4_9VIRU	Q7t3y4 grouper sle	190	25	86.2	109	2	Q650T2_ORYZA	Q650t2 oryza sativ
118	26	89.7	453	2	Q4KSP0_9VIRU	Q4ksf0 orange-spot	191	25	86.2	119	2	Q650T2_ORYZA	Q650t2 oryza sativ
119	26	89.7	457	1	TRME_LISIN	Q926u7 listeria in	192	25	86.2	120	1	COP1_STAAL	P03861 staphylococ
120	26	89.7	458	2	Q4TRD0_RSPHN	P4trd0 erythroblast	193	25	86.2	122	2	Q7QD79_ANOCA	Q7qd79 anopheles g
121	26	89.7	464	1	COAT_IRV1	P8182 tipula irid	194	25	86.2	122	2	Q4YZC4_PLABE	Q4yzc4 plasmodium
122	26	89.7	465	2	Q4U3U9_9VIRU	Q4u3u9 trichoplusi	195	25	86.2	128	2	Q4RIS1_TETNG	Q4ris1 tetraodon n
123	26	89.7	467	1	COAT_IRV6	Q831y5 shigella fl	196	25	86.2	128	2	Q4YR21_TETNG	Q4yr21 tetraodon n
124	26	89.7	468	2	Q831Y5_SHIPL	Q831y5 shigella fl	197	25	86.2	132	2	Q4M0F9_9BURK	Q4m0f9 burkholderi
125	26	89.7	472	1	COAT_IRV22	P22166 simulum ir	198	25	86.2	132	2	Q45455_BACSU	Q45455 bacillus su
126	26	89.7	479	2	Q9ZF52_RHOSH	Q9zfd8 rhodobacter	199	25	86.2	134	1	ACPS_ZYMMO	Q5nl87 zymomonas m
127	26	89.7	479	2	Q9ZF52_RHOSH	Q9zfd8 rhodobacter	200	25	86.2	141	2	Q96YD6_SULFO	Q96y46 sulfolobus
128	26	89.7	483	2	Q5FQ43_GLUOX	Q5fz52 rhodobacter	201	25	86.2	141	2	Q5ERC9_CARAU	Q5erc9 carassius a
129	26	89.7	487	2	Q8BTV9_MOUSE	Q8btv9 gluconobact	202	25	86.2	141	2	Q4SJV9_TETNG	Q4sjv9 tetraodon n
130	26	89.7	494	2	Q6NT77_HUMAN	Q6nt77 homo sapien	203	25	86.2	144	2	Q61G33_CAEBR	Q61g33 caenorhabdi
131	26	89.7	496	2	Q6C9A3_YARLI	Q6c9a3 varrowia li	204	25	86.2	144	2	Q9LA12_PASMU	Q9la12 pasteurella
132	26	89.7	496	2	Q8D2N2_WIGBR	Q8d2n2 wiggleswort	205	25	86.2	144	2	Q9CPF9_PASMU	Q9cpf9 pasteurella
133	26	89.7	498	2	Q3YZV4_NOCFA	Q3yzv4 nocardia fa	206	25	86.2	144	2	Q7W079_BORPE	Q7w079 bordetella
134	26	89.7	504	2	Q4H3G7_CIOIN	Q4h3g7 ciona intes	207	25	86.2	144	2	Q84L47_MIRJA	Q84l47 mirabilis j
135	26	89.7	525	2	Q5FVY8_XENTR	Q5fvy8 xenopus tro	208	25	86.2	160	2	Q4UDQ7_THEAN	Q4udq7 thelleria a
136	26	89.7	529	2	Q5B5V3_EMENI	Q5b5v3 aspergillus	209	25	86.2	162	2	Q965S0_CABEL	Q965s0 caenorhabdi
137	26	89.7	547	2	Q4TC12_TETNG	Q4tc12 tetraodon n	210	25	86.2	167	2	Q4N5T6_THEPA	Q4n5t6 thelleria p
138	26	89.7	555	2	Q9F103_HUMAN	Q9f103 homo sapien	211	25	86.2	167	2	Q92K27_RHIME	Q92k27 rhizobium p
139	26	89.7	555	2	Q8NCA4_HUMAN	Q8nca4 homo sapien	212	25	86.2	172	2	Q880L9_ARATH	Q880l9 arabidopsis
140	26	89.7	555	2	Q8BXN9_MOUSE	Q8bxn9 mus musculu	213	25	86.2	172	2	Q8L9P9_ARATH	Q8l9p9 arabidopsis
141	26	89.7	556	2	Q8R2P9_MOUSE	Q8r2p9 mus musculu	214	25	86.2	186	1	GL19_ORYSA	P29835 oryza sativ
142	26	89.7	558	2	Q8BU98_MOUSE	Q8bu98 mus musculu	215	25	86.2	186	2	P93414_ORYSA	P93414 oryza sativ
143	26	89.7	559	2	Q7NSY8_CHRVO	Q7nsy8 chromobacte	216	25	86.2	186	2	Q6MJF8_BDEBA	Q6mjf8 bdellovibri
144	26	89.7	564	2	Q8NBN3_HUMAN	Q8nbn3 homo sapien	217	25	86.2	190	2	Y1137_METJA	Q585j7 methanococc
145	26	89.7	634	2	Q7RY11_NEUCR	Q7ry11 neurospora	218	25	86.2	191	1	Q4FM11_RICK	Q4fm11 candidatus
146	26	89.7	646	2	Q5FS65_GLUOX	Q5fs65 gluconobact	219	25	86.2	192	2	Q4UMD0_RICPE	Q4umd0 rickettsia
147	26	89.7	647	2	Q8WU27_HUMAN	Q8wu27 homo sapien	220	25	86.2	192	2	Q7SE50_NEUCR	Q7se50 neurospora
148	26	89.7	679	2	Q5YV78_NOCFA	Q5yv78 nocardia fa	221	25	86.2	202	2	Q25798_HELPY	Q25798 heliobacte
149	26	89.7	715	2	Q5PCX6_SALPA	Q5pcx6 salmonella	222	25	86.2	202	2	Q67T36_SMYTH	Q67t36 symbiobacte
150	26	89.7	715	2	Q8Z4Z0_SALTI	Q8z4z0 salmonella	223	25	86.2	202	2	Q4FV94_PASMU	Q4fv94 psychrobact
151	26	89.7	728	2	Q7NBR7_MYCGA	Q7nbr7 mycoplasma	224	25	86.2	209	2	Q8YMX5_ANASP	Q8ymx5 anabaena sp
152	26	89.7	733	2	Q8KTJ9_MYCSY	Q8kti9 mycoplasma	225	25	86.2	209	2	Q5F654_NEIGI	Q5f654 neisseria g
153	26	89.7	742	2	Q8KTJ1_MYCSY	Q8ktj1 mycoplasma	226	25	86.2	210	2	Q9JSP2_NEIMA	Q9jsp2 neisseria m
154	26	89.7	743	2	Q6JEB3_9BURK	Q6jeb3 burkholderi	227	25	86.2	210	2	Q9K184_NEIMB	Q9k184 neisseria m
155	26	89.7	844	2	Q6AK45_DESPS	Q6ak45 desulfotale	228	25	86.2	212	2	Q57AX8_BRUAB	Q57ax8 bruceella ab
156	26	89.7	939	2	Q6AK45_DESPS	Q6ak45 desulfotale	229	25	86.2	212	2	Q8FYG0_BRUSU	Q8fyg0 bruceella su
157	26	89.7	960	2	Q41BE7_GIBZE	Q41be7 gibberella	230	25	86.2	212	2	Q9L6H7_BRUME	Q9l6h7 bruceella me
158	26	89.7	1041	2	Q5LD76_BACFN	Q5ld76 bacteroides	231	25	86.2	214	2	Q92LJ7_RHIME	Q92lj7 rhizobium m
159	26	89.7	1041	2	Q64U98_BACFR	Q64u98 bacteroides	232	25	86.2	220	2	Q8T3Z2_DROME	Q8t3z2 drosophila
160	26	89.7	1041	2	Q8A9Y5_BACTN	Q8a9y5 bacteroides	233	25	86.2	226	1	Y209_METTH	Q521s9 magnaporthe
161	26	89.7	1055	2	Q94887_HUMAN	Q94887 homo sapien	234	25	86.2	228	2	Q5AXR0_EMENI	Q5axr0 aspergillus
162	26	89.7	1055	2	Q91VS8_MOUSE	Q91vs8 mus musculu	235	25	86.2	231	2	Q4WVZ8_ASDFU	Q4wvz8 aspergillus
163	26	89.7	1139	1	SRBP2_CRIGR	Q60429 cricetus	236	25	86.2	231	2	Q8C6Y8_MOUSE	Q8c6y8 mus musculu
164	26	89.7	1411	2	Q73Y53_MYCPA	Q73y53 mycobacteri	237	25	86.2	234	2	Q5JEG7_PYRKO	Q5jeg7 pyrococcus
165	26	89.7	1701	2	Q61164_PLAYO	Q61164 plasmodium	238	25	86.2	234	2	Q8U3K3_PYRFO	Q8u3k3 pyrococcus
166	26	89.7	1701	2	Q7RC08_PLAYO	Q7rc08 plasmodium	239	25	86.2	240	2	Q6NUA9_XENLA	Q6nu9 xenopus lae
167	26	89.7	1723	2	Q8WRD0_PLABE	Q8wr0 plasmodium	240	25	86.2	246	2	Q9Y9U6_DROME	Q9y9u6 drosophila
168	26	89.7	1769	2	Q4YQ3_PLABE	Q4yq3 plasmodium	241	25	86.2	246	2	Q8SFZ1_9BACT	Q8sfz1 uncultured
169	26	89.7	1869	2	Q997D0_SCOMO	Q997d0 broad bean	242	25	86.2	246	2	Q93NM6_TREDE	Q93nm6 treponema d
170	26	89.7	2397	1	MOK11_SCHPO	Q09854 schistosacch	243	25	86.2	247	2	Q92K30_HELPJ	Q92k30 heliobacte
171	26	89.7	2601	2	Q4YQB7_PLABE	Q4yqb7 plasmodium	244	25	86.2	249	2	Q4NHD7_9MICC	Q4nhd7 arthrobacte
172	26	89.7	3888	2	Q51X35_MAGGR	Q51x35 magnaporthe	245	25	86.2	251	2	Q7N2P7_PHOLL	Q7n2p7 photorhabdu
173	26	89.7	4212	2	Q4V218_BURMA	Q4v218 burkholderi	246	25	86.2	252	2	Q7NUJ0_CHRVO	Q7nuj0 chromobacte
174	26	89.7	5835	2	Q63LX8_BURPS	Q63lx8 burkholderi	247	25	86.2	252	2	Q9ZILL_ACICA	Q9zill acinetobact
175	25	86.2	22	2	Q4YGG6_PLABE	Q4ygg6 plasmodium	248	25	86.2	255	2	Q5TU56_ANOCA	Q5tu56 anopheles g
176	25	86.2	42	2	Q7UKA9_RHOBA	Q7uka9 rhodospirell	249	25	86.2	255	2	Q9VHJ5_DROME	Q9vhj5 drosophila
177	25	86.2	46	2	Q73F18_BACCI1	Q73f18 bacillus ce	250	25	86.2	258	2	Q6G411_BARHE	Q6g411 bartonella
										260	2	Q50S14_ENTHI	Q50s14 entamoeba h

251	25	86.2	260	2	P94512_BACSU	P94512 bacillus s
252	25	86.2	263	2	Q92VA5_RHTE	Q92va5 rhizobium m
253	253	86.2	268	1	TRUA_TREDE	Q73ke3 treponema d
254	25	86.2	268	2	Q84148_MIRJA	Q84148 mirabilis j
255	255	86.2	268	2	Q52JPA_CHICK	Q52jpa gallus gall
256	25	86.2	270	2	Q4WEF8_ASPFU	Q4wef8 aspergillus
257	25	86.2	271	2	Q65GA6_BACLD	Q65ga6 bacillus li
258	258	86.2	276	2	Q68FV3_PARTE	Q68fv3 paramescium
259	259	86.2	276	2	Q94QO3_ARATH	Q940q3 arabidopsis
260	25	86.2	276	2	Q62RR1_BACLD	Q62rr1 bacillus li
261	261	86.2	282	1	PNWT_HUMAN	P11086 homo sapien
262	262	86.2	282	2	Q6FHD9_HUMAN	Q6fhd9 homo sapien
263	263	86.2	285	2	Q9KMB5_VIBCH	Q9kmb5 vibrio chol
264	264	86.2	291	2	Q87J38_VIBPA	Q87j38 vibrio para
265	25	86.2	293	2	Q924F0_9ZZZZ	Q924f0 plasmid col
266	266	86.2	293	2	Q9K130_STRCO	Q9k130 streptomyce
267	267	86.2	295	2	Q8D6B6_VIBVU	Q8d6e6 vibrio vuln
268	25	86.2	295	2	Q7MD99_VIBVY	Q7md99 vibrio vuln
269	269	86.2	297	2	Q8PID6_XANAC	Q8pid6 xanthomonas
270	25	86.2	298	2	Q97VK7_SULSO	Q97vk7 sulfolobus
271	25	86.2	299	2	Q5NTR3_9BACT	Q5ntr3 uncultured
272	272	86.2	300	2	Q4ZTF5_PSSXY	Q4ztf5 pseudomonas
273	25	86.2	300	2	Q8QB08_9POXY	Q8qb08 orf virus.
274	25	86.2	302	2	Q7AGM6_ECO57	Q7agm6 escherichia
275	25	86.2	303	2	Q9CLP3_PASMU	Q9clp3 pasteurella
276	25	86.2	303	2	Q6TWN6_9POXY	Q6tnv6 orf virus.
277	25	86.2	303	2	Q6TWN6_9POXY	Q6tnv6 orf virus.
278	25	86.2	307	2	Q6TV44_9POXY	Q6tv44 bovine papu
279	25	86.2	313	2	Q71KR8_KLEFL	Q71kr8 klebsormidi
280	25	86.2	317	2	Q4QEH6_LETMA	Q4qeh6 leishmania
281	25	86.2	321	2	Q9WZE8_THEMEA	Q9wze8 thermotoga
282	25	86.2	322	1	ORJ1XU_ECOM57	Q8ngs3 homo saplen
283	283	86.2	323	2	Q8X9H6_HUMAN	Q8x9h6 escherichia
284	25	86.2	324	2	Q41FV0_GIBZE	Q41fv0 gibberella
285	25	86.2	325	2	Q4TJG6_9SPHN	Q4tjg6 erythroba
286	25	86.2	326	1	PELA_EMENI	Q00645 emerice
287	25	86.2	326	2	Q5BFD9_EMENI	Q5bfd9 aspergillus
288	25	86.2	327	2	Q6FKK4_CANGA	Q6fkk4 candida gla
289	25	86.2	327	2	Q7W5S8_BORPA	Q7w5s8 bordetella
290	25	86.2	327	2	Q7WDB5_BORBR	Q7wdb5 bordetella
291	25	86.2	327	2	Q7VZ12_BORPE	Q7vz12 bordetella
292	291	86.2	331	2	Q4HS16_CAMUP	Q4hs16 campylobact
293	25	86.2	331	2	Q821X4_CHLCP	Q821x4 chlamydo
294	25	86.2	331	2	Q9Z6V0_CHLPN	Q9z6v0 chlamydia p
295	25	86.2	332	2	Q9ZCL2_ABRPE	Q9zcl2 aeropyrum p
296	25	86.2	333	2	Q5L571_CHLAB	Q5l571 chlamydo
297	25	86.2	334	2	Q6LH05_PHORP	Q6lh05 photobacter
298	25	86.2	337	2	Q4M1D9_9BUPK	Q4m1d9 burkholderi
299	25	86.2	340	1	YRU3_CREEL	Q10049 caenorhabdi
300	25	86.2	340	2	Q63KW3_BURPS	Q63kw3 burkholderi

ALIGNMENTS

RESULT 1	Q91Y69 MESAU PRELIMINARY;	PRT;	143 AA.
ID	Q91Y69 MESAU PRELIMINARY;		
AC	Q91Y69;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Matrix metalloproteinase-2 (Fragment)		
OS	Mesocricetus auratus (Golden hamster).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Roden-		
OC	tidae; Cricetinae; Mesocricetus.		
OX	NCBI_TaxID=10036;		
FN	(1)		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Tracheal surface;		
KA	CO K.H., Shin C.Y., Lee W.J., Yoo B.K., Ryu J.R., P		
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ datab		

```

DR EMBL; AF260254; AAK51635.1; -; mRNA.
DR HSSP; P08253; 1CK7.
DR MEROPS; M10.004; -.
DR InterPro; IPR000585; Hemopexin.
DR Pfam; PF00045; Hemopexin; 3.
DR SMART; SM00120; HK; 3.
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; - 16316 MW; 1B4310F9E6A023EF CRC64;

Query Match 100.0%; Score 29; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 21 KAVFFA 26

RESULT 2
Q9N284_BOVIN
ID Q9N284_BOVIN PRELIMINARY; PRT; 162 AA.
AC Q9N284;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MWP-2 (Fragment).
GN Name=bmp-2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP Sato T., Hirata M., Ito A., Hashizume K.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB043994; BAA96387.1; -; mRNA.
DR HSSP; P08253; 1CK7.
DR MEROPS; M10.003; -.
DR InterPro; IPR000585; Hemopexin.
DR Pfam; PF00045; Hemopexin; 3.
DR SMART; SM00120; HK; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
FT NON_TER 1
FT NON_TER 162
SQ SEQUENCE 162 AA; 18351 MW; B8898B49E5E5326A CRC64;

Query Match 100.0%; Score 29; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 33 KAVFFA 38

RESULT 3
Q9BGL4_SHEEP
ID Q9BGL4_SHEEP PRELIMINARY; PRT; 248 AA.
AC Q9BGL4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gelatinase A (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;

```

```

RX MEDLINE=21858324; PubMed=11870075;
RA Ricke W.A., Smith G.W., Smith M.F.;
RT "Matrix metalloproteinase expression and activity following
RT prostaglandin F(2 alpha)-induced luteolysis.";
RL Biol. Reprod. 66:685-691(2002).
DR EMBL; AF267159; AAG59847.1; -; mRNA.
DR HSSP; P08253; 1GXD.
DR MEROPS; M10_003; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00045; Hemopexin; 3.
DR Pfam; PF00413; Peptidase M10; 1.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 1.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00120; HX; 3.
DR SMART; SM00235; ZnMC; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 1
FT 248 1
FT 248 1
SQ SEQUENCE 248 AA; 28034 MW; 56F421C2D6DC133E CRC64;

Query Match 100.0%; Score 29; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 184 KAVFFA 189

RESULT 4
Y1086_HAEIN
ID Y1086_HAEIN STANDARD; PRT; 261 AA.
AC P45030;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical protein H1086.
GN OrderedLocNames=H1086;
OS Haemophilus influenzae;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=rd / KW20 / ATCC 51907;
RX Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.V., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RD rd.";
RL Science 269:496-512(1995).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: Belongs to the DUF140 family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration

```

```

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR EMBL; U32788; AAC22742.1; -; Genomic_DNA.
DR PIR; D64166; D64166.
DR TIGR; H11086; -.
DR InterPro; IPR003453; DUF140.
DR Pfam; PF02405; DUF140; 1.
DR TIGRFAMs; TIGR00056; DUF140; 1.
KW Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 13
FT TRANSMEM 50 70 Potential.
FT TRANSMEM 90 110 Potential.
FT TRANSMEM 148 168 Potential.
FT TRANSMEM 199 219 Potential.
FT TRANSMEM 239 259 Potential.
SQ SEQUENCE 261 AA; 28015 MW; 4BC3695F247A6BF6 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 205 KAVFFA 210

RESULT 5
Q4QLK2_HAE18
ID Q4QLK2_HAE18 PRELIMINARY; PRT; 261 AA.
AC Q4QLK2;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Conserved ABC-type transport system protein, permease component.
GN OrderedLocNames=NT11249;
OS Haemophilus influenzae (strain 86-028NP).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=281310;
[1]
NUCLEOTIDE SEQUENCE.
RP PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
RX Harrison A., Dyer D.W., Gillaspay A., Ray W.C., Mungur R., Carson M.B.,
RA Zhong H., Gibson J., Gibson M., Johnson L.S., Lewis L., Bakaitz L.O.,
RA Munson R.S. Jr.;
RT "Genomic sequence of an otitis media isolate of nontypeable
RT Haemophilus influenzae: comparative study with H. influenzae serotype
RT d, strain KW20."
RL J. Bacteriol. 187:4627-4636(2005).
DR EMBL; CP000057; AX88095.1; -; Genomic_DNA.
DR InterPro; IPR003453; DUF140.
DR Pfam; PF02405; DUF140; 1.
DR TIGRFAMs; TIGR00056; DUF140; 1.
KW Complete proteome.
SQ SEQUENCE 261 AA; 28075 MW; 0EB1BBD22FA133A CRC64;

Query Match 100.0%; Score 29; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 205 KAVFFA 210

RESULT 6
Q73KX6_TREDE
ID Q73KX6_TREDE PRELIMINARY; PRT; 277 AA.
AC Q73KX6;
DT 05-JUL-2004 (TRENBLrel. 27, Created)

```

DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Amino acid ABC transporter, amino acid-binding protein, putative.
 GN OrderedLocusNames=TDE2091;
 OS Treponema denticola.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=158;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 35405 / DSM 14222;
 RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
 RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
 RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
 RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
 RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
 RA Gebregorgis E., Geer K., Tsagaye G., Malek J.A., Ayodeji B.,
 RA Shateman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
 RA Vashisth P., McNeill T.Z., Xiang O., Sodergren E., Baca E.,
 RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
 RT "Comparison of the genome of the oral pathogen Treponema denticola
 with other spirochete genomes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).
 DR EMBL; AB017253; AAS12611.1; -; Genomic_DNA.
 DR TIGR; TDE2091; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001311; SBP_glu receptor.
 DR InterPro; IPR001638; SBP_bac_3.
 DR Pfam; PF00497; SBP_bac_3; 1.
 DR SMART; SM00062; PBPB; 1.
 DR PROSITE; PS01039; SBP_BACTERIAL_3; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 277 AA; 31013 MW; AC9F1BC5DB10A16E CRC64;

Query Match 100.0%; Score 29; DB 2; Length 277;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 DB 8 KAVFFA 13

RESULT 7
 Q9WY16 ARATH PRELIMINARY; PRT; 314 AA.
 AC Q9WY16;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE F3E22.6 protein.
 GN Name=F3E22.6;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B., Wu D.,
 RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
 RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC029912; AAP63818.1; -; Genomic_DNA.
 DR InterPro; IPR002575; APH trans.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF01636; APH; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; UNKNOWN_1.
 SQ SEQUENCE 314 AA; 34938 MW; B831A6DFA610A5DB CRC64;

Query Match 100.0%; Score 29; DB 2; Length 314;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 DB 282 KAVFFA 287

RESULT 8
 Q5L1A8 GEOKA PRELIMINARY; PRT; 381 AA.
 AC Q5L1A8;
 DT 01-FEB-2005 (TReMBLrel. 29, Created)
 DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
 DE Proton/sodium antiporter.
 GN OrderedLocusNames=GK0987;
 OS Geobacillus kaustophilus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 OX NCBI_TaxID=1462;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HTA426;
 RX PubMed=15576355; DOI=10.1093/nar/gkh970;
 RA Takami H., Takaki Y., Chee G.-J., Nishi S., Shimamura S., Suzuki H.,
 RA Matsui S., Uchiyama I.;
 RT "Thermoadaptation trait revealed by the genome sequence of
 thermophilic Geobacillus kaustophilus.";
 RL Nucleic Acids Res. 32:6292-6303 (2004).
 DR EMBL; BA000043; BAD75272.1; -; Genomic_DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
 DR GO; GO:0006885; P:regulation of pH; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR006153; Na_Hporter.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 381 AA; 39481 MW; AE3EA4252A7E367B CRC64;

Query Match 100.0%; Score 29; DB 2; Length 381;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 DB 179 KAVFFA 184

RESULT 9
 Q8KHB6 CLODI PRELIMINARY; PRT; 389 AA.
 AC Q8KHB6;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
 DE S-layer protein variable domain SlpA (fragment).
 GN Name=slpA;
 OS Clostridium difficile.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1496;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 43597, 90-111, and 93-136;
 RX MEDLINE=22083941; PubMed=12089261;
 RX DOI=10.1128/JCM.40.7.2452-2458.2002;
 RA Karjalainen T., Saunier N., Barc M.C., Delmee M., Collignon A.;
 RT "Clostridium difficile genotyping based on slpA variable region in S-
 layer gene sequence: an alternative to serotyping.";
 RL J. Clin. Microbiol. 40:2452-2458 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 43597, 90-111, and 93-136;

```

RA Karjalainen T.K., Saunier N.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458880; AAM75944.1; -; Genomic DNA.
DR EMBL; AF458881; AAM75945.1; -; Genomic DNA.
DR EMBL; AF458882; AAM75946.1; -; Genomic DNA.
FT NON_TER 1 389
FT NON_TER 389 389
SQ SEQUENCE 389 AA; 41788 MW; C5ED9F4901C18F8C CRC64;

Query Match 100.0%; Score 29; DB 2; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 340 KAVFFA 345

RESULT 10
Q8S8Q7 ARATH PRELIMINARY; PRT; 469 AA.
AC Q8S8Q7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Putative selenium-binding protein (Pentatricopeptide repeat-containing protein).
DE NCBI_TaxID=3702;
GN ORFNames=At2g34370;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN 1
RP NUCLEOTIDE SEQUENCE.
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN 2
RP NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
[3]
RN 3
RP NUCLEOTIDE SEQUENCE.
RA Underwood B.A., Xiao Y., Moskal W., Monaghan E., Wang W., Redman J.,
RA Wu H.C., Utterback T., Town C.D.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004481; AAM14949.1; -; Genomic DNA.
DR EMBL; DQ056566; AAY78716.1; -; mRNA.
DR PIR; T02325; T02325.
DR PIR; T02325; T02325.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR002885; PPR.
DR InterPro; IPR011990; TPR-like_helical.
DR Pfam; PF01535; PPR; 4.
DR TIGRFAMs; TIGR00756; PPR; 3.
KW Repeat.
SQ SEQUENCE 469 AA; 53856 MW; FB698FC9C0238437 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 213 KAVFFA 218

RESULT 11
Q9N1P6 CANFA PRELIMINARY; PRT; 632 AA.
AC Q9N1P6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

```

```

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Matrix metalloproteinase-2 (Fragment).
GN Name=MMP-2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN 1
RP NUCLEOTIDE SEQUENCE.
RA Tissue=Fibrosarcoma;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177217; AAF67517.1; -; mRNA.
DR HSSP; P08253; 1GXD.
DR MEROPS; M10_003; -.
DR Ensembl; ENSCAPG0000009421; Canis familiaris.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRXIN.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 632
SQ SEQUENCE 632 AA; 70991 MW; D8AE895497E129F3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 632;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 503 KAVFFA 508

RESULT 12
Q6U7G9 MELGA PRELIMINARY; PRT; 654 AA.
AC Q6U7G9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Gelatinase A.
OC Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN 1
RP NUCLEOTIDE SEQUENCE.
RA Monsonogo Ornan E., Tong A.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY376899; AAQ98971.1; -; mRNA.
DR HSSP; P08254; 1B3D.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

```


DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; Hemopexin; 3.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRILIX.
 DR ProDom; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMc; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
 SQ SEQUENCE 654 AA; 73956 MW; F9B0755F76B6F8DD CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 654;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVPFA 6
 |||||
 Db 533 KAVPFA 538

RESULT 13
 MMP2 HUMAN STANDARD; PRT; 660 AA.
 ID MMP2_HUMAN
 AC P08253;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE 72 kDa type IV collagenase precursor (BC 3.4.24.24) (72 kDa
 DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A) (TBB-
 DE 1).
 GN Name=MMP2; Synonyms=CLG4A;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 [1]
 RP NUCLEOTIDE SEQUENCE OF 19-660, AND PARTIAL PROTEIN SEQUENCE.
 RX MEDLINE=86198216; PubMed=2834383;
 RA Collier I.E., Wilhelm S.M., Eisen A.Z., Marmer B.L., Grant G.A.,
 RA Seltzer J.L., Kronberger A., He C., Bauer E.A., Goldberg G.I.;
 RT "H-ras oncogene-transformed human bronchial epithelial cells (TBB-1)
 RT secrete a single metalloprotease capable of degrading basement
 RT membrane collagen.";
 RL J. Biol. Chem. 263:6579-6587(1988).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91236162; PubMed=1851724;
 RA Collier I.E., Bruns G.A.P., Goldberg G.I., Gerhard D.S.;
 RT "On the structure and chromosome location of the 72- and 92-kDa human
 RT type IV collagenase genes.";
 RL Genomics 9:429-434(1991).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=90293047; PubMed=2162831;
 RA Huhtala P., Chow L.T., Tryggvason K.;
 RT "Structure of the human type IV collagenase gene.";
 RL J. Biol. Chem. 265:11077-11082(1990).
 [4]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS VAL-447 AND LEU-621.
 RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
 RA Nguyen C.P., Nguyen D.A., Poel C.L., Chambers S.W., Schackwitz W.S.,
 RA Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.;

"NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
 of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
 Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Bottrifield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RP NUCLEOTIDE SEQUENCE OF 1-51.
 RX MEDLINE=90228972; PubMed=2158484;
 RA Huhtala P., Eddy R.L., Fan Y.S., Byers M.G., Shows T.B.,
 RA Tryggvason K.;
 RT "Completion of the primary structure of the human type IV collagenase
 RT preproenzyme and assignment of the gene (CLG4) to the q21 region of
 RT chromosome 16.";
 RL Genomics 6:554-559(1990).
 [7]
 RP ENZYME REGULATION.
 RX PubMed=11179305; DOI=10.1128/IAI.69.3.1402-1408.2001;
 RA Gusman H., Travis J., Helmerhorst E.J., Potempa J., Troxler R.P.,
 RA Oppenheim F.G.;
 RT "Salivary histatin 5 is an inhibitor of both host and bacterial
 RT enzymes implicated in periodontal disease.";
 RL Infect. Immun. 69:1402-1408(2001).
 [8]
 RP PROCESSING OF KISS1.
 RX MEDLINE=22761370; PubMed=12879005; DOI=10.1038/sj.onc.1206542;
 RA Takino T., Koshikawa N., Miyamori H., Tanaka M., Sasaki T., Okada Y.,
 RA Seiki M., Sato H.;
 RT "Cleavage of metastasis suppressor gene product KiSS-1
 RT protein/metalin by matrix metalloproteinases.";
 RN Oncogene 22:4617-4626(2003).
 [9]
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 443-660.
 RX MEDLINE=96069777; PubMed=7583664;
 RA Libson A.M., Gittis A.G., Collier I.E., Marmer B.L., Goldberg G.I.,
 RA Lattman E.E.;
 RT "Crystal structure of the haemopexin-like C-terminal domain of
 RT gelatinase A.";
 RL Nat. Struct. Biol. 2:938-942(1995).
 [10]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 458-660.
 RX MEDLINE=96140723; PubMed=8549817; DOI=10.1016/0014-5793(95)01435-7;
 RA Gohlke U., Gomis-Rueth F.-X., Crabbe T., Murphy G., Docherty A.J.,
 RA Bode W.;
 RT "The C-terminal (haemopexin-like) domain structure of human gelatinase
 RT A (MMP2): structural implications for its function.";
 RL FEBS Lett. 378:126-130(1996).
 CC -|- FUNCTION: In addition to gelatin and collagens, it cleaves KiSS1
 CC at a Gly-|-Leu bond.
 CC -|- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types
 CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-|-
 CC Ile-Ala-Gly-Gln.

DR PROSITE; PS00142; ZINC_PROTEASE; 1.
3D-structure; Calcium; Collagen degradation;
KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW Hydrolase; Metal-binding; Metalloprotease; Polymorphism; Protease;
KW Repeat; Signal; Zinc; Zymogen.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 109 Activation peptide.
FT CHAIN 110 660 72 kDa type IV collagenase.
FT DOMAIN 228 276 Fibronectin type-II 1.
FT DOMAIN 286 334 Fibronectin type-II 2.
FT DOMAIN 344 392 Fibronectin type-II 3.
FT DOMAIN 466 660 Hemopexin-like.
FT REGION 110 221 Collagenase-like 1.

Query Match 100.0%; Score 29; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 3.1e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||
DB 531 KAVFFA 536

RESULT 14
Q5IV21_TUPGB
ID Q5IV21_TUPGB PRELIMINARY; PRT; 660 AA.
AC Q5IV21;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Matrix metalloproteinase 2.
OS Tupaia glis belangeri (Common tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupaia.
OX NCBI_TaxID=37347;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15621657; DOI=10.1080/10425170400012925;
RA Kenning M.S., Gentile A., McBrien N.A.;
RT "Expression and cDNA sequence of matrix metalloproteinase-2 (MMP-2) in
a mammalian model of human disease processes: Tupaia belangeri.";
RL DNA Seq. 15:332-337(2004).
DR ENBL; AY600958; AAT44903.1; -; mRNA.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:008270; F:zinc ion binding; IEA.
DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_type2_col_bd.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR Pfam; PF00040; fn2_3.
DR Pfam; PF00045; Hemopexin_4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00013; FNTYPEP1.
DR PRINTS; PR00138; MATRIXIN.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2_3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FN2_1; 2.
DR PROSITE; PS1092; FN2_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium; Hydrolase; Metal-binding; Metalloprotease; Protease; Zinc.
SQ SEQUENCE 660 AA; 73871 MW; FC7EB8481091C5ED CRC64;

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 3.1e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 KAVFFA 6
DB      531 KAVFFA 536

RESULT 15
Q95JA4_PIG PRELIMINARY; PRT; 661 AA.
AC Q95JA4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gelatinase A.
GN Name=MMP-2;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sub.
OC NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TSSUE=Tooth enamel organ;
RX MEDLINE=21480581; PubMed=11597028;
RA Caron C., Xue J., Sun X., Simmer J.P., Bartlett J.D.;
RT "Gelatinase A (MMP-2) in developing tooth tissues and amelogenin
RT hydrolysis.";
RL J. Dent. Res. 80:1660-1664 (2001).
DR EMBL; AF295805; AAK97133.1; -, mRNA.
DR HSSP; P08253; IGXD.
DR MEROPS; M10.003; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase M10; 1.
DR PRINTS; PR00138; FNTYPEII.
DR PRINTS; PR00138; MATRIXIN.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
DR Metalloprotease; Protease.
SQ SEQUENCE 661 AA; 73776 MW; 90545F7645E5F84D CRC64;

Query Match 100.0%; Score 29; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      532 KAVFFA 537

RESULT 17
MMP2_MOUSE STANDARD; PRT; 662 AA.
ID MMP2_MOUSE
AC P33434;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
GN Name=Mmp2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92218452; PubMed=1373140;
RA Reponen P., Sahlberg C., Huhtala P., Hurskainen T., Thesleff I.,
RA Tryggvason K.;
RT "Molecular cloning of murine 72-kDa type IV collagenase and its
RT expression during mouse development.";
RL J. Biol. Chem. 267:7856-7862 (1992).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

QY      1 KAVFFA 6
DB      532 KAVFFA 537

RESULT 16
Q9GLE5_BOVIN PRELIMINARY; PRT; 661 AA.
AC Q9GLE5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Matrix metalloprotease 2.
OS Bos taurus (Bovine).

```

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny N.B., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fabey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RN DEVELOPMENTAL STAGE.
RC TISSUE=Embryo;
RX PubMed:274464;
RA Brenner C.A., Adler R.R., Rappolee D.A., Pedersen R.A., Werb Z.;
RT "Genes for extracellular-matrix-degrading metalloproteinases and their
RT inhibitor, TIMP, are expressed during early mammalian development.";
RL Genes Dev. 3:848-859 (1989).
CC -|- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types
CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-|-
CC Ile-Ala-Gly-Gln.
CC -|- COFACTOR: Binds 4 calcium ions per subunit (By similarity).
CC -|- SUBUNIT: Binds 2 zinc ions per subunit (By similarity).
CC -|- SUBUNIT: Ligand for integrin alpha-V/beta-3.
CC -|- DEVELOPMENTAL STAGE: Present in unfertilized eggs and at the
CC zygote and cleavage stages. Levels increase at the blastocyst
CC stage and with endoderm differentiation.
CC -|- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-
CC MMP3) (By similarity).
CC -|- SIMILARITY: Belongs to the peptidase M10A family.
CC -|- SIMILARITY: Contains 3 fibronectin type-II domains.
CC -|- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M84324; AAA39338.1; -; mRNA.
DR EMBL; BC070430; AAH70430.1; -; mRNA.
DR PIR; A42496; A42496.
DR HSSP; P08253; 1RTG.
DR MEROPS; M10.003; -.
DR Ensembl; ENSMUSG0000031740; Mus musculus.
DR MGI; MGI:97009; Mmp2.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000562; FN_type2_col_bd.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRIXIN.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; Znmc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FN2_1; 3.

DR PROSITE; PS51092; FN2_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
KW Hydrolase; Metal-binding; Metalloprotease; Protease; Repeat; Signal;
KW Zinc; Zymogen.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 109 Activation peptide.
FT CHAIN 110 662 72 kDa type IV collagenase.
FT DOMAIN 228 276 Fibronectin type-II 1.
FT DOMAIN 286 334 Fibronectin type-II 2.
FT DOMAIN 344 392 Fibronectin type-II 3.
FT DOMAIN 468 662 Hemopexin-like 1.
FT REGION 110 221 Collagenase-like 1.
FT REGION 222 396 Collagen-binding 2.
FT REGION 397 467 Collagenase-like 2.
FT ACT_SITE 404 404 By similarity.
FT METAL 134 134 Calcium 1 (By similarity).
FT METAL 168 168 Calcium 2 (By similarity).
FT METAL 178 178 Zinc 1 (By similarity).
FT METAL 180 180 Zinc 1 (By similarity).
FT METAL 185 185 Calcium 3 (By similarity).
FT METAL 186 186 Calcium 3 (via carbonyl oxygen) (By
FT similarity).
FT METAL 193 193 Zinc 1 (By similarity).
FT METAL 200 200 Calcium 2 (via carbonyl oxygen) (By
FT similarity).
FT METAL 202 202 Calcium 2 (via carbonyl oxygen) (By
FT similarity).
FT METAL 204 204 Calcium 2 (By similarity).
FT METAL 206 206 Zinc 1 (By similarity).
FT METAL 208 208 Calcium 3 (By similarity).
FT METAL 209 209 Calcium 1 (By similarity).
FT METAL 211 211 Calcium 3 (By similarity).
FT METAL 403 403 Zinc 2 (catalytic) (By similarity).
FT METAL 407 407 Zinc 2 (catalytic) (By similarity).
FT METAL 413 413 Zinc 2 (catalytic) (By similarity).
FT METAL 478 478 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT METAL 523 523 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT METAL 571 571 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT METAL 620 620 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT SITE 102 102 Cysteine switch (Potential).
FT CARBOHYD 575 575 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 644 644 N-linked (GlcNAc...) (Potential).
FT DISULFID 471 662 By similarity.
SQ SEQUENCE 662 AA; 74102 MW; C630A7DBDB272F02 CRC64;
Query Match 100.0%; Score 29; DB 1; Length 662;
Best Local Similarity 100.0%; Pred. No. 3.le+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
QY 1 KAVPFA 6
Db 533 KAVPFA 538
RESULT 18
MMP2_RABIT
ID MMP2_RABIT STANDARD; PRT; 662 AA.
AC P50757;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
GN Name=MMP2;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;

OC Oryctolagus.
 OX NCBI_TaxID=9986;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=Japanese white; TISSUE=Articular joint;
 RX MEDLINE=56283805; PubMed=8679695; DOI=10.1016/0167-4781(96)00050-4;
 RA Matsumoto S.; Kato M.; Watanabe T.; Masuko Y.;
 RT "Molecular cloning of rabbit matrix metalloproteinase-2 and its broad
 expression at several tissues.";
 RL Biochim. Biophys. Acta 1307:137-139(1996).
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types
 IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-
 Ile-Ala-Gly-Gln.
 CC -1- COFACTOR: Binds 4 calcium ions per subunit (By similarity).
 CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
 CC -1- SUBUNIT: Ligand for integrin alpha-V/beta-3.
 CC -1- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-
 MMP3) (By similarity).
 CC -1- SIMILARITY: Belongs to the peptidase M10A family.
 CC -1- SIMILARITY: Contains 3 fibronectin type-II domains.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 DR EMBL: D63579; BAA09796.1; -; mRNA.
 DR F1R; S70365; S70365.
 DR HSP; P08253; 1Q1B.
 DR MEROPS; M10.003; -.
 DR InterPro; IPR000562; FN type2 col_bd.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR006026; Peptidase_M.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRILIX.
 DR ProDom; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMc; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00023; FN2_1; 3.
 DR PROSITE; PS1092; FN2_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
 KW Hydrolase; Metal-binding; Metalloprotease; Protease; Repeat; Signal;
 KW Zinc; Zymogen.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 109 Activation peptide.
 FT CHAIN 110 662 72 kDa type IV collagenase.
 FT DOMAIN 228 276 Fibronectin type-II 1.
 FT DOMAIN 286 334 Fibronectin type-II 2.
 FT DOMAIN 344 392 Fibronectin type-II 3.
 FT DOMAIN 468 662 Hemopexin-like.
 FT REGION 110 221 Collagenase-like 1.
 FT REGION 222 396 Collagen-binding.
 FT REGION 397 467 Collagenase-like 2.
 FT ACT_SITE 404 404 By similarity.
 FT METAL 134 134 Calcium 1 (By similarity).
 FT METAL 168 168 Calcium 2 (By similarity).
 FT METAL 178 178 Zinc 1 (By similarity).
 FT METAL 180 180 Zinc 1 (By similarity).
 FT METAL 185 185 Calcium 3 (By similarity).
 FT METAL 186 186 Calcium 3 (via carbonyl oxygen) (By
 similarity).

FT METAL 193 193 Zinc 1 (By similarity).
 FT METAL 200 200 Calcium 2 (via carbonyl oxygen) (By
 similarity).
 FT METAL 202 202 Calcium 2 (via carbonyl oxygen) (By
 similarity).
 FT METAL 204 204 Calcium 2 (By similarity).
 FT METAL 206 206 Zinc 1 (By similarity).
 FT METAL 208 208 Calcium 3 (By similarity).
 FT METAL 209 209 Calcium 1 (By similarity).
 FT METAL 211 211 Calcium 3 (By similarity).
 FT METAL 403 403 Zinc 2 (catalytic) (By similarity).
 FT METAL 407 407 Zinc 2 (catalytic) (By similarity).
 FT METAL 413 413 Zinc 2 (catalytic) (By similarity).
 FT METAL 478 478 Calcium 4 (via carbonyl oxygen) (By
 similarity).
 FT METAL 523 523 Calcium 4 (via carbonyl oxygen) (By
 similarity).
 FT METAL 571 571 Calcium 4 (via carbonyl oxygen) (By
 similarity).
 FT METAL 620 620 Calcium 4 (via carbonyl oxygen) (By
 similarity).
 FT SITE 102 102 Cysteine switch (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 644 644 N-linked (GlcNAc...) (Potential).
 FT DISULFID 471 662 By similarity.
 SQ SEQUENCE 662 AA; 73803 MW; 1CC246B270E440C8 CRC64;
 Query Match 100.0%; Score 29; DB 1; Length 662;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFPA 6
 DB 533 KAVFPA 538
 RESULT 19
 MMP2_RAT
 ID MMP2_RAT STANDARD; PRT; 662 AA.
 AC P33436; P97581;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
 gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
 OS Name=Mmp2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=93249363; PubMed=7916617;
 RA Marti H.P.; McNeil L.; Davies M.; Martin J.; Lovett D.H.;
 RT "Homology cloning of rat 72 kDa type IV collagenase: cytokine and
 second-messenger inducibility in glomerular mesangial cells.";
 Biochem. J. 291:441-446(1993).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Skin;
 RA Okada A.; Bassett P.;
 RT "The cloning of the cDNA encoding rat gelatinase A from a rat skin
 wound cDNA library.";
 Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types
 IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-
 Ile-Ala-Gly-Gln.
 CC -1- COFACTOR: Binds 4 calcium ions per subunit (By similarity).
 CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
 CC -1- SUBUNIT: Ligand for integrin alpha-V/beta-3.
 CC -1- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-
 MMP3) (By similarity).

CC -1- SIMILARITY: Belongs to the peptidase M10A family.
 CC -1- SIMILARITY: Contains 3 fibronectin type-II domains.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: X71466; CAA50583.1; -; mRNA.
 CC EMBL: U65656; AAB41692.1; -; mRNA.
 CC PIR: S34780; S34780.
 CC HSP: P08253; LRTG.
 CC MEROPS: M10.003; -.
 CC RGD: 621316; Mmp2.
 CC GO: GO:0004228; F:gelatinase A activity; IDA.
 CC GO: GO:0008237; F:metallopeptidase activity; TAS.
 CC InterPro: IPR000562; FN_type2_col_bd.
 CC InterPro: IPR000585; Hemopexin.
 CC InterPro: IPR001818; Pept_M10A_M12B.
 CC InterPro: IPR006025; Pept_M_Zn_BS.
 CC InterPro: IPR006026; Peptidase_M.
 CC Pfam: PF00040; fn2; 3.
 CC Pfam: PF00045; Hemopexin; 4.
 CC Pfam: PF00413; Peptidase M10; 1.
 CC Pfam: PF03933; Peptidase M10_N; 1.
 CC PRINTS: PR00013; FNTYPEII.
 CC PRINTS: PR00138; MATRXIN.
 CC ProDom: PD000395; FN_Type_II; 3.
 CC SMART: SM00059; FN2; 3.
 CC SMART: SM00120; HX; 4.
 CC SMART: SM00235; ZmC; 1.
 CC PROSITE: PS00546; CYSTEINE_SWITCH; 1.
 CC PROSITE: PS00023; FN2_1; 3.
 CC PROSITE: PS51092; FN2_2; 3.
 CC PROSITE: PS00024; HEMOPEXIN; 1.
 CC PROSITE: PS00142; ZINC_PROTEASE; 1.
 CC Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
 KW Hydrolase; Metal-binding; Metalloprotease; Protease; Repeat; Signal;
 KW Zinc; Zymogen.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 109 Activation peptide.
 FT CHAIN 110 662 72 kDa type IV collagenase.
 FT DOMAIN 228 276 Fibronectin type-II 1.
 FT DOMAIN 286 334 Fibronectin type-II 2.
 FT DOMAIN 344 392 Fibronectin type-II 3.
 FT DOMAIN 468 662 Hemopexin-like.
 FT REGION 110 221 Collagenase-like 1.
 FT REGION 222 396 Collagenase-like 2.
 FT REGION 397 467 By similarity.
 FT ACT_SITE 404 404 Calcium 1 (By similarity).
 FT METAL 134 134 Calcium 2 (By similarity).
 FT METAL 168 168 Zinc 1 (By similarity).
 FT METAL 178 178 Zinc 1 (By similarity).
 FT METAL 180 180 Calcium 3 (By similarity).
 FT METAL 185 185 Calcium 3 (via carbonyl oxygen) (By
 FT METAL 186 186 similarity).
 FT METAL 193 193 Zinc 1 (By similarity).
 FT METAL 200 200 Calcium 2 (via carbonyl oxygen) (By
 FT METAL 202 202 similarity).
 FT METAL 202 202 Calcium 2 (via carbonyl oxygen) (By
 FT METAL 204 204 similarity).
 FT METAL 204 204 Calcium 2 (By similarity).
 FT METAL 206 206 Zinc 1 (By similarity).
 FT METAL 208 208 Calcium 3 (By similarity).
 FT METAL 209 209 Calcium 3 (By similarity).
 FT METAL 211 211 Zinc 2 (catalytic) (By similarity).
 FT METAL 403 403 Zinc 2 (catalytic) (By similarity).
 FT METAL 407 407 Zinc 2 (catalytic) (By similarity).
 FT METAL 413 413 Zinc 2 (catalytic) (By similarity).
 FT METAL 478 478 Calcium 4 (via carbonyl oxygen) (By

FT METAL 523 523 similarity).
 FT METAL 571 571 Calcium 4 (via carbonyl oxygen) (By
 FT METAL 620 620 similarity).
 FT SITE 102 102 Calcium 4 (via carbonyl oxygen) (By
 FT CARBOHYD 575 575 similarity).
 FT CARBOHYD 644 644 Cysteine switch (Potential).
 FT DISULFID 471 662 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 42 42 By similarity.
 FT CONFLICT 286 286 A -> S (in Ref. 2).
 FT CONFLICT 369 369 A -> G (in Ref. 2).
 FT CONFLICT 435 435 N -> S (in Ref. 2).
 FT CONFLICT 586 586 H -> N (in Ref. 2).
 FT CONFLICT 586 586 A -> S (in Ref. 2).
 SQ SEQUENCE 662 AA; 74182 MW; 7496B34B0A21884B CRC64;
 Query Match 100.0%; Score 29; DB 1; Length 662;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 DB 533 KAVFFA 538
 RESULT 20
 Q6GM9 RAT PRELIMINARY; PRT; 662 AA.
 ID Q6GM9 RAT PRELIMINARY; PRT; 662 AA.
 AC Q6GM9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Mmp2 protein.
 GN Name=Mmp2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [2]
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Lung;
 RG NIH MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC074013; AAH74013.1; -; mRNA.
 DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO: GO:0004222; F:metalloendopeptidase activity; IEA.


```

FT METAL 572 572 similarity).
FT METAL 621 621 Calcium 4 (via carbonyl oxygen) (By
FT METAL 621 621 similarity).
FT SITE 99 99 Calcium 4 (via carbonyl oxygen) (By
FT DISULFID 472 663 similarity).
FT CONFLICT 40 40 Cysteine switch (Potential).
FT CONFLICT 116 116 By similarity.
FT CONFLICT 122 122 P -> Q (in Ref. 2).
FT CONFLICT 122 122 W -> T (in Ref. 2).
SQ SEQUENCE 663 AA; 74941 MW; 8D6FDA4E67C3EBCA CRC64;

Query Match 100.0%; Score 29; DB 1; Length 663;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 534 KAVFFA 539
|||||

RESULT 22
Q8K7W1 CLODI PRELIMINARY; PRT; 767 AA.
AC Q8K7W1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Surface layer protein A.
OS Clostridium difficile.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1496;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RX MEDLINE=22077258; PubMed=12081960;
RY DOI=10.1128/JB.184.14.3886-3897.2002;
RA Calabi E., Fairweather N.;
RT "Patterns of sequence conservation in the S-Layer proteins and related
RT sequences in Clostridium difficile."
RL J. Bacteriol. 184:3886-3897(2002).
DR EMBL; AF478571; AAM46790.1; -; Genomic_DNA.
DR InterPro; IPR007253; CW binding 2.
DR Pfam; PF04122; CW binding 2; 3.
SQ SEQUENCE 767 AA; 81461 MW; 7280626184495D70 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 767;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 358 KAVFFA 363
|||||

RESULT 23
Q7XX63 ORYSA PRELIMINARY; PRT; 770 AA.
AC Q7XX63;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE OSJNBa0052P16.14 protein.
GN Name=OSJNBa0052P16.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=12447439; DOI=10.1038/nature01183;

```

```

RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL; AL662936; CAD39717.1; -; Genomic_DNA.
DR Gramene; Q7XX63; -.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR001906; Terp synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth; 2.
SQ SEQUENCE 770 AA; 86960 MW; 6CFAB6855D904EE1 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 555 KAVFFA 560
|||||

RESULT 24
Q66QH3 ORYSA PRELIMINARY; PRT; 840 AA.
AC Q66QH3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Syn-pimara-7,15-diene synthase.
OS Oryza sativa (indica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39946;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=15299118; DOI=10.1104/pp.104.045971;
RX Wilderman P.R., Xu M., Jin Y., Coates R.M., Peters R.J.;
RA "Identification of syn-pimara-7,15-diene synthase reveals functional
RT clustering of terpene synthases involved in rice
RT phytoalexin/allelochemical biosynthesis.";
RL Plant Physiol. 135:2098-2105(2004).
DR EMBL; AY616862; AAU05906.1; -; mRNA.
DR Gramene; Q66QH3; -.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR001906; Terp synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth; 2.
SQ SEQUENCE 840 AA; 94757 MW; B0ECC89323C86ASE CRC64;

Query Match 100.0%; Score 29; DB 2; Length 840;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 625 KAVFFA 630
|||||

```



```
RESULT 25
Q60HB5_ORYSA
ID Q60HB5_ORYSA PRELIMINARY; PRT; 842 AA.
AC Q60HB5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 9b-plimara-7,15-diene synthase.
GN Name=OsK54;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15388982; DOI=10.1271/bbb.68.2001;
RA Oikawa K., Kanno Y., Moteji A., Kenmoku H., Yamane H., Mitsuhashi W.,
RA Okawa H., Toshima H., Itoh H., Matsuo M., Sassa T., Toyomasu T.;
RT "Diterpene cyclases responsible for the biosynthesis of phytoalexins,
RT momilactones A, B, and oryzalexins A-f in rice.";
RL Biosci. Biotechnol. Biochem. 68:2001-2006(2004).
DR EMBL; AB126934; BAD54751.1; -; mRNA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0002877; F:magnesium ion binding; IEA.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth_C; 1.
SQ SEQUENCE 842 AA; 94868 MW; 928F88F8FC335497 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 842;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 627 KAVFFA 632

RESULT 26
Q69DS7_ORYSA
ID Q69DS7_ORYSA PRELIMINARY; PRT; 842 AA.
AC Q69DS7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Ent-kaurene synthase like-4.
GN Name=OsK54;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15668792; DOI=10.1007/s00299-004-0896-6;
RA Margis-Pinheiro M., Zhou X.R., Zhu Q.H., Dennis E.S., Upadhyaya N.M.;
RT "Isolation and characterization of a Ds-tagged rice (Oryza sativa L.)
RT GA-responsive dwarf mutant defective in an early step of the
RT gibberellin biosynthesis pathway.";
RL Plant Cell Rep. 23:819-833(2005).
DR EMBL; AY347880; AAQ72563.1; -; mRNA.
DR Gramene; Q69DS7; -.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.

Query Match 100.0%; Score 29; DB 2; Length 842;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 627 KAVFFA 632

RESULT 27
Q9N175_SHEEP
ID Q9N175_SHEEP PRELIMINARY; PRT; 945 AA.
AC Q9N175;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inducible nitric oxide synthase (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22168784; PubMed=12181148;
RA Merhosh J.L., Baker R.S., Clark K.R.;
RT "Estrogen increases iNOS expression in the ovine coronary artery.";
RL Am. J. Physiol. Heart Circ. Physiol. 283:H1169-H1180(2002).
DR EMBL; AF223942; AAF34710.1; -; mRNA.
DR HSP; P35228; INSI.
DR SNR; Q9N175; 1-326.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0045585; P:positive regulation of cytotoxic T-cell dif. .; ISS.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001709; FPN_Cyt_redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; Oxired_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO synthase; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; PFNCR.
DR PROSITE; PS0902; FLAVODOXIN_LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 1
FT SEQUENCE 945 AA; 108001 MW; 9A5ACFD40440A74P CRC64;

Query Match 100.0%; Score 29; DB 2; Length 945;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 344 KAVFFA 349

RESULT 28
NOS2_RAT
```

ID NOS2_RAT STANDARD; PRT; 1147 AA.
AC Q06518; Q35765; Q35766; Q60591; Q60604; P97774; Q63267; Q64005;
AC Q64558;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1995 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
DE (Inducible NOS) (iNOS).
DE Name=Nos2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Vascular smooth muscle;
RX MEDLINE=93191721; PubMed=7680561;
RA Nunokawa Y., Ishida N., Tanaka S.;
RT "Cloning of inducible nitric oxide synthase in rat vascular smooth
RT muscle cells.";
RL Biochem. Biophys. Res. Commun. 191:89-94(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wistar; TISSUE=Pancreatic islets;
RX MEDLINE=95309542; PubMed=7540573;
RA Karlsson A.E., Andersen H.U., Viessing H., Larsen P.M., Fey S.J.,
RA Cuatrecasas B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,
RA Mandrup-Poulsen T., Boel E., Nerup J.;
RT "Cloning and expression of cytokine-inducible nitric oxide synthase
RT cDNA from rat islets of Langerhans.";
RL Diabetes 44:753-758(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Astrocytes;
RX MEDLINE=94231594; PubMed=7513745;
RA Galea E., Reis D.J., Feinstein D.L.;
RT "Cloning and expression of inducible nitric oxide synthase from rat
RT astrocytes.";
RL J. Neurosci. Res. 37:406-414(1994).
RN [4]
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94039059; PubMed=7693462;
RA Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki K.,
RA Kawasaki H., Sugimura T., Egumi H.;
RT "Molecular cloning of a cDNA encoding an inducible calmodulin-
RT dependent nitric-oxide synthase from rat liver and its expression in
RT COS 1 cells.";
RL Eur. J. Biochem. 217:37-43(1993).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Hepatocyte;
RX MEDLINE=93221515; PubMed=7682072;
RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
RT "Hepatocytes and macrophages express an identical cytokine inducible
RT nitric oxide synthase gene.";
RL Biochem. Biophys. Res. Commun. 191:767-774(1993).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Aorta;
RX MEDLINE=94325351; PubMed=7519448; DOI=10.1016/0167-4781(94)90196-1;
RA Geng Y.J., Almqvist M., Hansson G.K.;
RT "cDNA cloning and expression of inducible nitric oxide synthase from
RT rat vascular smooth muscle cells.";
RL Biochim. Biophys. Acta 1218:421-424(1994).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RA Kosuga K., Yui Y., Hattori R., Sase K., Bizawa H., Aoyama T.,
RA Inoue R., Sasayama S.;
RT "Cloning of an inducible nitric oxide synthase from rat
RT polymorphonuclear neutrophils.";
RL Endothelium 2:217-221(1994).

RN [8]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97070590; PubMed=8913516;
RA Tezumi-shita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,
RA Putaki S., Niwa M.;
RT "Sequence analysis of inducible nitric oxide synthase in rat kidney,
RT lung, and uterus.";
RL Biol. Pharm. Bull. 19:1374-1376(1996).
RN [9]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99066690; PubMed=9851365; DOI=10.1006/niox.1998.0184;
RA Adams V., Krabbes S., Jiang H., Yu J., Rahmel A., Giesen S.,
RA Schuler G., Hambrecht R.;
RT "Complete coding sequence of inducible nitric oxide synthase from
RT human heart and skeletal muscle of patients with chronic heart
RT failure.";
RL Nitric Oxide 2:242-249(1998).
RN [10]
RP NUCLEOTIDE SEQUENCE OF 426-788.
RC STRAIN=Dahl/Rapp salt sensitive strain; TISSUE=Vascular smooth muscle;
RX MEDLINE=98195092; PubMed=9535415;
RA Chen P.Y., Gladish R.D., Sanders P.W.;
RT "Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp
RT salt-sensitive rats.";
RL Hypertension 31:918-924(1998).
RN [11]
RP NUCLEOTIDE SEQUENCE OF 509-740.
RC STRAIN=Wistar; TISSUE=Renal glomerulus;
RA Saura M., Zaragoza C., Martinez-Dalmau R., Perez-Sala D., Lamas S.;
RT "Advances in the studies of NO synthesis regulation in mesangial
RT cells.";
RL Nefrologia 16:35-39(1996).
RN [12]
RP NUCLEOTIDE SEQUENCE OF 479-655.
RC STRAIN=Sprague-Dawley; TISSUE=Renal glomerulus;
RX MEDLINE=94276509; PubMed=7516453;
RA Morrissey J.J., McCracken R., Kaneto H., Vehaskari M., Montani D.,
RA Klahr S.;
RT "Location of an inducible nitric oxide synthase mRNA in the normal
RT kidney.";
RL Kidney Int. 45:998-1005(1994).
RN [13]
RP NUCLEOTIDE SEQUENCE OF 420-479.
RC TISSUE=Myocardium;
RA Michel T., Balligand J.-L.;
RT "Isolation and characterization of iNOS from rat cardiocytes.";
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule
CC with diverse functions throughout the body.
CC -!- CATALYTIC ACTIVITY: L-arginine + n NADPH + m O(2) = citrulline +
CC nitric oxide + n NADP(+).
CC -!- COFACTOR: Heme.
CC -!- COFACTOR: FAD. Binds 1 mole of FAD.
CC -!- COFACTOR: FMN. Binds 1 mole of FMN.
CC -!- COFACTOR: Tetrahydrobiopterin (BH4). May stabilize the dimeric
CC form of the enzyme.
CC -!- ENZYME REGULATION: Not stimulated by calcium/calmodulin. Aspirin
CC inhibits expression and function of this enzyme and effects may be
CC exerted at the level of translational/posttranslational
CC modification and directly on the catalytic activity (By
CC similarity).
CC -!- SUBUNIT: Homodimer. Binds SLC9A3R1 (By similarity).
CC -!- TISSUE SPECIFICITY: In normal kidney, expressed primarily in the
CC medullary thick ascending limb, with minor amounts in the
CC medullary collecting duct and vasa recta bundle.
CC -!- INDUCTION: By interferon gamma and lipopolysaccharides (LPS).
CC -!- SIMILARITY: Belongs to the NOS family.
CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.
CC -!- CAUTION: Ref.9 sequence was originally thought to originate from
CC human but appears to be from rat.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

```

-----
DR EMBL; D14051; BAA03138.1; -; mRNA.
DR EMBL; U28686; AA85861.1; -; mRNA.
DR EMBL; U03699; AAC13747.1; -; mRNA.
DR EMBL; D12520; BAA02090.1; -; mRNA.
DR EMBL; L12562; AAA41720.1; -; mRNA.
DR EMBL; X76881; CAA54208.1; -; mRNA.
DR EMBL; D44591; BAA07994.1; -; mRNA.
DR EMBL; D83661; BAA12035.1; -; mRNA.
DR EMBL; AF049656; AAC83553.1; -; mRNA.
DR EMBL; AF051164; AAC83554.1; -; mRNA.
DR EMBL; AF006619; AAC16401.1; -; mRNA.
DR EMBL; AF006620; AAC16402.1; -; mRNA.
DR EMBL; U48829; AAB18620.1; -; mRNA.
DR EMBL; S71597; AAB31028.2; -; mRNA.
DR EMBL; L36063; AAC02242.1; -; mRNA.
DR PIR; I53165; I53165.
DR PIR; I56575; I56575.
DR PIR; JC5027; JC5027.
DR PIR; S38253; S38253.
DR PIR; S47647; S47647.
DR HSSP; P29477; INOS.
DR SMR; Q06518; 80-499.
DR Ensembl; ENSRNOG0000011023; Rattus norvegicus.
DR RGD; 3185; Nos2.
DR GO; GO:0005829; Cytosol; ISS.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0008603; F:calmodulin-dependent protein kinase regulator act. .; IDA.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0004517; F:nitric-oxide synthase activity; IDA.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0007199; P:G-protein signaling, coupled to GMP nucleo. .; IDA.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0006809; P:nitric oxide biosynthesis; TAS.
DR GO; GO:0007165; P:signal transduction; IDA.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; PAD bd.
DR InterPro; IPR008254; Flav_nitox synth.
DR InterPro; IPR001094; Flavodoxin-like.
DR InterPro; IPR001709; FPN_cyt redctse.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR012144; NOS.
DR PANTHER; PTHR19386; NO synthase; 1.
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO synthase; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.

Query Match 100.0%; Score 29; DB 1; Length 1147;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 517 KAVFFA 522

RESULT 29
Q6XS76 RAT PRELIMINARY; PRT; 1147 AA.
AC Q6XS76;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Inducible nitric oxide synthase (fragment).
GN Name=Nos2;

Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
STRAIN=Wistar; TISSUE=Aortic smooth muscle;
RC Cui Z., Tulladhar R., Hart S., Marber M., Pearson J., Baydoun A.R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY211532; AAP43670.1; -; mRNA.
DR HSSP; P29477; 1JWK.
DR SMR; Q6XS76; 80-499.
DR GO; GO:0005516; F:calmodulin binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0010181; F:FMN binding; IEA.
DR GO; GO:0004517; F:nitric-oxide synthase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IEA.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin-like.
DR InterPro; IPR008254; Flav_nitox synth.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO synthase; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS0902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN_1.
DR NON_TER 1147 1147
SQ SEQUENCE 1147 AA; 130673 MW; 204484F2231D9ECA CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1147;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 517 KAVFFA 522

RESULT 30
Q9QW28_9MURI PRELIMINARY; PRT; 1147 AA.
AC Q9QW28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytokine inducible nitric oxide synthase, iNOS.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP NUCLEOTIDE SEQUENCE.
MEDLINE=93221515; PubMed=7682072;
RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
RT "Hepatocytes and macrophages express an identical cytokine inducible
RT nitric oxide synthase gene."
RL Biochem. Biophys. Res. Commun. 191:767-774 (1993).
DR HSSP; P29477; INOS.
DR SMR; Q9QW28; 80-499.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:00020037; F:heme binding; ISS.

```

```

DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0045585; P:positive regulation of cytotoxic T-cell dif. . .; ISS.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001709; FPN cyt redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO synthase; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PROSITE; PS00369; FLAVODOXIN.
DR PROSITE; PS00371; FPNCR.
DR PROSITE; PS0902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN 1.
SQ SEQUENCE 1147 AA; 130625 MW; 2CAPB983E56F651A CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1147;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 517 KAVFFA 522
|||||

RESULT 31
Q9ROW4_RAT PRELIMINARY; PRT; 1147 AA.
AC Q9ROW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE Inducible nitric oxide synthase.
GN Name=INOS;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wistar Kyoto;
RX MEDLINE=9326503; PubMed=10395902; DOI=10.1016/S0378-1119(99)00196-1;
RA Keinänen R.A., Vartiainen N., Koistinaho J.;
RT "Molecular cloning and characterization of the rat inducible nitric
oxide synthase (INOS) gene.";
RL Gene 234:297-305(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=864711;
RA Iwashina M., Hirata Y., Imai T., Sato K., Marumo F.;
RT "Molecular cloning of endothelial, inducible nitric oxide synthase
gene from rat aortic endothelial cell.";
RL Eur. J. Biochem. 237:668-673(1996).
DR EMBL; AJ230462; CAB46089.1; -; Genomic DNA.
DR EMBL; AJ230463; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230465; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230464; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230467; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230469; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230471; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230473; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230475; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230484; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230483; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230482; CAB46089.1; JOINED; Genomic DNA.

```

```

DR EMBL; AJ230481; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230480; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230479; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230478; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230477; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230476; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230487; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230486; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230485; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230474; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230472; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230470; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230468; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230466; CAB46089.1; JOINED; Genomic DNA.
DR PIR; JC5028; JC5028.
DR PIR; JC5029; JC5029.
DR PIR; S65440; S65440.
DR HSP; P29477; INOS.
DR SMR; Q9ROW4; 80-499.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD bd.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR001709; FPN cyt redctse.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR001433; Oxred_FAD_NAD_bd.
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO synthase; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS0902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN 1.
SQ SEQUENCE 1147 AA; 130614 MW; E76B3F8407D54CF6 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1147;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 517 KAVFFA 522
|||||

RESULT 32
Q8Y1S2_RALSO PRELIMINARY; PRT; 118 AA.
AC Q8Y1S2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE PROBABLE SIGNAL PEPTIDE PROTEIN.
OS OrderedLocustNames=RSC0617; ORFNames=RS01518;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Catolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunac S., Demange N.,

```

```

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguler P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646060; CAD14147.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 118 AA; 12054 MW; 955D9DEA2C16CF42 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 118;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 8 KAIFFA 13

RESULT 33
QBUI59_AGR75
ID QBUI59_AGR75 PRELIMINARY; PRT; 169 AA.
AC QBUI59;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Atu0441.
GN OrderedLocuNames=Atu0441;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Dupont;
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendinning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Neester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens C58."
RL Science 294:2317-2323(2001).
DR EMBL; AB090014; AAL41460.1; -; Genomic_DNA.
DR PIR; AF2630.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 169 AA; 19428 MW; FBD8B80BAC5D38EB CRC64;

Query Match 96.6%; Score 28; DB 2; Length 169;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 114 KAIFFA 119

RESULT 34
Q19334_CABEL
ID Q19334_CABEL PRELIMINARY; PRT; 283 AA.
AC Q19334; Q21599;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein M79.2.
GN ORFNames=M79.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

```

```

OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z50857; CAA90720.1; -; Genomic DNA.
DR EMBL; Z50806; CAA90692.1; -; Genomic DNA.
DR EMBL; Z50806; CAA90720.1; JOINED; Genomic DNA.
DR EMBL; Z50857; CAA90692.1; JOINED; Genomic DNA.
DR PIR; T20734; T20734.
DR Ensemble; M79.2; Caenorhabditis elegans.
DR WormBase; WBGene00010902; M79.2.
DR WormPep; M79.2; CR03507.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 283 AA; 32582 MW; 51638B43CB266860 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 283;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 157 KAIFFA 162

RESULT 35
Q8EM92_OCEIH
ID Q8EM92_OCEIH PRELIMINARY; PRT; 305 AA.
AC Q8EM92;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical conserved protein.
GN OrderedLocuNames=OB2966;
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; BA000028; BAC14922.1; -; Genomic DNA.
DR InterPro; IPR003507; Peptidase U61.
DR Pfam; PF02016; Peptidase U61.
DR Complete proteome; Hypothetical protein.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 305 AA; 33528 MW; 6A7F3E282B5580 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 305;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 75 KAIFFA 80

RESULT 36
Q6LJY6_PHOPR
ID Q6LJY6_PHOPR PRELIMINARY; PRT; 355 AA.
AC Q6LJY6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

```

DE Hypothetical protein.
 GN OrderedLocusNames=PBPRB0521;
 OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Photobacterium.
 OX NCBI_TaxID=74109;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15746425; DOI=10.1126/science.1103341;
 RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N.,
 RA Lauro F.M., Castaro S., Malacrida G., Simonati B., Cannata N.,
 RA Romaldi C., Barlett D.H., Valle G.;
 RT "Life at depth: Photobacterium profundum genome sequence and
 RT expression analysis."
 RL Science 307:1459-1461(2005).
 DR EMBL; CR378676; CAG22394.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein
 SQ SEQUENCE 355 AA; 40056 MW; 6A3C866307079447 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 355;
 Best Local Similarity 83.3%; Pred. No. 3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 ||:||||
 Db 316 KAIFPA 321

RESULT 37
 QXINS CLOPE
 ID Q8XINS CLOPE PRELIMINARY; PRT; 1044 AA.
 AC Q8XIN5;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alpha-mannosidase.
 GN OrderedLocusNames=CPE2080;
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=13 / Type A;
 RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL; BA000016; BAB81786.1; -; Genomic DNA.
 DR GO; GO:0004559; P:alpha-mannosidase activity; IEA.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0006013; P:mannose metabolism; IEA.
 DR InterPro; IPR000602; Glyco_hydro_38.
 DR InterPro; IPR011682; Glyco_hydro_38.
 DR Pfam; PF01074; Glyco_hydro_38; 1_
 DR Pfam; PF07748; Glyco_hydro_38C; 1_
 KW Complete proteome; Glycosidase; Hydrolase.
 SQ SEQUENCE 1044 AA; 121432 MW; 3CABB79447D42B6F CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1044;
 Best Local Similarity 83.3%; Pred. No. 8.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 ||:||||
 Db 666 KAIFPA 671

RESULT 38
 Q19641_CABEL

ID Q19641_CABEL PRELIMINARY; PRT; 85 AA.
 AC Q19641;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein F20D12.5.
 GN ORFNames=F20D12.5;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 CC -1- SIMILARITY: Contains 1 LIM zinc-binding domain.
 DR EMBL; U40933; AAL27241.1; -; Genomic_DNA.
 DR HSP; P04006; LIML.
 DR SMR; Q19641; 2-77.
 DR Ensembl; F20D12.5; Caenorhabditis elegans.
 DR WormBase; WBGene00017644; F20D12.5.
 DR WormPep; F20D12.5; CE29767.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR InterPro; IPR001781; LIM_Zn_bd.
 DR Pfam; PF00412; LIM; 1.
 DR ProDom; PD000094; LIM; 1.
 DR SMART; SM00132; LIM; 1.
 DR PROSITE; PS50023; LIM DOMAIN 2; 1.
 KW Complete proteome; Hypothetical protein; LIM domain; Metal-binding;
 Zinc.
 SQ SEQUENCE 85 AA; 9479 MW; 83B934A0C82AE849 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 85;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 ||:||||
 Db 9 KAVFFA 14

RESULT 39
 Q731J0 WOLP
 ID Q731J0 WOLP PRELIMINARY; PRT; 99 AA.
 AC Q731J0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Oxidoreductase, putative.
 GN OrderedLocusNames=WD0173;
 OS Wolbachia pipiens wMel.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Rickettsiaceae; Wolbachiae; Wolbachia.
 OX NCBI_TaxID=66077;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15024419; DOI=10.1371/journal.pbio.0020069;
 RA Wu M., Sun L.V., Vamathevan J.J., Riegler M., DeBoy R.T.,
 RA Brownlie J.C., McGraw E.A., Martin W., Esser C., Ahmadijad N.,
 RA Wiegand C., Madupu R., Beanan M.J., Brinkac L.M., Daugherty S.C.,
 RA Durkin A.S., Kolonay J.F., Nelson W.C., Mohamoud Y., Lee P.,
 RA Berry K.J., Young M.B., Utterback T.R., Weidman J.F., Nierman W.C.,
 RA Paulsen I.T., Nelson K.E., Tettelin H., O'Neill S.B., Eisen J.A.;
 RT "Phylogenomics of the reproductive parasite Wolbachia pipiens wMel:
 RT a streamlined genome overrun by mobile genetic elements."
 RL PLOS Biol. 2:327-341(2004).
 DR EMBL; AE017256; AAS13922.1; -; Genomic_DNA.
 DR TIGR; WD0173; -.

```

DR GO; GO:0016651; F:oxidoreductase activity, acting on NADH or . . . ; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006885; ETC CI 21.
DR Pfam; PF04800; ETC_CI_NDUF4; 1.
DR Complete proteome.
SQ SEQUENCE 99 AA; 11504 MW; FFB301D34D6C8F84 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 99;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 65 KAVFFA 70

RESULT 40
Q8XQ19_RALSO
ID Q8XQ19_RALSO PRELIMINARY; PRT; 109 AA.
AC Q8XQ19;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PUTATIVE TRANSMEMBRANE PROTEIN.
GN OrderedLocusNames=Rsp1467; ORFNames=RS03077;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
R1 NUCLEOTIDE SEQUENCE.
RC STRAIN=GMI1000;
RX MEDLINE=12681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Guzy J., Mangenot S.,
RA Aliat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646085; CAD18618.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
KW Complete proteome; Plasmid; Transmembrane.
SQ SEQUENCE 109 AA; 11658 MW; BEDB6D1DBFF1EB13 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 109;
Best Local Similarity 83.3%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 10 KSVFFA 15

RESULT 41
Q6G347_BARHE
ID Q6G347_BARHE PRELIMINARY; PRT; 126 AA.
AC Q6G347;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BH09610;
OS Bartonella henselae (Rochalimaea henselae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bartonellaceae; Bartonella.
OX NCBI_TaxID=38323;
RN [1]
R1 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 49882 / Houston 1;

```

```

RX PubMed=15210978; DOI=10.1073/pnas.0305659101;
RA Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,
RA La Scola B., Holmberg M., Andersson S.G.E.;
RT "The louse-borne human pathogen Bartonella quintana is a genomic
RT derivative of the zoonotic agent Bartonella henselae.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
DR EMBL; BX897699; CAF27754.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 126 AA; 14027 MW; 7A632D838151FFAE CRC64;

Query Match      89.7%; Score 26; DB 2; Length 126;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 34 RAVFFA 39

RESULT 42
Q6C1M8_YARLI
ID Q6C1M8_YARLI PRELIMINARY; PRT; 131 AA.
AC Q6C1M8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to w|NCU06209.1 Neurospora crassa NCU06209.1 hypothetical
DE protein.
GN OrderedLocusNames=YALI0P14905g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
R1 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Sennen D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR382132; CAG78243.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 131 AA; 14843 MW; 5D7F9328DBC87E19 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 131;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 126 RAVFFS 131

RESULT 43
Q6G346_BARHE
ID Q6G346_BARHE PRELIMINARY; PRT; 131 AA.
AC Q6G346;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

```

```

DE Hypothetical protein.
GN OrderedLocusNames=BH09620;
OS Bartonella henselae (Rochalimaea henselae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bartonellaceae; Bartonella.
OX NCBI_TaxID=38323;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 49882 / Houston 1;
RX PubMed=15210978; DOI=10.1073/pnas.0305659101;
RA Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,
RA La Scala B., Holmberg M., Andersson S.G.E.;
RT "The louse-borne human pathogen Bartonella quintana is a genomic
RT derivative of the zoonotic agent Bartonella henselae.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
DR EMBL; BX897699; CAF27755.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 131 AA; 14730 MW; 48D91F115B667439 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 131;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   :|||||
Db 34 RAVFFA 39

RESULT 44
QSKK3_THET8
ID Q5SKK3_THET8 PRELIMINARY; PRT; 137 AA.
AC Q5SKK3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein TTHA0640.
GN OrderedLocusNames=TTHA0640;
OS Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=300852;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HB8;
RA Masui R., Kurokawa K., Nakagawa N., Tokunaga F., Koyama Y.,
RA Shibata T., Oshima T., Yokoyama S., Yasunaga T., Kuramitsu S.;
RT "Complete genome sequence of Thermus thermophilus HB8.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP008226; BAD70463.1; -; Genomic_DNA.
DR InterPro; IPR007842; HEPN.
DR Pfam; PF05168; HEPN; 1.
DR PROSITE; PS00910; HEPN; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 137 AA; 15304 MW; 37D01C6D9C3287FA CRC64;

Query Match      89.7%; Score 26; DB 2; Length 137;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   :|||||
Db 43 KAVFFA 48

RESULT 45
QAJC95_SULAC
ID QAJC95_SULAC PRELIMINARY; PRT; 142 AA.
AC QAJC95;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Conserved membrane protein.

```

```

GN OrderedLocusNames=Saci_0164;
OS Sulfolobus acidocaldarius.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2285;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 33909 / NCIB 11770 / DSM 639;
RX PubMed=1595215; DOI=10.1128/JB.187.14.4992-4999.2005;
RA Chen L., Bruggger K., Skovgaard M., Redder P., She Q., Torarinsson E.,
RA Greve B., Awavez M., Zibat A., Klenk H.-P., Garrett R.A.;
RT "The genome of Sulfolobus acidocaldarius, a model organism of the
RT Crenarchaeota.";
RL J. Bacteriol. 187:4992-4999(2005).
DR EMBL; CP000077; AAY79584.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 142 AA; 16221 MW; 5E92483FA7F864C4 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 142;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   :|||||
Db 82 KSVFFA 87

RESULT 46
QSWU01_LEGPL
ID QSWU01_LEGPL PRELIMINARY; PRT; 149 AA.
AC QSWU01;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=lp12372;
OS Legionella pneumophila (strain Lens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297245;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
DR EMBL; CR628337; CAH16612.1; -; Genomic_DNA.
DR LegioList; lp12372; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 149 AA; 16274 MW; F698CCE732B0837 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 149;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   :|||||
Db 37 KSVFFA 42

RESULT 47
Q5X274_LEGPA
ID Q5X274_LEGPA PRELIMINARY; PRT; 149 AA.
AC Q5X274;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=lp2519;
OS Legionella pneumophila (strain Paris).

```



```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297246;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazalet C., Rumiok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glauser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
DR EMBL; CR628336; CAH13672.1; -; Genomic_DNA.
DR Legionellist; lpp2519; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 149 AA; 16323 MW; 8489CE2861AD3D5A CRC64;

Query Match 89.7%; Score 26; DB 2; Length 149;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 37 KSVFFA 42

RESULT 48
Q5ZSR4 LEGPH
ID Q5ZSR4_LEGPH PRELIMINARY; PRT; 149 AA.
AC Q5ZSR4
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN OrderedLocustNames=lp92453;
OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /
ATCC 33152).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=272624;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15448271; DOI=10.1126/science.1099776;
RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA Asamani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,
RA Stehenko V., Park S.H., Zhao B., Teplickaya E., Edwards J.R.,
RA Pampou S., Georgiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
RA Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
RA Segal G., Qu X., Rzhetsky A., Zhang P., Cayanis E., De Jong P.J.,
RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
RT "The genomic sequence of the accidental pathogen Legionella
RT pneumophila.";
RL Science 305:1966-1968(2004).
DR EMBL; AB01354; AAU28513.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 149 AA; 16374 MW; 76C1CB2C5D08BDF23 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 149;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 37 KSVFFA 42

RESULT 49
Q51314 9NOSO
ID Q51314_9NOSO PRELIMINARY; PRT; 150 AA.
AC Q51314;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```

```

DE SdNA replicating plasmid encoding a replication-associated protein
DE (repA) and three ORFs, complete cds.
OC Nostoc sp.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=1180;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Walton D.K., Gendel S.M., Atherly A.G.;
RL Submitted (F88-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M81381; AAA25514.1; -; Genomic_DNA.
DR PIR; S27597; S27597.
SQ SEQUENCE 150 AA; 16660 MW; 7C34D00291E436A6 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 150;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 36 KALFFA 41

RESULT 50
GUAD_BACSU
ID GUAD_BACSU STANDARD; PRT; 156 AA.
AC C34598;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Guanine deaminase (EC 3.5.4.3) (Guanase) (Guanine aminase) (Guanine
DE aminohydrolase) (GAH) (GDEase).
GN Name=guad; Synonyms=gde; OrderedLocustNames=BSU13170;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=168;
RC Devine K.M.;
RT "Sequence of the Bacillus subtilis genome between xlyA and ykoR.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=168;
RC MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RX Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Besterio M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Duesterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Gim S.-Y., Glauser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.-P., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Szor S.J., Serror P.,
RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler H.,
RA Waitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,

```

```

RT KEM-KL6." ;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006627; BAD66350.1; -; Genomic DNA.
DR GO; GO:000892; F:guanine deaminase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR002125; dCMP/cyt deam.
DR Pfam; PF00383; dCMP_cyt_deam; 1.
DR PROSITE; PS00903; Cyt dCMP DEAMINASES; UNKNOWN_1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 156 AA; 17287 MW; F2BPFPPF2FB4B28A1 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 156;
Best Local Similarity 83.3%; Pred.No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

Qy 1 KAVFFFA 6
Db 96 KAVFFA 101
|||||

RESULT 52
O59317_PYRHO
ID O59317_PYRHO PRELIMINARY; PRT; 166 AA.
AC O59317;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 166aa long hypothetical L(+) -tartrate dehydratase.
GN OrderedLocustNames=PH1684;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
NCBI_TaxID=53953;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Rep. 5:53-76 (1998).
DR EMBL; BA000001; BAA30796.1; -; Genomic DNA.
DR PIR; D71049;
DR GO; GO:0016829; F:lyase activity; IEA.
DR InterPro; IPR004647; TtdB_fumA_fumB.
DR Pfam; PF05683; Fumerase_C1.
DR TIGRFAMs; TIGR00723; ttdB_fumA_fumB; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 166 AA; 18250 MW; A2A70CF533DD166 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 166;
Best Local Similarity 83.3%; Pred.No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

Qy 1 KAVFFFA 6
Db 107 KAVFFA 112
|||||

RESULT 53
O67590_AQUAE
ID O67590_AQUAE PRELIMINARY; PRT; 185 AA.
AC O67590;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-terminal fumarate hydratase. Class I.

```

```

GN Name=fumX; OrderedLocusNames=AQ_1679;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=VPS; GenBank=U00001; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeck R., Snead M.A., Keller M., Auway M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus";
RL Nature 392:353-358(1998).
DR EMBL; AB000750; AAC07546.1; -; Genomic_DNA.
DR PIR; E70445; E70445.
DR GO; GO:0016829; P:lyase activity; IEA.
DR InterPro; IPR004647; TcdB_fumA_fumB.
DR Pfam; PF05683; Fumerase_C_1.
DR TIGRPFAMs; TIGR00723; tcdB_fumA_fumB; 1.
KW Complete proteome.
SQ SEQUENCE 185 AA; 20441 MW; CBA8320A226E2558 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 185;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPFA 6
|||:|
Db 117 KAVYFA 122

RESULT 54
CSRPI CHICK STANDARD; PRT; 191 AA.
AC P67965; P32965;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cysteine-rich protein 1 (CRP1) (CRP).
GN Name=CSRPI; Synonyms=CSRPN;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryonic fibroblast;
RX MEDLINE=94124603; PubMed=8294495; DOI=10.1083/jcb.124.1.117;
RA Crawford A.W., Pino J.D., Beckerle M.C.;
RT "Biochemical and molecular characterization of the chicken cysteine-
RT rich protein, a developmentally regulated LIM-domain protein that is
RT associated with the actin cytoskeleton.";
RL J. Cell Biol. 124:117-127(1994).
[2]
RN PROTEIN SEQUENCE OF 1-49; 69-83; 111-129 AND 177-188.
RX MEDLINE=93107157; PubMed=1469049; DOI=10.1083/jcb.119.6.1573;
RA Sadler I., Crawford A.W., Michelsen J.W., Beckerle M.C.;
RT "Zyxin and cCRP: two interactive LIM domain proteins associated with
RT the cytoskeleton.";
RL J. Cell Biol. 119:1573-1587(1992).
[3]
RN ZINC-BINDING.
RX MEDLINE=93281587; PubMed=8506279;
RA Michelsen J.W., Schmeichel K.L., Beckerle M.C., Winge D.R.;
RT "The LIM motif defines a specific zinc-binding protein domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:4404-4408(1993).
[4]
RN MUTAGENESIS.
RX MEDLINE=94209279; PubMed=8157637;
RA Michelsen J.W., Sewell A.K., Louis H.A., Olsen J.I., Davis D.R.,
RA Winge D.R., Beckerle M.C.;

```

```

RT "Mutational analysis of the metal sites in an LIM domain.";
RL J. Biol. Chem. 269:11108-11113(1994).
[5]
RN STRUCTURE BY NMR OF C-TERMINAL LIM DOMAIN.
RX MEDLINE=95393167; PubMed=7664053;
RA Perez-Alvarado G.C., Miles C., Michelsen J.W., Louis H.A., Winge D.R.;
RT "Structure of the carboxy-terminal LIM domain from the cysteine rich
RT protein CRP.";
RL Nat. Struct. Biol. 1:388-398(1994).
CC -1- FUNCTION: Heat stable protein, that interacts with zyxin. May be a
CC component of a signal transduction pathway that mediates adhesion-
CC stimulated changes in gene expression.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Associates with the actin cytoskeleton.
CC -1- TISSUE SPECIFICITY: Most prominent in tissues that are enriched in
CC smooth muscle cells, such as gizzard, stomach, and intestine.
CC Lower level in the heart, no expression in liver, skeletal muscle,
CC or brain.
CC -1- DEVELOPMENTAL STAGE: Expression levels increase dramatically
CC during smooth muscle maturation.
CC -1- DOMAIN: Glycine-rich repeats mediate the association with the
CC actin cytoskeleton (Probable).
CC -1- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR EMBL; X73831; CAAS2053.1; -; mRNA.
DR PIR; A49648; A49648.
DR PIR; B44358; B44358.
DR PIR; C44358; C44358.
DR PDB; 1B8T; NMR; A=1-191.
DR PDB; 1CTU; NMR; @=107-191.
DR InterPro; IPR001781; LIM_Zn_bd.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00023; LIM_DOMAIN_1; 2.
DR PROSITE; PS00023; LIM_DOMAIN_2; 2.
KW 3D-structure; Direct protein sequencing; LIM domain; Metal-binding;
KW Nuclear protein; Repeat; Zinc.
FT INIT MET 0 0
FT DOMAIN 9 60 LIM zinc-binding 1.
FT DOMAIN 117 168 LIM zinc-binding 2.
FT MOTIF 63 68 Nuclear localization signal (Potential).
FT COMPBIAS 62 77 Gly-rich.
FT COMPBIAS 174 185 Gly-rich.
FT STRAND 7 8
FT TURN 10 12
FT STRAND 15 16
FT STRAND 22 24
FT TURN 25 26
FT STRAND 27 29
FT TURN 31 33
FT STRAND 35 35
FT TURN 37 39
FT STRAND 42 42
FT STRAND 48 51
FT TURN 52 53
FT STRAND 54 57
FT HELIX 58 65
FT STRAND 115 116
FT TURN 118 120
FT STRAND 123 124
FT STRAND 130 132
FT TURN 133 134
FT STRAND 135 137
FT TURN 139 141
FT STRAND 143 143
FT TURN 145 147

```

FT STRAND 150 150
 FT TURN 156 159
 FT TURN 160 161
 FT STRAND 162 165
 FT HELIX 166 172
 FT TURN 173 173
 SQ SEQUENCE 191 AA; 20254 MW; BC1A45013C7BDA38 CRC64;

Query Match 89.7%; Score 26; DB 1; Length 191;
 Best Local Similarity 83.3%; Pred. No. 5.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||:|
 Db 14 KAVYFA 19

RESULT 55

CSRP1_COTJUA STANDARD; PRT; 191 AA.
 AC P67967; P32965; (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 47, Last annotation update)
 DE 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Cysteine-rich protein 1 (CRP1) (CRP).
 GN Name=CSRP1; Synonyms=CSR1;
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Coturnix.
 OC NCBI_TaxID=93934;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryonic fibroblast;
 RX MEDLINE=96081967; PubMed=7499435; DOI=10.1074/jbc.270.48.28946;
 RA Weiskirchen R., Pino J.D., Macalima T., Bister K., Beckerle M.C.;
 RT "The cysteine-rich protein family of highly related LIM domain proteins";
 RL J. Biol. Chem. 270:28946-28954(1995).
 CC -!- FUNCTION: Heat stable protein, that interacts with zyxin. May be a component of a signal transduction pathway that mediates adhesion-stimulated changes in gene expression.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Associates with the actin cytoskeleton (By similarity).
 CC -!- DOMAIN: Glycine-rich repeats mediate the association with the actin cytoskeleton (Probable).
 CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.

 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

DR EMBL; Z28333; CAA82187.1; -; mRNA.
 DR PIR; S38879; S38879.
 DR InterPro; IPR001781; LIM_Zn_bd.
 DR Pfam; PF00412; LIM; 2.
 DR ProDom; PD000094; LIM; 2.
 DR SMART; SM00132; LIM; 2.
 DR PROSITE; PS00478; LIM DOMAIN 1; 2.
 DR PROSITE; PS50023; LIM DOMAIN 2; 2.
 KW LIM domain; Metal-binding; Nuclear protein; Repeat; Zinc.
 FT INIT_MET 0 0 By similarity.
 FT DOMAIN 9 60 LIM zinc-binding 1.
 FT DOMAIN 117 168 LIM zinc-binding 2.
 FT MOTIF 63 68 Nuclear localization signal (Potential).
 FT COMPIAS 62 77 Gly-rich.
 FT COMPIAS 174 185 Gly-rich.
 SQ SEQUENCE 191 AA; 20254 MW; BC1A45013C7BDA38 CRC64;

Query Match 89.7%; Score 26; DB 1; Length 191;

Best Local Similarity 83.3%; Pred. No. 5.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 |||:|
 Db 14 KAVYFA 19

RESULT 56

Q9RR88_DEIRA PRELIMINARY; PRT; 229 AA.
 AC Q9RR88;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Molybdenum cofactor biosynthesis protein D/E.
 GN OrderedLocusNames=DR2607;
 OS Deinococcus radiodurans.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OC NCBI_TaxID=1299;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
 RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1";
 RL Science 286:1571-1577(1999).
 DR EMBL; AE002090; AAF12145.1; -; Genomic_DNA.
 DR PIR; E75252; E75252.
 DR HSSP; P30748; 1NVI.
 DR TIGR; DR2607; -.
 DR GO; GO:0006777; P-Mo-molybdopter in cofactor biosynthesis; IEA.
 DR GO; GO:0006790; P-sulfur metabolism; IEA.
 DR InterPro; IPR003448; Mb_biosynth_Moae.
 DR InterPro; IPR010034; Moad.
 DR InterPro; IPR003749; This.
 DR PANTHER; PTHR10311; Mb_biosynth_Moae; 1.
 DR Pfam; PF02391; Moae; 1.
 DR Pfam; PF02597; ThisS; 1.
 DR TIGRFAMs; TIGR01682; moad; 1.
 KW Complete proteome.
 SQ SEQUENCE 229 AA; 25311 MW; CD0F8B7060118B38 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 229;
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 :|||
 Db 4 RAVFFA 9

RESULT 57

Q67QUL_SYTH PRELIMINARY; PRT; 232 AA.
 AC Q67QUL;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE Hypothetical protein.
 GN OrderedLocusNames=STH967;
 OS Symbiobacterium thermophilum.
 OC Bacteria; Actinobacteria; Symbiobacterium.
 OC NCBI_TaxID=2734;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1AM14863; DOI=10.1093/nar/gkh830;
RX PubMed=15383646; DOI=10.1093/nar/gkh830;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watauji T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Genome sequence of *Symbiobacterium thermophilum*, an uncultivable
RT bacterium that depends on microbial commensalism.";
RL Nucleic Acids Res. 32:4937-4944 (2004).
DR EMBL; AP006840; BAD39952.1; -; Genomic_DNA.
DR InterPro; IPR005834; Dehal_like_hydro.
DR Pfam; PF00702; Hydrolase; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 232 AA; 24811 MW; D830F748F8D4D67B CRC64;

Query Match 89.7%; Score 26; DB 2; Length 232;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
DB 3 KALFFA 8
|||||

RESULT 58
Q527F8_MAGGR PRELIMINARY; PRT; 233 AA.
AC Q527F8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG05732.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_TaxID=242507;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachanteang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Bouhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Darjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamvasselis M., Karlsson E.,
RA Kelle C., Kieu A., Kiser P., Kodira C., Kulbosa E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Landblad-toh K., Liu X., Lokitysang T., Lokitysang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., McGhee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihalov A., Minova T., Mikkelsen T., Mienga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okawa O., O'leary S., Onotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settippalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnev C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoultsang Y., Topham K.,
RA Towey S., Teamla T., Tsomo N., Vallee D., Vassiliev H.,

RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Zander E.;
RT "The genome sequence of *Magnaporthe grisea*.";
RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AACU01000565; EAA54941.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 25744 MW; C25C024868B86B34C CRC64;

Query Match 89.7%; Score 26; DB 2; Length 233;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
DB 192 RAVFFA 197
|||||

RESULT 59
O30760_RHOSH PRELIMINARY; PRT; 233 AA.
AC O30760;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Autoinducer synthesis regulator.
GN Names=cerR;
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=98053869; PubMed=9393720;<

```

DR PRINTS; PR00038; HTHLUXR..
DR ProDom; PD000307; HTH LuxR; 1.
DR SMART; SM00421; HTH LUXR; 1.
SQ SEQUENCE 233 AA; 26080 MW; 127DDE8E6DB8D48 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 233;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db :|||||
92 RAVFFA 97

RESULT 60
Q9N2Y5 CAEEL PRELIMINARY; PRT; 235 AA.
AC Q9N2Y5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Y71G10AR.3.
GN ORFNames=Y71G10AR.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=981916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AC024856; AAF60868.4; -; Genomic_DNA.
DR Ensembl; Y71G10AR.3; Caenorhabditis elegans.
DR WormBase; WBGene0022137; Y71G10AR.3.
DR WormPep; Y71G10AR.3; CE36900.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 235 AA; 27638 MW; 206BEC3C9570D089 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 235;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db :|||||
47 KAVFFS 52

RESULT 61
Q5UEW2 9PROT PRELIMINARY; PRT; 266 AA.
AC Q5UEW2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative sulfatase (fragment).
GN ORFNames=Red2C11_75;
OS uncultured alpha proteobacterium EBAC2C11.
OC Bacteria; Proteobacteria; Alphaproteobacteria; SAR116 cluster;
OC environmental samples.
OX NCBI_TaxID=295349;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sabeni G., Beja O.;
RT "SAR116.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY744399; AAV31659.1; -; Genomic DNA.
DR GO; GO:0008484; F:sulfuric ester hydrolase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000917; Sulfatase.

DR PRINTS; PF00884; Sulfatase; 1.
DR NON TER 266
SQ SEQUENCE 266 AA; 29908 MW; 518924D95F9043A7 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 266;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db :|||||
232 KALFFA 237

RESULT 62
Q5GU79 XANOR PRELIMINARY; PRT; 268 AA.
AC Q5GU79;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=XO04490;
OS Xanthomonas oryzae (pv. oryzae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=64187;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KACC10331 / KX085;
RX PubMed=15673718; DOI=10.1093/nar/gki206;
RA Lee B.-M., Park Y.-J., Park D.-S., Kang H.-W., Kim J.-G., Song E.-S.,
RA Park I.-C., Yoon U.-H., Hahn J.-H., Koo B.-S., Lee G.-B., Kim H.,
RA Park H.-S., Yoon K.-O., Kim J.-H., Jung C.-H., Koh N.-H., Seo J.-S.,
RA Go S.-J.;
RT "The genome sequence of Xanthomonas oryzae pathovar oryzae KACC10331,
RT the bacterial blight pathogen of rice.";
RL Nucleic Acids Res. 33:577-586(2005).
DR EMBL; AE013598; AAW77744.1; -; Genomic_DNA.
DR InterPro; IPR005184; DUF306_Meta_HslJ.
DR Pfam; PF03724; META; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 268 AA; 28691 MW; 7757E113FF1816E9 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 268;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db :|||||
2 RAVFFA 7

RESULT 63
Q7QS35 GIALA PRELIMINARY; PRT; 276 AA.
AC Q7QS35;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP_661_5852.6682.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

```

DR EMBL; AACB01000125; EAA37819.1; -; Genomic_DNA.
 DR InterPro; IPR001498; UPF0029.
 DR Pfam; PF01205; UPF0029; 1.
 DR PROSITE; PS00910; UPF0029; UNKNOWN 1.
 SQ SEQUENCE 276 AA; 30612 MW; 09078636BAID9667 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 276;
 Best Local Similarity 83.3%; Pred. No. 7.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 Db 155 KSVFFA 160
 |||:|

RESULT 64

O48777 ARATH
 ID O48777 ARATH PRELIMINARY; PRT; 285 AA.
 AC O48777;
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein At2g32880.
 GN Name=At2g32880;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.J.,
 RA Wu D., Maiti R., Roming C.M., Koo H., Fujii C.Y., Utterback T.R.,
 RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RA Town C.D., Kaul S.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC003033; AAB91985.1; -; Genomic_DNA.
 DR PIR; T01119; T01119.
 DR PIR; T01119; T01119.
 DR InterPro; IPR002083; MATH.
 DR Pfam; PF00917; MATH; 1.
 DR SMART; SM0061; MATH; 2.
 DR PROSITE; PS0144; MATH; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 285 AA; 32882 MW; 192157DB0D30FE27 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 285;
 Best Local Similarity 83.3%; Pred. No. 7.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 Db 137 KAVFYA 142
 |||:|

RESULT 65

Q5ASP9 CANAL
 ID Q5ASP9 CANAL PRELIMINARY; PRT; 290 AA.
 AC Q5ASP9;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein CTX3.
 GN Name=CTX3; ORFNames=CA019.12810, CA019.5350;
 OS Candida albicans SC5314.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=237561;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SC5314;

Qy 1 KAVFFA 6
 Db 137 KAVFYA 142
 |||:|

Query Match 89.7%; Score 26; DB 2; Length 296;
 Best Local Similarity 83.3%; Pred. No. 7.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 Db 137 KAVFYA 142
 |||:|

RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
 RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
 RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
 RA Davis R.W., Scherer S.;
 RT "The diploid genome sequence of *Candida albicans*";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=SC5314;
 RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
 RA Roberts J., Persson K., Donnelly S., Favoreto S., Tsung K.-W.,
 RA Jones T., Scherer S., Agabian N.;
 RT "Annotation of the Genome of *Candida albicans*";
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AACQ01000059; EAK98097.1; -; Genomic_DNA.
 DR EMBL; AACQ01000058; EAK98178.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 290 AA; 34139 MW; 41D96D679D453249 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 290;
 Best Local Similarity 83.3%; Pred. No. 7.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 Db 26 KAVFYA 31
 |||:|

RESULT 66

Q75IV7 ORYZA
 ID Q75IV7 ORYZA PRELIMINARY; PRT; 296 AA.
 AC Q75IV7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative 6-phosphogluconolactonase (With alternative splicing).
 GN Names=OSUNB0059G13.23;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
 RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
 RA Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Haiao J., Blunt S.,
 RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
 RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
 RA White O., Salzberg S.L., Fraser C.M.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RA Buell R.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC120538; AAS07092.1; -; Genomic_DNA.
 DR Gramene; Q75IV7; -;
 DR GO; GO:0017057; F:6-phosphogluconolactonase activity; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
 DR InterPro; IPR006148; Gluc_gal_isom.
 DR InterPro; IPR005900; Phosphogluconlac.
 DR Pfam; PF01182; Glucosamine iso; 1.
 DR TIGRFAMs; TIGR01198; pgl; 1.
 SQ SEQUENCE 296 AA; 33270 MW; 36B72EAB4C2FE65A CRC64;

Query Match 89.7%; Score 26; DB 2; Length 296;
 Best Local Similarity 83.3%; Pred. No. 7.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 Db 26 KAVFYA 31
 |||:|

Db 240 KAVYFA 245

RESULT 67
VG12 ICHV1
ID VG12 ICHV1 STANDARD; PRT; 299 AA.
AC Q00165;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypothetical gene 12 zinc-binding protein.
GN Name=12;
OS Ictalurid herpesvirus 1 (ICHV-1) (Channel catfish herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Ictalurivirus.
ON NCBI_TaxID=10401;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=Auburn 1;
RX MEDLINE=92087490; PubMed=1727613;
RA Davison A.J.;
RL "Channel catfish virus: a new type of herpesvirus.";
RL Virology 186:9-14(1992).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; W75136; AAA88193.1; -; Genomic DNA.
CC EMBL; W75136; AAA88115.1; -; Genomic DNA.
CC PIR; D36787; ZBBE13.
CC InterPro; IPR001841; Znf_RING.
CC SMART; SM00184; RING; 1_RING.
CC Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 299 AA; 33108 MW; B78295A904A647EB CRC64;

Query Match 89.7%; Score 26; DB 1; Length 299;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVYFA 6
:|||||
39 KAVYFA 44

Db 318 AA.

RESULT 68
Q8GX90 ARATH
ID Q8GX90 ARATH PRELIMINARY; PRT; 318 AA.
AC Q8GX90;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein Atg32880.
GN Name=Atg32880;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
ON NCBI_TaxID=3702;
RN NUCLEOTIDE SEQUENCE.
RP Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK118361; BAC42975.1; -; mRNA.
DR InterPro; IPR002083; MATH.
DR Pfam; PF00917; MATH; 2.
DR SMART; SM00061; MATH; 2.
DR PROSITE; PS0144; MATH; 2.
KW Hypothetical protein.
SQ SEQUENCE 318 AA; 36701 MW; 14B0D9BF9BE0C7BD CRC64;

Query Match 89.7%; Score 26; DB 2; Length 318;
Best Local Similarity 83.3%; Pred. No. 8.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVYFA 6
:|||||
137 KAVYFA 142

Db 321 AA.

RESULT 69
Q6ASCI DESPS
ID Q6ASCI DESPS PRELIMINARY; PRT; 321 AA.
AC Q6ASCI;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Related to glycosyltransferase involved capsular polysaccharide
DE biosynthesis.
GN OrderedLocusNames=DP0013;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobubaceae; Desulfotalea.
ON NCBI_TaxID=84980;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=LSV54 / DSM 12343;
RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner P.-O., Lupas A.N., Amann R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:887-902(2004).
DR EMBL; CR522870; CAG34742.1; -; Genomic DNA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001173; Glyco trans 2.
DR Pfam; PF00535; Glycos transf 2; I.
KW Complete proteome; Transferase.
SQ SEQUENCE 321 AA; 37861 MW; B3DEC2F91FB040BD CRC64;

Query Match 89.7%; Score 26; DB 2; Length 321;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVYFA 6
:|||||
190 KAVYFA 195

Db 340 AA.

RESULT 70
Q9EZ99 ZYMO
ID Q9EZ99 ZYMO PRELIMINARY; PRT; 340 AA.
AC Q9EZ99; Q5NLZ6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Tryptophanyl-tRNA synthase (EC 6.1.1.2).
GN Name=trps; OrderedLocusNames=ZMO1640;
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
ON NCBI_TaxID=542;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ZM4;
RA Shin I.S., Kang H.S.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 31821 / ZM4 / CP4;
RX PubMed=15592456; DOI=10.1038/ndt1045;


```

RA Seo J.-S., Chong H., Park H.S., Yoon K.-O., Jung C., Kim J.J.,
RA Hong J.H., Kim H., Kim J.-H., Kil J.-I., Park C.J., Oh H.-M.,
RA Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.Y.,
RA Kang H.L., Lee S.Y., Lee K.J., Kang H.S.;
RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis
RT ZMA."
RL Nat. Biotechnol. 23:63-68(2005).
CC -1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA (Trp) = AMP +
CC diphosphate + L-tryptophyl-tRNA(Trp).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL; AF300471; AA42413.1; -; Genomic DNA.
DR EMBL; AE008692; AA90264.1; -; Genomic DNA.
DR HSSP; P00953; 1MAU.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004830; F:tryptophan-tRNA ligase activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006436; P:tryptophanyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002305; tRNA-synt_1b.
DR InterPro; IPR001412; tRNA-synt_1b.
DR InterPro; IPR002306; Trp tRNA-synt_1b.
DR Pfam; PF00579; tRNA-synt_1b; 1.
DR PRINTS; PR01039; TRNASYNTHTRP.
DR TIGRFAMs; TIGR00233; trps; 1.
DR PROSITE; PS00178; AA TRNA LIGASE I; 1.
DR ATP-binding; Aminoacyl-tRNA synthetase; Complete proteome; Ligase;
KW Nucleotide-binding; Protein biosynthesis.
FT DOMAIN 3 237 ABC transporter.
FT NP BIND 35 42 ATP (By similarity).
SQ SEQUENCE 340 AA; 37475 MW; 363EACB6A6EB883 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 340;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 81 RAVFFA 86

RESULT 71
CYSA METCA STANDARD; PRT; 348 AA.
ID Q609Q1;
AC Q609Q1;
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Sulfate/thiosulfate import ATP-binding protein cysA (EC 3.6.3.25)
DE (Sulfate-transferring ATPase).
GN Name=cysA; OrderedLocNames=MCAL181;
OS Methylococcus capsulatus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
OC Methylococcaceae; Methylococcus.
OX NCBI_TaxID=414;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bath / NCIMB 11132;
RC PubMed=15383840; DOI=10.1371/journal.pbio.0020303;
RA Ward N.L., Larsen O., Sakwa J., Brueseth L., Khouri H.M., Durkin A.S.,
RA Dimitrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E.,
RA Methe B.A., Wu M., Heidelberg J.F., Paulsen I.F., Fouts D.E.,
RA Ravel J., Tettelin H., Ren Q., Read T.D., DeBoy R.T., Seehadri R.,
RA Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J.,
RA Grindhaug S.H., Holt I.B., Eidhammer I., Jonassen I., Vanaken S.,
RA Utterback T.R., Feldblyum T.V., Fraser C.M., Lillehaug J.R.,
RA Eisen J.A.;
RT "Genomic insights into methanotrophy: the complete genome sequence of
RT Methylococcus capsulatus (Bath).";
RL PLOS Biol. 2:1616-1628(2004).
CC -1- FUNCTION: Part of the ABC transporter complex cysAWTP involved in
CC sulfate/thiosulfate import. Responsible for energy coupling to the
CC transport system (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + sulfate(Out) = ADP + phosphate +
CC sulfate(In).

RA Seo J.-S., Chong H., Park H.S., Yoon K.-O., Jung C., Kim J.J.,
RA Hong J.H., Kim H., Kim J.-H., Kil J.-I., Park C.J., Oh H.-M.,
RA Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.Y.,
RA Kang H.L., Lee S.Y., Lee K.J., Kang H.S.;
RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis
RT ZMA."
RL Nat. Biotechnol. 23:63-68(2005).
CC -1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA (Trp) = AMP +
CC diphosphate + L-tryptophyl-tRNA(Trp).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL; AF300471; AA42413.1; -; Genomic DNA.
DR EMBL; AE008692; AA90264.1; -; Genomic DNA.
DR HSSP; P00953; 1MAU.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004830; F:tryptophan-tRNA ligase activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006436; P:tryptophanyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002305; tRNA-synt_1b.
DR InterPro; IPR001412; tRNA-synt_1b.
DR InterPro; IPR002306; Trp tRNA-synt_1b.
DR Pfam; PF00579; tRNA-synt_1b; 1.
DR PRINTS; PR01039; TRNASYNTHTRP.
DR TIGRFAMs; TIGR00233; trps; 1.
DR PROSITE; PS00178; AA TRNA LIGASE I; 1.
DR ATP-binding; Aminoacyl-tRNA synthetase; Complete proteome; Ligase;
KW Nucleotide-binding; Protein biosynthesis.
FT DOMAIN 3 237 ABC transporter.
FT NP BIND 35 42 ATP (By similarity).
SQ SEQUENCE 340 AA; 37475 MW; 363EACB6A6EB883 CRC64;

Query Match 89.7%; Score 26; DB 1; Length 348;
Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 271 KALFFA 276

RESULT 72
Q83MJ3_SHIFL PRELIMINARY; PRT; 352 AA.
ID Q83MJ3_SHIFL PRELIMINARY;
AC Q83MJ3; Q7UB67;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Putative resistance protein.
GN Name=yihN; OrderedLocNames=S3802, SF3944;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=301 / Serotype 2a;
RC PubMed=2272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2457T / ATCC 700930 / Serotype 2a;
RC PubMed=22590274; PubMed=12704152;
RA DOI=10.1128/JAI.71.5.2775-2786-2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

```

```

RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RL flexneri serotype 2a strain 2457T.",
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AS005674; AAN45379.2; -; Genomic DNA.
DR EMBL; AS015990; AAP18819.1; -; Genomic DNA.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
KW Complete proteome.
SQ SEQUENCE 352 AA; 38913 MW; 2CEA79CE6252270B CRC64;

Query Match      89.7%; Score 26; DB 2; Length 352;
Best Local Similarity 83.3%; Pred. No. 9.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 332 RAVFFA 337
:|||||

RESULT 73
Q72FT5 DESVH
ID Q72FT5_DESVH PRELIMINARY; PRT; 352 AA.
AC Q72FT5_27
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Membrane protein, putative.
DE OrderedLocusNames=DVU0128;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS 8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15077118; DOI=10.1038/nbt959;
RA Heideberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RA "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough."
RL Nat. Biotechnol. 22:554-559(2004).
DR EMBL; AS017309; AAS94612.1; -; Genomic DNA.
DR TIGR; DVU0128; -.
DR InterPro; IPR002549; UPF0118.
DR Pfam; PF01594; UPF0118; 1.
KW Complete proteome.
SQ SEQUENCE 352 AA; 36026 MW; 787856A87410B493 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 352;
Best Local Similarity 83.3%; Pred. No. 9.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 23 KALFFA 28
:|||||

RESULT 74
Q6MI90 BDEBA
ID Q6MI90_BDEBA PRELIMINARY; PRT; 383 AA.
AC Q6MI90_27
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative polysaccharide deacetylase precursor (EC 3.5.1.-).
GN OrderedLocusNames=Bd3279;
OS Bdellovibrio bacteriovorus.

```

```

OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Gpplinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.",
RT Science 303:689-692(2004).
RL EMBL; BX842655; CAE78090.1; -; Genomic DNA.
DR GO; GO:0016810; F:hydrolase activity, acting on carbon-nitrog. . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR002509; PolySac deacet.
DR Pfam; PF01522; PolySacc_deac_1; 1.
KW Complete proteome; Hydrolase; Signal.
FT SIGNAL 1
FT SIGNAL 11 Potential.
SQ SEQUENCE 383 AA; 42819 MW; 7A1A4BF645C565BC CRC64;

Query Match      89.7%; Score 26; DB 2; Length 383;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 197 KAMFFA 202
:|||||

RESULT 75
Q4HML6 CAMLA
ID Q4HML6_CAMLA PRELIMINARY; PRT; 390 AA.
AC Q4HML6_31
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Cyanate MFS transporter, putative.
GN ORFNames=CLA1389;
OS Campylobacter lari RM2100.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=306263;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RM2100;
RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
RA Nelson K.E.;
RT "Major structural and novel potential virulence mechanisms from the
RT genomes of multiple Campylobacter species.",
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAPK0100001; EAL55536.1; -; Genomic DNA.
SQ SEQUENCE 390 AA; 42990 MW; 29E9CF925C147383 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 390;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 75 KALFFA 80
:|||||

Search completed: December 29, 2005, 17:47:28
Job time : 78.1936 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: December 29, 2005, 17:49:38 ; Search time 3.83871 Seconds
(without alignments)
13.656 Million cell updates/sec

Title: US-10-009-122-18
Perfect score: 34
Sequence: 1 KLVFFAQ 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues
Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : Published Applications AA.New.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	91.2	19	6	US-10-923-605-5
2	31	91.2	19	6	US-10-934-818-5
3	31	91.2	40	7	US-11-016-706-36
4	31	91.2	40	7	US-11-098-674-12
5	31	91.2	42	6	US-10-923-605-1
6	31	91.2	42	6	US-10-934-818-1
7	31	91.2	42	7	US-11-016-706-37
8	31	91.2	43	6	US-10-934-818-6
9	31	91.2	43	6	US-10-250-581-1
10	31	91.2	43	6	US-10-250-581-1
11	31	91.2	770	6	US-10-982-545-15
12	31	91.2	770	6	US-10-789-273-38
13	26	76.5	525	7	US-11-082-389-350
14	26	76.5	858	6	US-10-613-744-6
15	25	73.5	5	7	US-11-098-674-1
16	25	73.5	179	6	US-10-467-657-306
17	25	73.5	179	6	US-10-467-657-6422
18	25	73.5	325	6	US-10-454-437-142
19	25	73.5	485	6	US-10-204-029-7
20	25	73.5	528	6	US-10-793-626-1930
21	25	73.5	721	6	US-10-467-962B-49
22	24	70.6	71	7	US-11-000-463-765
23	24	70.6	197	5	US-09-940-308-3
24	24	70.6	211	6	US-10-467-657-6932
25	24	70.6	215	6	US-10-131-826A-4

26	24	70.6	221	6	US-10-467-657-290	Sequence 290, App
27	24	70.6	221	6	US-10-467-657-5750	Sequence 5750, App
28	24	70.6	228	6	US-10-467-657-568	Sequence 568, App
29	24	70.6	228	6	US-10-467-657-4838	Sequence 4838, App
30	24	70.6	233	6	US-10-821-234-1322	Sequence 1322, App
31	24	70.6	252	6	US-10-467-657-3128	Sequence 3128, App
32	24	70.6	338	6	US-10-878-556A-19	Sequence 19, Appl
33	24	70.6	344	6	US-10-131-826A-376	Sequence 376, App
34	24	70.6	389	5	US-09-940-308-6	Sequence 6, Appl
35	24	70.6	453	7	US-11-082-389-198	Sequence 198, App
36	24	70.6	481	6	US-10-995-561-959	Sequence 959, App
37	24	70.6	505	6	US-10-873-528-120	Sequence 120, App
38	24	70.6	547	6	US-10-770-726-87	Sequence 87, Appl
39	24	70.6	558	7	US-11-078-189-19	Sequence 19, Appl
40	24	70.6	588	6	US-10-821-234-1337	Sequence 1337, App
41	24	70.6	590	5	US-09-940-308-2	Sequence 2, Appl
42	24	70.6	660	7	US-11-186-284-125	Sequence 125, App
43	24	70.6	708	6	US-10-821-234-917	Sequence 917, App
44	23	67.6	47	6	US-10-467-657-5436	Sequence 5436, App
45	23	67.6	57	6	US-10-467-657-5448	Sequence 5448, App
46	23	67.6	104	6	US-10-689-742-206	Sequence 206, App
47	23	67.6	143	6	US-10-793-626-370	Sequence 370, App
48	23	67.6	155	6	US-10-467-657-2420	Sequence 2420, App
49	23	67.6	194	6	US-10-467-657-3978	Sequence 3978, App
50	23	67.6	195	7	US-11-019-955-24	Sequence 24, Appl
51	23	67.6	211	6	US-10-821-234-1372	Sequence 1372, App
52	23	67.6	216	6	US-10-467-657-8102	Sequence 8102, App
53	23	67.6	223	7	US-11-112-882-88	Sequence 88, Appl
54	23	67.6	241	7	US-11-019-955-27	Sequence 27, Appl
55	23	67.6	258	6	US-10-793-626-2360	Sequence 2360, App
56	23	67.6	268	7	US-11-019-955-28	Sequence 28, Appl
57	23	67.6	269	6	US-10-467-657-330	Sequence 330, App
58	23	67.6	272	6	US-10-632-150-46	Sequence 46, Appl
59	23	67.6	272	7	US-11-073-457-46	Sequence 46, Appl
60	23	67.6	272	7	US-11-073-460-46	Sequence 1105, App
61	23	67.6	370	6	US-10-821-234-1105	Sequence 1105, App
62	23	67.6	400	6	US-10-793-626-1056	Sequence 1056, App
63	23	67.6	463	6	US-10-467-657-6352	Sequence 6352, App
64	23	67.6	463	6	US-10-467-657-7604	Sequence 7604, App
65	23	67.6	522	6	US-10-995-561-1030	Sequence 1030, App
66	23	67.6	582	7	US-11-090-439-58	Sequence 58, Appl
67	23	67.6	585	6	US-10-967-457-18	Sequence 18, Appl
68	23	67.6	585	6	US-10-939-890-500	Sequence 500, App
69	23	67.6	585	7	US-11-078-663-18	Sequence 18, Appl
70	23	67.6	585	7	US-11-078-914-18	Sequence 18, Appl
71	23	67.6	615	6	US-10-995-561-940	Sequence 940, App
72	23	67.6	662	6	US-10-995-561-943	Sequence 943, App
73	23	67.6	690	6	US-10-939-890-501	Sequence 501, App
74	23	67.6	702	6	US-10-995-561-942	Sequence 942, App
75	23	67.6	754	6	US-10-995-561-941	Sequence 941, App
76	22	64.7	35	6	US-10-821-234-1704	Sequence 1704, App
77	22	64.7	50	6	US-10-467-657-7892	Sequence 7892, App
78	22	64.7	106	7	US-11-064-174-50	Sequence 50, Appl
79	22	64.7	117	6	US-10-467-657-2282	Sequence 2282, App
80	22	64.7	122	6	US-10-467-657-606	Sequence 606, App
81	22	64.7	127	6	US-10-467-657-3152	Sequence 3152, App
82	22	64.7	134	6	US-10-467-657-6860	Sequence 6860, App
83	22	64.7	150	6	US-10-467-657-2040	Sequence 2040, App
84	22	64.7	175	6	US-10-873-528-90	Sequence 90, Appl
85	22	64.7	183	6	US-10-980-388-89	Sequence 89, Appl
86	22	64.7	183	6	US-10-467-657-8825	Sequence 8825, App
87	22	64.7	189	6	US-10-467-657-6854	Sequence 6854, App
88	22	64.7	189	6	US-10-467-657-7856	Sequence 7856, App
89	22	64.7	204	6	US-10-980-388-102	Sequence 102, App
90	22	64.7	208	6	US-10-467-657-3098	Sequence 3098, App
91	22	64.7	220	6	US-10-467-657-8734	Sequence 8734, App
92	22	64.7	239	6	US-10-467-657-8743	Sequence 8743, App
93	22	64.7	271	6	US-10-793-626-1156	Sequence 1156, App
94	22	64.7	276	6	US-10-873-528-134	Sequence 134, App
95	22	64.7	347	6	US-10-467-657-2014	Sequence 2014, App
96	22	64.7	352	7	US-11-191-072-4	Sequence 4, Appl
97	22	64.7	358	6	US-10-467-657-7030	Sequence 7030, App
98	22	64.7	362	6	US-10-467-657-6880	Sequence 6880, App

99	22	64.7	366	6	US-10-467-657-7024	Sequence 7024, Ap	172	21	61.8	433	6	US-10-821-234-1429	Sequence 1429, Ap
100	22	64.7	366	6	US-10-467-657-7964	Sequence 7964, Ap	173	21	61.8	446	6	US-10-467-657-930	Sequence 930, Ap
101	22	64.7	392	6	US-10-467-657-2726	Sequence 2726, Ap	174	21	61.8	447	7	US-11-112-882-4	Sequence 4, Appl
102	22	64.7	402	6	US-10-467-657-9070	Sequence 9070, Ap	175	21	61.8	448	6	US-10-467-657-1096	Sequence 1096, Ap
103	22	64.7	409	6	US-10-821-234-1425	Sequence 1425, Ap	176	21	61.8	460	6	US-10-467-657-3136	Sequence 3136, Ap
104	22	64.7	413	6	US-10-467-657-1858	Sequence 1858, Ap	177	21	61.8	475	6	US-11-174-150-45	Sequence 45, Appl
105	22	64.7	425	7	US-11-055-822-1104	Sequence 1104, Ap	178	21	61.8	476	6	US-10-763-712A-107	Sequence 107, App
106	22	64.7	426	6	US-10-467-657-2120	Sequence 2120, Ap	179	21	61.8	481	6	US-10-467-657-3292	Sequence 3292, Ap
107	22	64.7	444	6	US-10-467-657-2141	Sequence 2141, Ap	180	21	61.8	481	6	US-10-467-657-4660	Sequence 4660, Ap
108	22	64.7	445	6	US-10-873-528-30	Sequence 30, Appl	181	21	61.8	489	6	US-10-793-626-2632	Sequence 2632, Ap
109	22	64.7	524	6	US-10-689-742-13	Sequence 13, Appl	182	21	61.8	522	7	US-11-080-991-104	Sequence 104, App
110	22	64.7	525	7	US-11-112-882-27	Sequence 27, Appl	183	21	61.8	525	6	US-10-763-712A-108	Sequence 108, App
111	22	64.7	576	6	US-10-508-442-2	Sequence 2, Appl	184	21	61.8	529	7	US-11-174-150-46	Sequence 46, Appl
112	22	64.7	616	6	US-10-131-826A-206	Sequence 206, App	185	21	61.8	533	6	US-10-467-657-2868	Sequence 2868, Ap
113	22	64.7	672	6	US-10-467-657-8280	Sequence 8280, Ap	186	21	61.8	554	7	US-11-000-463-240	Sequence 240, App
114	22	64.7	677	6	US-10-131-826A-230	Sequence 230, App	187	21	61.8	560	7	US-11-080-991-62	Sequence 62, Appl
115	22	64.7	708	7	US-11-174-150-25	Sequence 25, Appl	188	21	61.8	592	6	US-10-467-657-4888	Sequence 4888, Ap
116	22	64.7	710	7	US-11-078-189-18	Sequence 18, Appl	189	21	61.8	594	6	US-10-467-657-3952	Sequence 3952, Ap
117	22	64.7	736	7	US-11-174-150-26	Sequence 26, Appl	190	21	61.8	602	7	US-11-055-822-74	Sequence 74, Appl
118	22	64.7	737	7	US-11-078-189-9	Sequence 9, Appl	191	21	61.8	626	7	US-10-512-184-49	Sequence 49, Appl
119	22	64.7	739	7	US-11-078-189-12	Sequence 12, Appl	192	21	61.8	707	7	US-11-186-284-132	Sequence 132, App
120	22	64.7	745	6	US-11-147-109-2	Sequence 2, Appl	193	21	61.8	738	7	US-11-147-047-48	Sequence 48, Appl
121	22	64.7	856	6	US-10-467-657-8534	Sequence 8534, Ap	194	21	61.8	747	7	US-11-018-018-1	Sequence 1, Appl
122	22	64.7	989	6	US-10-821-234-975	Sequence 975, App	195	21	61.8	747	7	US-11-047-757-1	Sequence 1, Appl
123	22	64.7	1167	6	US-10-601-368-18	Sequence 18, Appl	196	21	61.8	823	6	US-10-467-657-2526	Sequence 2526, Ap
124	22	64.7	2504	6	US-10-647-956A-8	Sequence 8, Appl	197	21	61.8	1016	7	US-11-103-957-41	Sequence 41, Appl
125	21	61.8	26	6	US-10-986-501-303	Sequence 303, App	198	21	61.8	1070	7	US-11-147-047-49	Sequence 49, Appl
126	21	61.8	45	6	US-10-467-657-8626	Sequence 8626, Ap	199	21	61.8	1113	7	US-11-067-811-4	Sequence 4, Appl
127	21	61.8	50	6	US-10-467-657-9144	Sequence 9144, Ap	200	21	61.8	1196	6	US-10-613-744-9	Sequence 9, Appl
128	21	61.8	101	6	US-10-467-657-6722	Sequence 6722, Ap	201	21	61.8	1259	6	US-10-467-657-5510	Sequence 5510, Ap
129	21	61.8	104	6	US-10-793-626-2512	Sequence 2512, Ap	202	21	61.8	1510	7	US-11-055-822-72	Sequence 72, Appl
130	21	61.8	105	6	US-10-467-657-9209	Sequence 9209, Ap	203	21	61.8	1766	7	US-11-075-185-10	Sequence 10, Appl
131	21	61.8	133	7	US-11-069-834-2	Sequence 2, Appl	204	21	61.8	2261	6	US-10-995-561-600	Sequence 600, App
132	21	61.8	147	7	US-11-000-463-758	Sequence 758, App	205	21	61.8	2261	7	US-11-055-309A-9	Sequence 9, Appl
133	21	61.8	179	6	US-10-793-626-3052	Sequence 3052, Ap	206	21	61.8	2261	7	US-11-055-309A-10	Sequence 10, Appl
134	21	61.8	183	7	US-11-000-463-286	Sequence 286, App	207	21	61.8	2333	7	US-11-096-281-13	Sequence 13, Appl
135	21	61.8	190	6	US-10-467-657-3436	Sequence 3436, Ap	208	21	61.8	2339	7	US-11-096-281-11	Sequence 11, Appl
136	21	61.8	193	6	US-10-467-657-8294	Sequence 8294, Ap	209	21	61.8	3623	6	US-10-995-561-593	Sequence 593, App
137	21	61.8	194	7	US-11-103-957-57	Sequence 57, Appl	210	20	58.8	11	7	US-11-074-176-377	Sequence 377, App
138	21	61.8	199	6	US-10-467-657-4532	Sequence 4532, Ap	211	20	58.8	19	6	US-10-467-657-8712	Sequence 8712, Ap
139	21	61.8	204	6	US-10-467-657-8687	Sequence 8687, Ap	212	20	58.8	28	6	US-10-250-581-14	Sequence 14, Appl
140	21	61.8	205	6	US-10-873-528-52	Sequence 52, Appl	213	20	58.8	28	6	US-10-250-581-17	Sequence 17, Appl
141	21	61.8	207	6	US-10-858-730-136	Sequence 136, App	214	20	58.8	28	6	US-10-250-581-14	Sequence 14, Appl
142	21	61.8	208	6	US-10-467-657-2658	Sequence 2658, Ap	215	20	58.8	28	6	US-10-250-581-17	Sequence 17, Appl
143	21	61.8	210	6	US-10-793-626-972	Sequence 972, App	216	20	58.8	28	6	US-10-250-581-15	Sequence 15, Appl
144	21	61.8	213	6	US-10-467-657-1194	Sequence 1194, Ap	217	20	58.8	40	6	US-10-250-581-18	Sequence 18, Appl
145	21	61.8	220	6	US-10-467-657-3154	Sequence 3154, Ap	218	20	58.8	40	6	US-10-250-581-15	Sequence 15, Appl
146	21	61.8	224	6	US-10-793-626-2684	Sequence 2684, Ap	219	20	58.8	40	6	US-10-250-581-18	Sequence 18, Appl
147	21	61.8	229	6	US-10-131-826A-410	Sequence 410, App	220	20	58.8	42	6	US-10-250-581-16	Sequence 16, Appl
148	21	61.8	231	6	US-10-467-657-7406	Sequence 7406, Ap	221	20	58.8	42	6	US-10-250-581-19	Sequence 19, Appl
149	21	61.8	248	6	US-10-793-626-3218	Sequence 3218, Ap	222	20	58.8	42	6	US-10-250-581-16	Sequence 16, Appl
150	21	61.8	249	7	US-11-113-424-30	Sequence 30, Appl	223	20	58.8	42	6	US-10-250-581-19	Sequence 19, Appl
151	21	61.8	258	6	US-10-467-657-6180	Sequence 6180, Ap	224	20	58.8	44	7	US-11-000-463-372	Sequence 372, App
152	21	61.8	258	6	US-10-467-657-7572	Sequence 7572, Ap	225	20	58.8	47	6	US-10-467-657-9186	Sequence 9186, Ap
153	21	61.8	259	6	US-10-512-184-34	Sequence 34, Appl	226	20	58.8	52	6	US-10-467-657-2216	Sequence 2216, Ap
154	21	61.8	267	6	US-10-821-234-1683	Sequence 1683, Ap	227	20	58.8	53	6	US-10-467-657-6120	Sequence 6120, Ap
155	21	61.8	269	6	US-10-467-657-2198	Sequence 2198, Ap	228	20	58.8	54	6	US-10-467-657-4978	Sequence 4978, Ap
156	21	61.8	298	6	US-10-793-626-1298	Sequence 1298, Ap	229	20	58.8	54	6	US-10-467-657-8560	Sequence 8560, Ap
157	21	61.8	311	6	US-10-793-626-2450	Sequence 2450, Ap	230	20	58.8	56	6	US-10-467-657-1050	Sequence 1050, Ap
158	21	61.8	327	6	US-10-793-626-1104	Sequence 1104, Ap	231	20	58.8	56	6	US-10-467-657-5386	Sequence 5386, Ap
159	21	61.8	348	6	US-10-467-657-6602	Sequence 6602, Ap	232	20	58.8	76	6	US-10-467-657-5690	Sequence 5690, Ap
160	21	61.8	348	6	US-10-467-657-7662	Sequence 7662, Ap	233	20	58.8	80	7	US-11-123-896-89	Sequence 89, Appl
161	21	61.8	349	6	US-10-515-419-2	Sequence 2, Appl	234	20	58.8	90	7	US-11-020-772-33	Sequence 33, Appl
162	21	61.8	352	6	US-10-515-419-3	Sequence 3, Appl	235	20	58.8	92	6	US-10-467-657-2378	Sequence 2378, Ap
163	21	61.8	355	6	US-10-467-657-7996	Sequence 7996, Ap	236	20	58.8	98	6	US-10-467-657-4746	Sequence 4746, Ap
164	21	61.8	355	7	US-11-055-822-162	Sequence 162, App	237	20	58.8	100	7	US-11-123-896-137	Sequence 137, App
165	21	61.8	371	6	US-10-512-184-71	Sequence 71, Appl	238	20	58.8	104	6	US-10-467-657-6866	Sequence 6866, Ap
166	21	61.8	373	6	US-10-858-730-20	Sequence 20, Appl	239	20	58.8	105	7	US-11-155-775-12	Sequence 12, Appl
167	21	61.8	378	6	US-10-467-657-1796	Sequence 1796, Ap	240	20	58.8	106	6	US-10-467-657-3052	Sequence 3052, Ap
168	21	61.8	395	6	US-10-793-626-664	Sequence 664, App	241	20	58.8	107	7	US-11-064-174-36	Sequence 36, Appl
169	21	61.8	417	6	US-10-467-657-2112	Sequence 2112, Ap	242	20	58.8	112	7	US-11-054-669-113	Sequence 113, App
170	21	61.8	428	6	US-10-821-234-997	Sequence 997, App	243	20	58.8	114	6	US-10-467-657-9012	Sequence 9012, Ap
171	21	61.8	433	6	US-10-652-893-4	Sequence 4, Appl	244	20	58.8	115	6	US-10-793-626-1554	Sequence 1554, Ap

```
245 20 58.8 119 7 US-11-084-508-23
246 20 58.8 122 6 US-10-632-150-38
247 20 58.8 122 7 US-11-073-457-38
248 20 58.8 122 7 US-11-073-460-38
249 20 58.8 123 6 US-10-793-626-354
250 20 58.8 123 6 US-10-467-657-1528
251 20 58.8 123 6 US-10-467-657-5166
252 20 58.8 123 6 US-10-467-657-5166
253 20 58.8 126 6 US-10-793-626-2786
254 20 58.8 127 7 US-11-106-796-10
255 20 58.8 129 6 US-10-501-039-8
256 20 58.8 134 6 US-10-793-626-432
257 20 58.8 137 6 US-10-793-626-530
258 20 58.8 137 6 US-10-793-626-1980
259 20 58.8 138 6 US-10-467-657-2928
260 20 58.8 139 6 US-10-467-657-28
261 20 58.8 139 6 US-10-467-657-8188
262 20 58.8 157 6 US-10-467-657-5104
263 20 58.8 167 7 US-11-210-316-18
264 20 58.8 175 6 US-10-873-528-97
265 20 58.8 178 6 US-10-892-379-4
266 20 58.8 179 6 US-10-467-657-5942
267 20 58.8 182 6 US-10-793-626-2836
268 20 58.8 183 6 US-10-467-657-6906
269 20 58.8 191 6 US-10-467-657-818
270 20 58.8 193 6 US-10-467-657-2700
271 20 58.8 205 6 US-10-689-742-72
272 20 58.8 208 6 US-10-510-386-172
273 20 58.8 210 6 US-10-467-657-6318
274 20 58.8 215 6 US-10-467-657-5460
275 20 58.8 215 7 US-11-008-331-5
276 20 58.8 222 6 US-10-467-657-7608
277 20 58.8 223 6 US-10-467-657-5212
278 20 58.8 229 6 US-10-510-386-228
279 20 58.8 230 7 US-11-170-653-59
280 20 58.8 239 6 US-10-467-657-432
281 20 58.8 242 6 US-10-821-234-1073
282 20 58.8 242 6 US-10-467-657-5676
283 20 58.8 243 6 US-10-512-109-23
284 20 58.8 243 6 US-10-512-109-48
285 20 58.8 245 6 US-10-467-657-4742
286 20 58.8 256 7 US-11-054-515-1027
287 20 58.8 263 6 US-10-467-657-6188
288 20 58.8 265 6 US-10-793-626-2500
289 20 58.8 271 6 US-10-821-234-1419
290 20 58.8 274 7 US-11-132-142-1
291 20 58.8 288 6 US-10-467-657-1272
292 20 58.8 291 7 US-11-102-883-22
293 20 58.8 292 7 US-11-102-883-24
294 20 58.8 294 6 US-10-467-657-7686
295 20 58.8 299 6 US-10-467-657-2190
296 20 58.8 299 6 US-10-873-528-106
297 20 58.8 302 6 US-10-467-657-5794
298 20 58.8 313 6 US-10-467-657-3982
299 20 58.8 313 6 US-10-467-657-8140
300 20 58.8 320 6 US-10-467-657-424
301 20 58.8 321 6 US-10-467-657-2504
```

ALIGNMENTS

```
RESULT 1
US-10-923-605-5
; Sequence 5, Application US/10923605
; Publication No. US20050245727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
```

```
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abetal3-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)_RES
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-923-605-5
```

```
Query Match 91.2%; Score 31; DB 6; Length 19;
Best Local Similarity 85.7%; Pred. No. 0.32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
||| |||
Db 4 KLVFFAE 10
```

RESULT 2

```
US-10-934-818-5
; Sequence 5, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/667,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abetal3-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)_RES
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5
```

```
Query Match 91.2%; Score 31; DB 6; Length 19;
Best Local Similarity 85.7%; Pred. No. 0.32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
||| |||
Db 4 KLVFFAE 10
```

RESULT 3

```
US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
```

; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; PRIOR FILING DATE: 2004-12-16
; CURRENT APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-36

Query Match 91.2%; Score 31; DB 7; Length 40;
Best Local Similarity 85.7%; Pred. No. 0.66;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 16 KLVFFAE 22

RESULT 4
US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elmova, Elena
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTQ-0086
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

Query Match 91.2%; Score 31; DB 7; Length 40;
Best Local Similarity 85.7%; Pred. No. 0.66;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 16 KLVFFAE 22

RESULT 5
US-10-923-605-1
; Sequence 1, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152700-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605

; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-923-605-1

Query Match 91.2%; Score 31; DB 6; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 16 KLVFFAE 22

RESULT 6
US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152700-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1

Query Match 91.2%; Score 31; DB 6; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 16 KLVFFAE 22

RESULT 7
US-11-016-706-37
; Sequence 37, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24

; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-37

Query Match 91.2%; Score 31; DB 7; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||||:
Db 16 KLVFFPAE 22

RESULT 8

US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match 91.2%; Score 31; DB 6; Length 43;
Best Local Similarity 85.7%; Pred. No. 0.71;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||||:
Db 16 KLVFFPAE 22

RESULT 9

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 91.2%; Score 31; DB 6; Length 43;
Best Local Similarity 85.7%; Pred. No. 0.71;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||||:
Db 16 KLVFFPAE 22

RESULT 10

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 91.2%; Score 31; DB 6; Length 43;
Best Local Similarity 85.7%; Pred. No. 0.71;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||||:
Db 16 KLVFFPAE 22

RESULT 11

US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:

; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease

```
/ OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
/ OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
/ OTHER INFORMATION: Alzheimer's disease amyloid protein
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: (1)..(17)
/ OTHER INFORMATION: signal peptide
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (1)..(40)
/ OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40
/ OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (18)..(687)
/ OTHER INFORMATION: soluble APP-alpha
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (18)..(671)
/ OTHER INFORMATION: soluble APP-beta
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (672)..(770)
/ OTHER INFORMATION: C99
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (672)..(713)
/ OTHER INFORMATION: beta-amyloid protein 42
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (672)..(711)
/ OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
/ OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (688)..(770)
/ OTHER INFORMATION: C83
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (688)..(713)
/ OTHER INFORMATION: P3(42)
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (688)..(711)
/ OTHER INFORMATION: P3(40)
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (712)..(770)
/ OTHER INFORMATION: gamma-CTF(59)
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (714)..(770)
/ OTHER INFORMATION: gamma-CTF(57)
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (721)..(770)
/ OTHER INFORMATION: gamma-CTF(50)
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (740)..(770)
/ OTHER INFORMATION: C31
/ OTHER INFORMATION: C31
US-10-982-545-15
```

```
Query Match          91.2%; Score 31; DB 6; Length 770;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 KLVFFPAQ 7

Db 687 KLVFFFAE 693

RESULT 12

```
US-10-789-273-38
/ Sequence 38, Application US/10789273
/ Publication No. US20050249725A1
/ GENERAL INFORMATION:
/ APPLICANT: Basi, Gurig
/ APPLICANT: Saidanha, Jose
/ APPLICANT: Yednock, Ted
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
/ TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
/ FILE REFERENCE: ELN-002CP
/ CURRENT APPLICATION NUMBER: US/10/789,273
/ CURRENT FILING DATE: 2004-02-27
/ PRIOR APPLICATION NUMBER: US/10/388,389
/ PRIOR FILING DATE: 2003-03-12
/ PRIOR APPLICATION NUMBER: US 10/010,942
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: US 60/251,892
/ PRIOR FILING DATE: 2000-12-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 38
/ LENGTH: 770
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-789-273-38
```

```
Query Match          91.2%; Score 31; DB 6; Length 770;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 KLVFFPAQ 7

Db 687 KLVFFFAE 693

RESULT 13

```
US-11-082-389-350
/ Sequence 350, Application US/11082389
/ Publication No. US20050244935A1
/ GENERAL INFORMATION:
/ APPLICANT: Pompejus, Markus
/ APPLICANT: Kroger, Burkhard
/ APPLICANT: Schroder, Hartwig
/ APPLICANT: Zelder, Oskar
/ APPLICANT: Haberhauer, Gregor
/ TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
/ TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
/ TITLE OF INVENTION: TRANSPORT
/ FILE REFERENCE: BGI-131PCPN
/ CURRENT APPLICATION NUMBER: US/11/082,389
/ CURRENT FILING DATE: 2005-03-16
/ PRIOR APPLICATION NUMBER: US 09/603024
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 60/141031
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: US 60/143262
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: US 60/151281
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: DE 19930487.4
/ PRIOR FILING DATE: 1999-07-01
/ PRIOR APPLICATION NUMBER: DE 19930489.0
/ PRIOR FILING DATE: 1999-07-01
/ PRIOR APPLICATION NUMBER: DE 19931549.3
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931550.7
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19932134.5
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19941379.7
/ PRIOR FILING DATE: 1999-08-31
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 446
```



```
; SEQ ID NO 350
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-350

Query Match          76.5%; Score 26; DB 7; Length 525;
Best Local Similarity 71.4%; Pred. No. 95;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      230 KYVFFAQ 236
      |||||

RESULT 14
US-10-613-744-6
; Sequence 6, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-613-744-6

Query Match          76.5%; Score 26; DB 6; Length 858;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFAQ 7
Db      348 LVFFAE 353
      |||||

RESULT 15
US-11-098-674-1
; Sequence 1, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; TITLE OF INVENTION: Compounds Which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTO-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-098-674-1

Query Match          73.5%; Score 25; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFF 5
Db      1 KLVFF 5
      |||||

RESULT 16
US-10-467-657-306
; Sequence 306, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 306
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-306

Query Match          73.5%; Score 25; DB 6; Length 179;
Best Local Similarity 57.1%; Pred. No. 55;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      30 KLVYFAQ 36
      ||::||

RESULT 17
US-10-467-657-6422
; Sequence 6422, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6422
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6422

Query Match          73.5%; Score 25; DB 6; Length 179;
Best Local Similarity 57.1%; Pred. No. 55;
```

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
||:|
Db 30 KLLYYAQ 36

RESULT 18

US-10-454-437-142
; Sequence 142, Application US/10454437
; Publication No. US20050277115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128PCPN
; CURRENT APPLICATION NUMBER: US/10/454,437
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 142
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-142

Query Match 73.5%; Score 25; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VFFAQ 7
|||
Db 55 VFFAQ 59

RESULT 19

US-10-204-029-7
; Sequence 7, Application US/10204029
; Publication No. US20050261487A1
; GENERAL INFORMATION:
; APPLICANT: Cully, Doris F.
; APPLICANT: Priest, Birgit
; APPLICANT: Yuan, Jeffrey
; APPLICANT: Zheng, Yingsong
; TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND-GATED ION
; TITLE OF INVENTION: CHANNELS FROM DROSOPHILA MELANOGASTER
; FILE REFERENCE: 20615P
; CURRENT APPLICATION NUMBER: US/10/204,029
; CURRENT FILING DATE: 2002-08-15

; PRIOR APPLICATION NUMBER: PCT/US01/06096
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/186645
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Drosophila Melanogaster
US-10-204-029-7

Query Match 73.5%; Score 25; DB 6; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VFFAQ 7
|||
Db 78 VFFAQ 82

RESULT 20

US-10-793-626-1930
; Sequence 1930, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1930
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1930

Query Match 73.5%; Score 25; DB 6; Length 528;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFF 5
|||
Db 477 KLVFF 481

RESULT 21

US-10-467-962B-49
; Sequence 49, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000 857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 49
; LENGTH: 721
; TYPE: PRT

```

; ORGANISM: Arabidopsis thaliana
US-10-467-962B-49

Query Match      73.5%; Score 25; DB 6; Length 721;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VFPAQ 7
Db 286 VFPAQ 290

RESULT 22
US-11-000-463-765
; Sequence 765, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radjoe T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785C1P4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 765
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-765

Query Match      70.6%; Score 24; DB 7; Length 71;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 LVFFAQ 7
Db 44 LVFFLQ 49

RESULT 23
US-09-940-308-3
; Sequence 3, Application US/09940308
; Publication No. US20040092437A1
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as
; FILE OF INVENTION: an Immunosuppressive Agent
; FILE REFERENCE: 06727/005003
; CURRENT APPLICATION NUMBER: US/09/940,308

; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 09/186,723
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 08/377,309
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-940-308-3

Query Match      70.6%; Score 24; DB 5; Length 197;
Best Local Similarity 80.0%; Pred. No. 99;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VFPAQ 7
Db 30 VFPAQ 34

RESULT 24
US-10-467-657-6932
; Sequence 6932, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6932
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6932

Query Match      70.6%; Score 24; DB 6; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFPA 6
Db 19 LVFFPA 23

RESULT 25
US-10-131-826A-4
; Sequence 4, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.

```

```
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 4
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-4

Query Match          70.6%; Score 24; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFFA 6
DB      166 LVFFFA 170

RESULT 26
US-10-467-657-290
; Sequence 290, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 290
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-290

Query Match          70.6%; Score 24; DB 6; Length 221;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFFA 6
DB      166 LVFFFA 170

RESULT 27
US-10-467-657-5750
; Sequence 5750, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5750
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5750

Query Match          70.6%; Score 24; DB 6; Length 221;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFFA 7
DB      41 LIFFFAR 46

RESULT 28
US-10-467-657-568
; Sequence 568, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 568
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-568

Query Match          70.6%; Score 24; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFFA 6
DB      156 LVFFFA 160

RESULT 29
```

```
US-10-467-657-4838
; Sequence 4838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838

Query Match      70.6%; Score 24; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFPA 6
Db      156 LVFFPA 160
|||||

RESULT 30
US-10-821-234-1322
; Sequence 1322, Application US/10821234
; Publication No. US2005025511A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1322
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1322

Query Match      70.6%; Score 24; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFPA 6
Db      166 LVFFPA 170
|||||

RESULT 31
US-10-467-657-3128
; Sequence 3128, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

US-10-467-657-3128
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3128
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3128

Query Match      70.6%; Score 24; DB 6; Length 252;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KLVFFPA 7
Db      202 KLVFFPA 208
|||||

RESULT 32
US-10-878-556A-19
; Sequence 19, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/cn03_human
; DATABASE ENTRY DATE: 2001-10-16
US-10-878-556A-19

Query Match      70.6%; Score 24; DB 6; Length 338;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFP 5
Db      76 KLVFFP 80
|||||

RESULT 33
US-10-131-826A-376
; Sequence 376, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
```

```
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 376
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-376

Query Match          70.6%; Score 24; DB 6; Length 344;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFF 5
      |||
Db      279 KLIFF 283

RESULT 34
US-09-940-308-6
; Sequence 6, Application US/09940308
; Publication No. US20040092437A1
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as
; FILE REFERENCE: 06727/005003
; CURRENT APPLICATION NUMBER: US/09/940,308
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 09/186,723
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 08/377,309
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-940-308-6

Query Match          70.6%; Score 24; DB 5; Length 389;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 VFPPA 7
```

```
Db      30 IFFAQ 34
      :|||
      30 IFFAQ 34

RESULT 35
US-11-082-389-198
; Sequence 198, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131PCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 198
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-198

Query Match          70.6%; Score 24; DB 7; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFA 6
      |||
Db      401 LVFFA 405

RESULT 36
US-10-995-561-959
; Sequence 959, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 959
; LENGTH: 481
```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-959

Query Match 70.6%; Score 24; DB 6; Length 481;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 275 KLVFFA 280

RESULT 37

US-10-873-528-120
; Sequence 120, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; PRIOR FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-120

Query Match 70.6%; Score 24; DB 6; Length 505;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VFFFA 7
Db 241 IFFFA 245

RESULT 38

US-10-770-726-87
; Sequence 87, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-87

Query Match 70.6%; Score 24; DB 6; Length 547;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 537 KLIGFAQ 543

RESULT 39

US-11-078-189-19
; Sequence 19, Application US/11078189
; Publication No. US20050277167A1
; GENERAL INFORMATION:
; APPLICANT: Bachinger, Hans Peter
; APPLICANT: Vranka, Janice
; TITLE OF INVENTION: PROLYL 3-HYDROXYLASES
; FILE REFERENCE: 08062-020001 US/11/078,189
; CURRENT APPLICATION NUMBER: US/11/078,189
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/552,409
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
US-11-078-189-19

Query Match 70.6%; Score 24; DB 7; Length 558;
Best Local Similarity 57.1%; Pred. No. 2.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 278 ELLFFAE 284

RESULT 40

US-10-821-234-1137
; Sequence 1137, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pt_SEQ_genes Version 1.0
; SEQ ID NO 1137
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1137

Query Match 70.8%; Score 24; DB 6; Length 588;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 578 KLIGFAQ 584

RESULT 41

US-09-940-308-2
; Sequence 2, Application US/09940308
; Publication No. US20040092437A1

```
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as
; FILE OF INVENTION: an Immunosuppressive Agent
; FILE REFERENCE: 06727/005003
; CURRENT APPLICATION NUMBER: US/09/940,308
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 09/186,723
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 08/377,309
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-940-308-2

Query Match          70.6%; Score 24; DB 5; Length 590;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 VFFAQ 7
DB      30 IFFAQ 34

RESULT 42
US-11-186-284-125
; Sequence 125, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: BURGART, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-125

Query Match          70.6%; Score 24; DB 7; Length 660;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KLVFFA 6
DB      531 KAVFFA 536

RESULT 43
```

```
US-10-821-234-917
; Sequence 917, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 917
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-917

Query Match          70.6%; Score 24; DB 6; Length 708;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KLVFFA 6
DB      579 KAVFFA 584

RESULT 44
US-10-467-657-5436
; Sequence 5436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5436
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5436

Query Match          67.6%; Score 23; DB 6; Length 47;
Best Local Similarity 80.0%; Pred. No. 41;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFF 5
DB      36 KLVFF 40

RESULT 45
US-10-467-657-5448
; Sequence 5448, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
```


; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5448
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5448

Query Match 67.6%; Score 23; DB 6; Length 57;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LVFFAQ 7
Db 51 LVFYAE 56

RESULT 46

US-10-689-742-206
; Sequence 206, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaVallie, Edward R
; APPLICANT: Ragie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 206
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-206

Query Match 67.6%; Score 23; DB 6; Length 104;
Best Local Similarity 66.7%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LVFFAQ 7
Db 21 LMFFSQ 26

RESULT 47

US-10-793-626-370
; Sequence 370, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 370
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-370

Query Match 67.6%; Score 23; DB 6; Length 143;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LVFFAQ 7
Db 101 LVFLAQ 106

RESULT 48

US-10-467-657-2420
; Sequence 2420, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2420
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2420

Query Match 67.6%; Score 23; DB 6; Length 155;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LVFFAQ 7
Db 18 MVFFAK 23

RESULT 49

US-10-467-657-3978
; Sequence 3978, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3978
; LENGTH: 194
; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3978

Query Match 67.6%; Score 23; DB 6; Length 194;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
: |||||
Db 13 REAFFAQ 19

RESULT 50

US-11-019-955-24
; Sequence 24, Application US/11019955
; Publication No. US20050282763A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
; FILE REFERENCE: 08191-022001
; CURRENT APPLICATION NUMBER: US/11/019,955
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US/10/074,956
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,175
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-019-955-24

Query Match 67.6%; Score 23; DB 7; Length 195;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
: |||||
Db 153 ELLFFAK 159

RESULT 51

US-10-821-234-1372
; Sequence 1372, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1372
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1372

Query Match 67.6%; Score 23; DB 6; Length 211;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
: |||||
Db 33 KTVYFAE 39

RESULT 52

US-10-467-657-8102
; Sequence 8102, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8102
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8102

Query Match 67.6%; Score 23; DB 6; Length 216;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFPA 6
: |||||
Db 18 LVFFPA 22

RESULT 53

US-11-112-882-88
; Sequence 88, Application US/11112882
; Publication No. US20050273885A1
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Research Organisation
; TITLE OF INVENTION: Synthesis of Long-Chain Polyunsaturated Fatty Acids in Recombinant
; FILE REFERENCE: 503244
; CURRENT APPLICATION NUMBER: US/11/112,882
; CURRENT FILING DATE: 2005-04-22
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Melosira sp.
US-11-112-882-88

Query Match 67.6%; Score 23; DB 7; Length 223;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LVFFPAQ 7
: |||||
Db 199 LVLFFAQ 204

RESULT 54

US-11-019-955-27
; Sequence 27, Application US/11019955
; Publication No. US20050282763A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
; FILE REFERENCE: 08191-022001
; CURRENT APPLICATION NUMBER: US/11/019,955
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US/10/074,956

```
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,175
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-019-955-27

Query Match      67.6%; Score 23; DB 7; Length 241;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
DB      177 ELFFAK 183

RESULT 55
US-10-793-626-2360
; Sequence 2360, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2360
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2360

Query Match      67.6%; Score 23; DB 6; Length 258;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFAQ 7
DB      158 LVFFSE 163

RESULT 56
US-11-019-955-28
; Sequence 28, Application US/11019955
; Publication No. US20050282763A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
; FILE REFERENCE: 08191-022001
; CURRENT APPLICATION NUMBER: US/11/019,955
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US/10/074,956
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,175
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-019-955-28

; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,175
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-019-955-27

Query Match      67.6%; Score 23; DB 7; Length 241;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
DB      177 ELFFAK 183

RESULT 57
US-10-467-657-330
; Sequence 330, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 330
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-330

Query Match      67.6%; Score 23; DB 6; Length 269;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFF 5
DB      11 KLVFF 15

RESULT 58
US-10-632-150-46
; Sequence 46, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chlaur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-46

Query Match      67.6%; Score 23; DB 6; Length 272;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
```


FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6352
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6352

Query Match 67.6%; Score 23; DB 6; Length 463;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LVFFA 6
Db 369 LIFFA 373

RESULT 64
US-10-467-657-7604
; Sequence 7604, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7604
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7604

Query Match 67.6%; Score 23; DB 6; Length 463;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LVFFA 6
Db 369 LIFFA 373

RESULT 65
US-10-995-561-1030
; Sequence 1030, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 1030
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-995-561-1030

Query Match 67.6%; Score 23; DB 6; Length 522;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LVFFA 6
Db 353 LIFFA 357

RESULT 66
US-11-090-439-58
; Sequence 58, Application US/11090439
; Publication No. US20050266442A1
; GENERAL INFORMATION:
; APPLICANT: Squillace, Rachel P.
; APPLICANT: Weiner, Michael P.
; TITLE OF INVENTION: Immortalized Human Tuberos Sclerosis Null
; TITLE OF INVENTION: Angiomyolipoma Cell and Method of Use Thereof
; FILE REFERENCE: 24318-502
; CURRENT APPLICATION NUMBER: US/11/090,439
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/556,344
; PRIOR FILING DATE: 2004-03-25
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-439-58

Query Match 67.6%; Score 23; DB 7; Length 582;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LVFFAQ 7
Db 178 MIFFAE 183

RESULT 67
US-10-967-457-18
; Sequence 18, Application US/10967457
; Publication No. US20050244931A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF545PCT
; CURRENT APPLICATION NUMBER: US/10/967,457
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: US/09/833,041
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-967-457-18

Query Match 67.6%; Score 23; DB 6; Length 585;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7

```
; :|||:
Db      153 ELLFFAK 159

RESULT 68
US-10-939-890-500
; Sequence 500, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen B.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 500
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo sapiens
US-10-939-890-500

Query Match      67.6%; Score 23; DB 6; Length 585;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      153 ELLFFAK 159

RESULT 69
US-11-078-663-18
; Sequence 18, Application US/11078663
; Publication No. US20050266532A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Sadeghi, Homa
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF543
; CURRENT APPLICATION NUMBER: US/11/078,663
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US/09/833,117
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-078-663-18

Query Match      67.6%; Score 23; DB 7; Length 585;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      153 ELLFFAK 159

RESULT 70
US-11-078-914-18
; Sequence 18, Application US/11078914
; Publication No. US20050268533A1
; GENERAL INFORMATION:
; APPLICANT: Ballance, David J.
; APPLICANT: Sleep, Darrell
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homa
; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF542
; CURRENT APPLICATION NUMBER: US/11/078,914
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US/09/832,501
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-078-914-18

Query Match      67.6%; Score 23; DB 7; Length 585;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      153 ELLFFAK 159

RESULT 71
US-10-995-561-940
; Sequence 940, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: PF543
; CURRENT APPLICATION NUMBER: US/11/078,663
```

```

; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 940
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-940

Query Match      67.6%; Score 23; DB 6; Length 615;
Best Local Similarity 80.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LVFFA 6
      |::|
Db      502 LIFFA 506

RESULT 72
US-10-995-561-943
; Sequence 943, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 943
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-943

Query Match      67.6%; Score 23; DB 6; Length 662;
Best Local Similarity 80.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LVFFA 6
      |::|
Db      547 LIFFA 551

RESULT 73
US-10-939-890-501
; Sequence 501, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.

```

```

; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 501
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HSA-Linked Dimer
US-10-939-890-501

Query Match      67.6%; Score 23; DB 6; Length 690;
Best Local Similarity 57.1%; Pred. No. 5.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
      |::|
Db      205 ELLFFAK 211

RESULT 74
US-10-995-561-942
; Sequence 942, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 942
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-942

Query Match      67.6%; Score 23; DB 6; Length 702;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LVFFA 6
      |::|
Db      587 LIFFA 591

RESULT 75
US-10-995-561-941
; Sequence 941, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559

```

```
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 941
; LENGTH: 754
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)---(754)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-995-561-941

Query Match      67.6%; Score 23; DB 6; Length 754;
Best Local Similarity 80.0%; Pred. No. 6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVFFA 6
Db      587 LVFFA 591
```

Search completed: December 29, 2005, 18:50:22
Job time : 4.83871 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 77.3387 Seconds
(without alignments)
37.818 Million cell updates/sec

Title: US-10-009-122-18
Perfect score: 34
Sequence: 1 KLVFFAQ 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : Published_applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	7	3	US-09-867-847-27
2	34	100.0	7	3	US-09-867-847-28
3	34	100.0	7	3	US-09-915-092-17
4	34	100.0	7	3	US-09-915-092-18
5	34	100.0	7	3	US-09-747-408-18
6	34	100.0	7	3	US-09-747-408-19
7	34	100.0	7	5	US-10-728-028-17
8	34	100.0	7	5	US-10-728-028-18
9	34	100.0	10	3	US-09-867-847-29
10	34	100.0	10	3	US-09-915-092-19
11	34	100.0	10	5	US-10-728-028-19
12	34	100.0	35	6	US-11-066-697-979
13	34	100.0	35	6	US-11-066-697-1006
14	34	100.0	42	4	US-10-217-584-8
15	34	100.0	42	5	US-10-853-593-1
16	34	100.0	42	5	US-10-969-898-1
17	34	100.0	100	4	US-10-975-025-7
18	34	100.0	108	4	US-10-275-025-15
19	31	91.2	7	5	US-10-825-558-25
20	31	91.2	7	5	US-10-825-558-26
21	31	91.2	8	4	US-10-235-483-1
22	31	91.2	8	4	US-10-281-092-42
23	31	91.2	8	5	US-10-810-881A-125
24	31	91.2	8	5	US-10-817-979-73
25	31	91.2	9	3	US-09-859-815-2
26	31	91.2	9	4	US-10-235-483-64
27	31	91.2	9	4	US-10-619-454-3
28	31	91.2	9	4	US-10-619-454-25
29	31	91.2	9	4	US-10-619-454-57
30	31	91.2	9	4	US-10-619-454-157
31	31	91.2	10	5	US-10-889-999-21
32	31	91.2	10	5	US-10-889-999-22
33	31	91.2	10	5	US-10-889-999-23
34	31	91.2	10	5	US-10-889-999-24
35	31	91.2	10	5	US-10-890-070-21
36	31	91.2	10	5	US-10-890-070-22
37	31	91.2	10	5	US-10-890-070-23
38	31	91.2	10	5	US-10-890-070-24
39	31	91.2	10	5	US-10-890-000-21
40	31	91.2	10	5	US-10-890-000-22
41	31	91.2	10	5	US-10-890-000-23
42	31	91.2	10	5	US-10-890-000-24
43	31	91.2	10	5	US-10-823-463-21
44	31	91.2	10	5	US-10-823-463-22
45	31	91.2	10	5	US-10-823-463-23
46	31	91.2	10	5	US-10-823-463-24
47	31	91.2	10	5	US-10-822-968-21
48	31	91.2	10	5	US-10-822-968-22
49	31	91.2	10	5	US-10-822-968-23
50	31	91.2	10	5	US-10-822-968-24
51	31	91.2	10	5	US-10-777-792-21
52	31	91.2	10	5	US-10-777-792-22
53	31	91.2	10	5	US-10-777-792-23
54	31	91.2	10	5	US-10-777-792-24
55	31	91.2	10	5	US-10-825-958-27
56	31	91.2	10	5	US-10-890-071-21
57	31	91.2	10	5	US-10-890-071-22
58	31	91.2	10	5	US-10-890-071-23
59	31	91.2	10	5	US-10-890-071-24
60	31	91.2	10	5	US-10-890-024-21
61	31	91.2	10	5	US-10-890-024-22
62	31	91.2	10	5	US-10-890-024-23
63	31	91.2	10	5	US-10-890-024-24
64	31	91.2	10	5	US-10-828-926-21
65	31	91.2	10	5	US-10-828-926-22
66	31	91.2	10	5	US-10-828-926-23
67	31	91.2	10	5	US-10-828-926-24
68	31	91.2	10	6	US-11-058-757-21
69	31	91.2	10	6	US-11-058-757-22
70	31	91.2	10	6	US-11-058-757-23
71	31	91.2	11	3	US-09-888-842-9
72	31	91.2	11	3	US-09-888-842-25
73	31	91.2	11	4	US-10-235-483-14
74	31	91.2	11	4	US-10-237-673-20
75	31	91.2	11	5	US-10-464-117-13
76	31	91.2	11	5	US-10-772-230-9
77	31	91.2	11	5	US-10-772-230-25
78	31	91.2	12	5	US-10-810-881A-117
79	31	91.2	13	4	US-10-281-458-1
80	31	91.2	13	5	US-10-625-854-140
81	31	91.2	13	5	US-10-625-854-128
82	31	91.2	14	3	US-09-892-800-5
83	31	91.2	14	3	US-09-892-994-5
84	31	91.2	14	4	US-10-385-065-5
85	31	91.2	14	5	US-10-810-881A-114
86	31	91.2	14	5	US-10-505-313-2
87	31	91.2	14	5	US-10-625-854-141
88	31	91.2	14	6	US-11-063-350-5
89	31	91.2	14	6	US-09-972-475-14
90	31	91.2	15	3	US-09-996-357-9
91	31	91.2	15	3	US-10-235-483-56
92	31	91.2	15	4	US-10-235-483-57
93	31	91.2	15	4	US-10-235-483-58
94	31	91.2	15	4	US-10-235-483-61
95	31	91.2	15	4	US-10-235-483-63
96	31	91.2	15	4	US-10-235-483-65
97	31	91.2	15	4	US-10-463-729-14
98	31	91.2	15	5	US-10-625-854-116
99	31	91.2	15	5	US-10-625-854-129
100	31	91.2	15	5	US-10-625-854-129

101	31	91.2	15	5	US-10-625-854-142	Sequence 142, App	174	31	91.2	28	6	US-11-066-697-992	Sequence 992, App
102	31	91.2	16	5	US-10-625-854-104	Sequence 104, App	175	31	91.2	28	6	US-11-066-697-1003	Sequence 1003, App
103	31	91.2	16	5	US-10-625-854-117	Sequence 117, App	176	31	91.2	30	3	US-09-861-847-1	Sequence 1, Appli
104	31	91.2	16	5	US-10-625-854-130	Sequence 130, App	177	31	91.2	30	4	US-10-301-488A-1	Sequence 1, Appli
105	31	91.2	16	5	US-10-625-854-143	Sequence 143, App	178	31	91.2	30	4	US-10-666-423-1	Sequence 1, Appli
106	31	91.2	17	3	US-09-992-800-3	Sequence 3, Appli	179	31	91.2	30	4	US-10-617-876-9	Sequence 9, Appli
107	31	91.2	17	3	US-09-992-994-3	Sequence 3, Appli	180	31	91.2	30	4	US-10-619-454-24	Sequence 24, Appli
108	31	91.2	17	3	US-09-998-491-8	Sequence 8, Appli	181	31	91.2	30	4	US-10-301-448-1	Sequence 1, Appli
109	31	91.2	17	4	US-10-385-065-3	Sequence 3, Appli	182	31	91.2	30	5	US-10-775-562-5	Sequence 5, Appli
110	31	91.2	17	4	US-10-475-281-8	Sequence 8, Appli	183	31	91.2	32	4	US-10-732-862A-99	Sequence 99, Appli
111	31	91.2	17	4	US-10-810-919-3	Sequence 3, Appli	184	31	91.2	33	3	US-09-930-915A-295	Sequence 295, App
112	31	91.2	17	5	US-10-684-346-24	Sequence 24, Appli	185	31	91.2	33	4	US-10-082-014-84	Sequence 84, Appli
113	31	91.2	17	5	US-10-997-078-46	Sequence 46, Appli	186	31	91.2	33	4	US-10-372-076-85	Sequence 85, Appli
114	31	91.2	17	5	US-10-997-700-19	Sequence 19, Appli	187	31	91.2	33	4	US-10-732-862A-98	Sequence 98, Appli
115	31	91.2	17	6	US-11-063-350-3	Sequence 3, Appli	188	31	91.2	33	4	US-10-806-006-295	Sequence 295, App
116	31	91.2	17	6	US-11-066-697-950	Sequence 950, App	189	31	91.2	33	4	US-10-677-074-85	Sequence 85, Appli
117	31	91.2	17	6	US-11-066-697-983	Sequence 983, App	190	31	91.2	33	4	US-10-805-913-295	Sequence 295, App
118	31	91.2	19	3	US-09-825-242-5	Sequence 5, Appli	191	31	91.2	35	3	US-09-867-847-3	Sequence 3, Appli
119	31	91.2	19	4	US-10-429-216-5	Sequence 5, Appli	192	31	91.2	35	3	US-09-972-475-16	Sequence 16, Appli
120	31	91.2	19	4	US-10-816-022-5	Sequence 5, Appli	193	31	91.2	35	4	US-10-463-729-16	Sequence 16, Appli
121	31	91.2	19	4	US-10-816-529-5	Sequence 5, Appli	194	31	91.2	35	5	US-10-825-958-3	Sequence 3, Appli
122	31	91.2	19	4	US-10-815-353-5	Sequence 5, Appli	195	31	91.2	36	3	US-09-861-847-6	Sequence 6, Appli
123	31	91.2	19	4	US-10-815-391-5	Sequence 5, Appli	196	31	91.2	36	3	US-09-861-847-11	Sequence 11, Appli
124	31	91.2	19	5	US-10-828-548-5	Sequence 5, Appli	197	31	91.2	36	4	US-10-301-488A-6	Sequence 6, Appli
125	31	91.2	19	5	US-10-816-380-5	Sequence 5, Appli	198	31	91.2	36	4	US-10-301-488A-11	Sequence 11, Appli
126	31	91.2	19	5	US-10-889-999-75	Sequence 75, Appli	199	31	91.2	36	4	US-10-666-423-6	Sequence 6, Appli
127	31	91.2	19	5	US-10-890-070-75	Sequence 75, Appli	200	31	91.2	36	4	US-10-666-423-11	Sequence 11, Appli
128	31	91.2	19	5	US-10-890-000-75	Sequence 75, Appli	201	31	91.2	36	4	US-10-301-448-6	Sequence 6, Appli
129	31	91.2	19	5	US-10-788-666-5	Sequence 5, Appli	202	31	91.2	36	4	US-10-301-448-11	Sequence 11, Appli
130	31	91.2	19	5	US-10-923-471-5	Sequence 5, Appli	203	31	91.2	36	4	US-10-732-862A-436	Sequence 436, App
131	31	91.2	19	5	US-10-823-463-75	Sequence 75, Appli	204	31	91.2	38	6	US-11-066-697-975	Sequence 975, App
132	31	91.2	19	5	US-10-923-469-5	Sequence 5, Appli	205	31	91.2	38	6	US-11-066-697-1002	Sequence 1002, Ap
133	31	91.2	19	5	US-10-933-559-5	Sequence 5, Appli	206	31	91.2	39	4	US-10-051-496-5	Sequence 5, Appli
134	31	91.2	19	5	US-10-815-404-5	Sequence 5, Appli	207	31	91.2	39	4	US-10-190-548A-5	Sequence 5, Appli
135	31	91.2	19	5	US-10-934-609-5	Sequence 5, Appli	208	31	91.2	40	3	US-09-861-847-7	Sequence 7, Appli
136	31	91.2	19	5	US-10-923-474-5	Sequence 5, Appli	209	31	91.2	40	3	US-09-861-847-8	Sequence 8, Appli
137	31	91.2	19	5	US-10-884-892-5	Sequence 5, Appli	210	31	91.2	40	3	US-09-867-847-2	Sequence 2, Appli
138	31	91.2	19	5	US-10-822-968-75	Sequence 75, Appli	211	31	91.2	40	3	US-09-988-842-3	Sequence 3, Appli
139	31	91.2	19	5	US-10-777-792-75	Sequence 75, Appli	212	31	91.2	40	3	US-09-851-071-3	Sequence 3, Appli
140	31	91.2	19	5	US-10-890-071-75	Sequence 75, Appli	213	31	91.2	40	3	US-09-962-955C-36	Sequence 36, Appli
141	31	91.2	19	5	US-10-890-024-75	Sequence 75, Appli	214	31	91.2	40	3	US-09-792-079-12	Sequence 12, Appli
142	31	91.2	19	5	US-10-934-819-5	Sequence 5, Appli	215	31	91.2	40	4	US-10-007-779A-1	Sequence 1, Appli
143	31	91.2	19	5	US-10-923-267-5	Sequence 5, Appli	216	31	91.2	40	4	US-10-051-496-4	Sequence 4, Appli
144	31	91.2	19	5	US-10-928-926-75	Sequence 75, Appli	217	31	91.2	40	4	US-10-217-584-3	Sequence 3, Appli
145	31	91.2	19	6	US-11-058-757-75	Sequence 75, Appli	218	31	91.2	40	4	US-10-169-580-1	Sequence 1, Appli
146	31	91.2	20	3	US-11-108-102-5	Sequence 5, Appli	219	31	91.2	40	4	US-10-143-534-3	Sequence 3, Appli
147	31	91.2	20	3	US-09-908-943A-75	Sequence 25, Appli	220	31	91.2	40	4	US-10-190-548A-4	Sequence 4, Appli
148	31	91.2	20	5	US-10-801-487-25	Sequence 25, Appli	221	31	91.2	40	4	US-10-051-663-3	Sequence 3, Appli
149	31	91.2	20	5	US-10-801-938-25	Sequence 25, Appli	222	31	91.2	40	4	US-10-151-614-1	Sequence 1, Appli
150	31	91.2	20	5	US-10-801-509-25	Sequence 25, Appli	223	31	91.2	40	4	US-10-159-279-12	Sequence 12, Appli
151	31	91.2	20	5	US-10-801-486-25	Sequence 25, Appli	224	31	91.2	40	4	US-10-301-488A-7	Sequence 7, Appli
152	31	91.2	20	5	US-10-801-493-25	Sequence 25, Appli	225	31	91.2	40	4	US-10-301-488A-8	Sequence 8, Appli
153	31	91.2	24	5	US-10-728-246-5	Sequence 5, Appli	226	31	91.2	40	4	US-10-455-218-1	Sequence 1, Appli
154	31	91.2	24	5	US-10-728-246-6	Sequence 6, Appli	227	31	91.2	40	4	US-10-366-125-27	Sequence 27, Appli
155	31	91.2	26	3	US-09-792-079-11	Sequence 11, Appli	228	31	91.2	40	4	US-10-337-261-1	Sequence 1, Appli
156	31	91.2	26	4	US-10-159-279-11	Sequence 11, Appli	229	31	91.2	40	4	US-10-666-423-7	Sequence 7, Appli
157	31	91.2	28	3	US-09-867-847-4	Sequence 4, Appli	230	31	91.2	40	4	US-10-666-423-8	Sequence 8, Appli
158	31	91.2	28	3	US-09-865-294-66	Sequence 66, Appli	231	31	91.2	40	4	US-10-301-448-7	Sequence 7, Appli
159	31	91.2	28	3	US-09-792-079-5	Sequence 5, Appli	232	31	91.2	40	4	US-10-301-448-8	Sequence 8, Appli
160	31	91.2	28	4	US-10-159-279-5	Sequence 5, Appli	233	31	91.2	40	4	US-10-683-815-1	Sequence 1, Appli
161	31	91.2	28	4	US-10-363-082-2	Sequence 2, Appli	234	31	91.2	40	4	US-10-683-815-14	Sequence 14, Appli
162	31	91.2	28	4	US-10-433-385-7	Sequence 7, Appli	235	31	91.2	40	4	US-10-683-815-15	Sequence 15, Appli
163	31	91.2	28	4	US-10-390-472-4	Sequence 4, Appli	236	31	91.2	40	4	US-10-683-815-16	Sequence 16, Appli
164	31	91.2	28	4	US-10-741-205-36	Sequence 36, Appli	237	31	91.2	40	4	US-10-683-815-17	Sequence 17, Appli
165	31	91.2	28	4	US-10-416-262B-7	Sequence 7, Appli	238	31	91.2	40	4	US-10-683-815-18	Sequence 18, Appli
166	31	91.2	28	4	US-10-478-308-4	Sequence 4, Appli	239	31	91.2	40	4	US-10-810-919-1	Sequence 1, Appli
167	31	91.2	28	4	US-10-478-307-4	Sequence 4, Appli	240	31	91.2	40	5	US-10-864-107-1	Sequence 1, Appli
168	31	91.2	28	5	US-10-861-614-66	Sequence 66, Appli	241	31	91.2	40	5	US-10-485-310-18	Sequence 18, Appli
169	31	91.2	28	5	US-10-825-958-4	Sequence 4, Appli	242	31	91.2	40	5	US-10-481-387-1	Sequence 1, Appli
170	31	91.2	28	6	US-11-091-309-3	Sequence 3, Appli	243	31	91.2	40	5	US-10-481-954-5	Sequence 5, Appli
171	31	91.2	28	6	US-11-066-697-959	Sequence 959, App	244	31	91.2	40	5	US-10-698-259A-1	Sequence 1, Appli
172	31	91.2	28	6	US-11-066-697-965	Sequence 965, App	245	31	91.2	40	5	US-10-884-729-1	Sequence 1, Appli
173	31	91.2	28	6	US-11-066-697-976	Sequence 976, App	246	31	91.2	40	5	US-10-728-246-4	Sequence 4, Appli

247 31 91.2 40 5 US-10-772-230-3 Sequence 3, Appli
248 31 91.2 40 5 US-10-333-206-36 Sequence 36, Appl
249 31 91.2 40 5 US-10-825-958-2 Sequence 2, Appli
250 31 91.2 40 5 US-10-775-562-2 Sequence 2, Appli
251 31 91.2 40 5 US-10-296-168-1 Sequence 1, Appli
252 31 91.2 40 6 US-11-004-053-36 Sequence 36, Appl
253 31 91.2 40 6 US-11-007-643-36 Sequence 36, Appl
254 31 91.2 40 6 US-11-007-644-36 Sequence 36, Appl
255 31 91.2 40 6 US-11-007-669-36 Sequence 36, Appl
256 31 91.2 40 6 US-11-066-697-956 Sequence 956, App
257 31 91.2 40 6 US-11-066-697-962 Sequence 962, App
258 31 91.2 40 6 US-11-066-697-968 Sequence 968, App
259 31 91.2 40 6 US-11-066-697-978 Sequence 978, App
260 31 91.2 40 6 US-11-066-697-989 Sequence 989, App
261 31 91.2 40 6 US-11-066-697-995 Sequence 995, App
262 31 91.2 40 6 US-11-066-697-1005 Sequence 1005, App
263 31 91.2 41 4 US-10-051-496-3 Sequence 3, Appli
264 31 91.2 41 4 US-10-190-548A-3 Sequence 13, Appl
265 31 91.2 41 4 US-10-683-815-13 Sequence 2, Appli
266 31 91.2 42 2 US-08-922-330-2 Sequence 2, Appli
267 31 91.2 42 2 US-08-923-055-2 Sequence 1, Appli
268 31 91.2 42 3 US-09-867-847-1 Sequence 26, Appl
269 31 91.2 42 3 US-09-956-625-26 Sequence 1, Appli
270 31 91.2 42 3 US-09-731-460-1 Sequence 1, Appli
271 31 91.2 42 3 US-09-962-955C-37 Sequence 37, Appl
272 31 91.2 42 3 US-09-848-616-174 Sequence 174, App
273 31 91.2 42 3 US-09-865-294-65 Sequence 65, Appl
274 31 91.2 42 3 US-09-792-079-13 Sequence 13, Appl
275 31 91.2 42 3 US-09-825-242-1 Sequence 1, Appli
276 31 91.2 42 3 US-09-930-915A-293 Sequence 2, Appli
277 31 91.2 42 4 US-10-051-496-2 Sequence 7, Appli
278 31 91.2 42 4 US-10-082-804-7 Sequence 2, Appli
279 31 91.2 42 4 US-10-217-584-2 Sequence 11, Appl
280 31 91.2 42 4 US-10-217-584-11 Sequence 2, Appli
281 31 91.2 42 4 US-10-169-580-2 Sequence 1, Appli
282 31 91.2 42 4 US-10-278-181-1 Sequence 2, Appli
283 31 91.2 42 4 US-10-143-534-2 Sequence 1, Appli
284 31 91.2 42 4 US-10-130-548A-1 Sequence 2, Appli
285 31 91.2 42 4 US-10-051-663-2 Sequence 2, Appli
286 31 91.2 42 4 US-10-159-279-13 Sequence 13, Appl
287 31 91.2 42 4 US-10-318-302-4 Sequence 4, Appli
288 31 91.2 42 4 US-10-050-902-220 Sequence 220, App
289 31 91.2 42 4 US-10-050-898-220 Sequence 82, Appl
290 31 91.2 42 4 US-10-082-014-81 Sequence 81, Appl
291 31 91.2 42 4 US-10-372-076-82 Sequence 2, Appli
292 31 91.2 42 4 US-10-455-218-2 Sequence 15, Appl
293 31 91.2 42 4 US-10-231-298B-15 Sequence 15, Appl
294 31 91.2 42 4 US-10-231-470C-15 Sequence 15, Appl
295 31 91.2 42 4 US-10-231-663C-15 Sequence 15, Appl
296 31 91.2 42 4 US-10-366-125-28 Sequence 28, Appl
297 31 91.2 42 4 US-10-411-544-2 Sequence 2, Appli
298 31 91.2 42 4 US-10-231-213D-15 Sequence 15, Appl
299 31 91.2 42 4 US-10-231-114C-15 Sequence 15, Appl
300 31 91.2 42 4 US-10-337-261-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-867-847-27
; Sequence 27, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-27

Query Match 100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 1 KLVFFAQ 7

RESULT 2

US-09-867-847-28
; Sequence 28, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (7)
; OTHER INFORMATION: AMIDATION
US-09-867-847-28

Query Match 100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 1 KLVFFAQ 7

RESULT 3

US-09-915-092-17
; Sequence 17, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert

```
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-17

Query Match      100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      1 KLVFFAQ 7
      |||||

RESULT 4
US-09-915-092-18
; Sequence 18, Application US/09915092
; Publication No. US2002011517A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-18

Query Match      100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      1 KLVFFAQ 7
      |||||

RESULT 5
US-09-747-408-18
; Sequence 18, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-747-408-18

Query Match      100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      1 KLVFFAQ 7
      |||||

RESULT 6
US-09-747-408-19
; Sequence 19, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-19

Query Match      100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      1 KLVFFAQ 7
      |||||

RESULT 7
US-10-728-028-17
; Sequence 17, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-10-728-028-17
```

```
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-17

Query Match      100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
Db 1 KLVFFPAQ 7

RESULT 8
US-10-728-028-18
; Sequence 18, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USSES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; PRIOR FILING DATE: 2003-12-03
; PRIOR FILING DATE: 2003-01-29
; PRIOR FILING DATE: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-18

Query Match      100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
Db 1 KLVFFPAQ 7

RESULT 9
US-09-867-847-29
; Sequence 29, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 29

; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-19

Query Match      100.0%; Score 34; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
Db 4 KLVFFPAQ 10

RESULT 10
US-09-915-092-19
; Sequence 19, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneaault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USSES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Synthetic Construct
US-09-915-092-19

Query Match      100.0%; Score 34; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
Db 4 KLVFFPAQ 10

RESULT 11
US-10-728-028-19
; Sequence 19, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USSES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
```

```

; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-19
Query Match      100.0%; Score 34; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 4 KLVFFAQ 10

RESULT 12
US-11-066-697-979
; Sequence 979, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 979
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-979
Query Match      100.0%; Score 34; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 11 KLVFFAQ 17

RESULT 13
US-11-066-697-1006
; Sequence 1006, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697

```

```

; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1006
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1006
Query Match      100.0%; Score 34; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 11 KLVFFAQ 17

RESULT 14
US-10-217-584-8
; Sequence 8, Application US/10217584
; Publication No. US20030077261A1
; GENERAL INFORMATION:
; APPLICANT: Paris, Daniel
; APPLICANT: Mullan, Michael
; TITLE OF INVENTION: Modulation of Angiogenesis by A-Beta Peptides
; FILE REFERENCE: USP-T161XCI
; CURRENT APPLICATION NUMBER: US/10/217,584
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 60/311,656
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 22Q-A-beta 1-42 (Dutch) mutant
US-10-217-584-8
Query Match      100.0%; Score 34; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 16 KLVFFAQ 22

RESULT 15
US-10-853-593-1
; Sequence 1, Application US/10853593
; Publication No. US20040250302A1
; GENERAL INFORMATION:
; APPLICANT: Envivo Pharmaceuticals
; APPLICANT: Lowe, David
; APPLICANT: Cummings, Christopher
; APPLICANT: Koenig, Gerhard
; TITLE OF INVENTION: Transgenic Flies Expressing AB42Dutch
; FILE REFERENCE: 9000-2202
; CURRENT APPLICATION NUMBER: US/10/853,593
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: 60/512,972

```

; PRIOR FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-853-593-1

Query Match 100.0%; Score 34; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 16 KLVFFAQ 22

RESULT 16
US-10-969-898-1
; Sequence 1, Application US/10969898
; Publication No. US2005013242A1
; GENERAL INFORMATION:
; APPLICANT: Envivo Pharmaceuticals
; APPLICANT: Lowe, David
; APPLICANT: Cummings, Christopher
; APPLICANT: Koenig, Gerhard
; TITLE OF INVENTION: Transgenic Flies Expressing AB42Dutch
; FILE REFERENCE: 9000-2202
; CURRENT APPLICATION NUMBER: US/10/969,898
; CURRENT FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: 60/512,972
; PRIOR FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-969-898-1

Query Match 100.0%; Score 34; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 16 KLVFFAQ 22

RESULT 17
US-10-275-025-7
; Sequence 7, Application US/10275025
; Publication No. US20030215896A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yueming
; APPLICANT: Xu, Min
; APPLICANT: Huang, Qian
; APPLICANT: Gardell, Stephen J.
; TITLE OF INVENTION: GAMMA SECRETASE SUBSTRATES AND IN VITRO
; TITLE OF INVENTION: ASSAYS
; FILE REFERENCE: 20507P
; CURRENT APPLICATION NUMBER: US/10/275,025
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US01/13332
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/201,053
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 100
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-CTF domain
US-10-275-025-7

Query Match 100.0%; Score 34; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 17 KLVFFAQ 23

RESULT 18
US-10-275-025-15
; Sequence 15, Application US/10275025
; Publication No. US20030215896A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yueming
; APPLICANT: Xu, Min
; APPLICANT: Huang, Qian
; APPLICANT: Gardell, Stephen J.
; TITLE OF INVENTION: GAMMA SECRETASE SUBSTRATES AND IN VITRO
; TITLE OF INVENTION: ASSAYS
; FILE REFERENCE: 20507P
; CURRENT APPLICATION NUMBER: US/10/275,025
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US01/13332
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/201,053
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Gamma-secretase substrate
US-10-275-025-15

Query Match 100.0%; Score 34; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 17 KLVFFAQ 23

RESULT 19
US-10-825-958-25
; Sequence 25, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 7

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-25

Query Match          91.2%; Score 31; DB 5; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 1 KLVFFAE 7
|||||:

RESULT 20
US-10-825-958-26
; Sequence 26, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Hebert, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)_
; OTHER INFORMATION: AMIDATION
US-10-825-958-26

Query Match          91.2%; Score 31; DB 5; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 1 KLVFFAE 7
|||||:

RESULT 21
US-10-235-483-1
; Sequence 1, Application US/10235483
; Publication No. US20030087407A1
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Bias
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIK
; DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
```

```
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/235,483
; FILING DATE: 06-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-235-483-1

Query Match          91.2%; Score 31; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 1 KLVFFAE 7
|||||:

RESULT 22
US-10-281-092-42
; Sequence 42, Application US/10281092
; Publication No. US20040121947A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Arun K.
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Bilcer, Geoffrey
; APPLICANT: Chang, Waupin
; APPLICANT: Hong, Lin
; APPLICANT: Koelsch, Gerald E.
; APPLICANT: Loy, Jeffrey A.
; APPLICANT: Turner, Robert T., III
; APPLICANT: Devasumadrum, Thippeswamy
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT BETA-SECRETASE
; FILE REFERENCE: 2932.1001-004
; CURRENT APPLICATION NUMBER: US/10/281,092
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 10/032,818
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: PCT US01/50826
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/258,705
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/275,756
```



```
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/335,952
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/333,545
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 60/348,464
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/348,615
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/390,804
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 60/397,557
; PRIOR FILING DATE: 2002-07-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-10-281-092-42

Query Match          91.2%; Score 31; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 1 KLVFFAE 7

RESULT 23
US-10-810-881A-125
; Sequence 125, Application US/10810881A
; Publication No. US20050129695A1
; GENERAL INFORMATION:
; APPLICANT: Mercken, Marc; Benson, Jacqueline M.
; TITLE OF INVENTION: ANTI-AMYLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5021 NP
; CURRENT APPLICATION NUMBER: US/10/810,881A
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/458,474
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,469
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,509
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,510
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 125
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PEPTIDE
US-10-810-881A-125

Query Match          91.2%; Score 31; DB 5; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 1 KLVFFAE 7

RESULT 24
US-10-817-979-73
; Sequence 73, Application US/10817979
```

```
; Publication No. US20050196398A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, et al
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/40065
; CURRENT APPLICATION NUMBER: US/10/817,979
; CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 09/668,314
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/169,232
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-817-979-73

Query Match          91.2%; Score 31; DB 5; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 1 KLVFFAE 7

RESULT 25
US-09-899-815-2
; Sequence 2, Application US/09899815
; Patent No. US20020162129A1
; GENERAL INFORMATION:
; APPLICANT: LANNFELT, Lars
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: LANNFELT-1A
; CURRENT APPLICATION NUMBER: US/09/899,815
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/217,098
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: EP 00202387.7
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (16-24 of SEQ ID NO:1)
US-09-899-815-2

Query Match          91.2%; Score 31; DB 3; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 1 KLVFFAE 7
```

```
RESULT 26
US-10-235-483-64
; Sequence 64, Application US/10235483
; Publication No. US20030087407A1
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; BAUMANN, Marc
; BAUMANN, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/235,483
; FILING DATE: 06-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-10-235-483-64

Query Match 91.2%; Score 31; DB 4; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 2 KLVFFAE 8

RESULT 27
US-10-454-3
; Sequence 3, Application US/10619454
; Publication No. US20040091945A1
; GENERAL INFORMATION:
; APPLICANT: Mindset
; APPLICANT: Fitzer Attas, Cheryl
; APPLICANT: Chain, Daniel
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES A
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES A

RESULT 28
US-10-619-454-25
; Sequence 25, Application US/10619454
; Publication No. US20040091945A1
; GENERAL INFORMATION:
; APPLICANT: Mindset
; APPLICANT: Fitzer Attas, Cheryl
; APPLICANT: Chain, Daniel
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES A
; TITLE OF INVENTION: AD IN WHICH T-CELL EPITOPES ARE REDUCED
; FILE REFERENCE: P-5202-US
; CURRENT APPLICATION NUMBER: US/10/619,454
; CURRENT FILING DATE: 2003-07-16
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: algorithm generated
US-10-619-454-25

Query Match 91.2%; Score 31; DB 4; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 1 KLVFFAE 7

RESULT 29
US-10-619-454-57
; Sequence 57, Application US/10619454
; Publication No. US20040091945A1
; GENERAL INFORMATION:
; APPLICANT: Mindset
; APPLICANT: Fitzer Attas, Cheryl
; APPLICANT: Chain, Daniel
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES A
; TITLE OF INVENTION: AD IN WHICH T-CELL EPITOPES ARE REDUCED
; FILE REFERENCE: P-5202-US
; CURRENT APPLICATION NUMBER: US/10/619,454
; CURRENT FILING DATE: 2003-07-16
; PRIOR FILING DATE: 2002-07-17
```

```
; FILE REFERENCE: P-5202-US
; CURRENT APPLICATION NUMBER: US/10/619,454
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: US 60/396,245
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: algorithm generated
US-10-619-454-3
```

```
Query Match 91.2%; Score 31; DB 4; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
DB 1 KLVFFAE 7
```

```
RESULT 28
US-10-619-454-25
; Sequence 25, Application US/10619454
; Publication No. US20040091945A1
; GENERAL INFORMATION:
; APPLICANT: Mindset
; APPLICANT: Fitzer Attas, Cheryl
; APPLICANT: Chain, Daniel
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES A
; TITLE OF INVENTION: AD IN WHICH T-CELL EPITOPES ARE REDUCED
; FILE REFERENCE: P-5202-US
; CURRENT APPLICATION NUMBER: US/10/619,454
; CURRENT FILING DATE: 2003-07-16
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: algorithm generated
US-10-619-454-25
```

```
Query Match 91.2%; Score 31; DB 4; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
DB 1 KLVFFAE 7
```

```
RESULT 29
US-10-619-454-57
; Sequence 57, Application US/10619454
; Publication No. US20040091945A1
; GENERAL INFORMATION:
; APPLICANT: Mindset
; APPLICANT: Fitzer Attas, Cheryl
; APPLICANT: Chain, Daniel
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES A
; TITLE OF INVENTION: AD IN WHICH T-CELL EPITOPES ARE REDUCED
; FILE REFERENCE: P-5202-US
; CURRENT APPLICATION NUMBER: US/10/619,454
; CURRENT FILING DATE: 2003-07-16
; PRIOR FILING DATE: 2002-07-17
```

```
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: algorithm generated
US-10-619-454-57

Query Match          91.2%; Score 31; DB 4; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
Db 1 KLVFFPAE 7

RESULT 30
US-10-619-454-157
; Sequence 157, Application US/10619454
; Publication No. US20040091945A1
; GENERAL INFORMATION:
; APPLICANT: Mindset
; APPLICANT: Fitzer Attas, Cheryl
; APPLICANT: Chain, Daniel
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES
; TITLE OF INVENTION: AD IN WHICH T-CELL EPITOPES ARE REDUCED
; FILE REFERENCE: P-5202-US
; CURRENT APPLICATION NUMBER: US/10/619,454
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: US 60/396,245
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 157
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: algorithm generated
US-10-619-454-157

Query Match          91.2%; Score 31; DB 4; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
Db 1 KLVFFPAE 7

RESULT 31
US-10-889-999-21
; Sequence 21, Application US/10889999
; Publication No. US20040247590A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/889,999
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10

Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
Db 4 KLVFFPAE 10

RESULT 32
US-10-889-999-22
; Sequence 22, Application US/10889999
; Publication No. US20040247590A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/889,999
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-889-999-22

Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
Db 3 KLVFFPAE 9

RESULT 33
US-10-889-999-23
; Sequence 23, Application US/10889999
; Publication No. US20040247590A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/889,999
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
```

```
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-889-999-23
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
    |||||:
DB 2 KLVFFAE 8
```

```
RESULT 34
US-10-889-999-24
; Sequence 24, Application US/10889999
; Publication No. US20040247590A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/889,999
; PRIOR FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-889-999-24
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
    |||||:
DB 1 KLVFFAE 7
```

```
RESULT 35
US-10-890-070-21
; Sequence 21, Application US/10890070
; Publication No. US20040247591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,070
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-070-21
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
    |||||:
DB 4 KLVFFAE 10
```

```
RESULT 36
US-10-890-070-22
; Sequence 22, Application US/10890070
; Publication No. US20040247591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,070
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-070-22
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
    |||||:
DB 3 KLVFFAE 9
```

```
RESULT 37
US-10-890-070-23
; Sequence 23, Application US/10890070
; Publication No. US20040247591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,070
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
```

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 23

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)

US-10-890-070-23

Query Match

Best Local Similarity 91.2%; Score 31; DB 5; Length 10;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7

Db 2 KLVFFAE 8

RESULT 38

US-10-890-070-24

; Sequence 24, Application US/10890070

; Publication No. US20040247591A1

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/10/890,070

; CURRENT FILING DATE: 2004-07-12

; PRIOR APPLICATION NUMBER: US/09/580,018

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 24

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)

US-10-890-070-24

Query Match

Best Local Similarity 91.2%; Score 31; DB 5; Length 10;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7

Db 1 KLVFFAE 7

RESULT 39

US-10-890-000-21

; Sequence 21, Application US/10890000

; Publication No. US20040265301A1

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/10/890,000

; CURRENT FILING DATE: 2004-07-12

; PRIOR APPLICATION NUMBER: US/09/580,018

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 21

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)

US-10-890-000-21

Query Match

Best Local Similarity 91.2%; Score 31; DB 5; Length 10;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7

Db 4 KLVFFAE 10

RESULT 40

US-10-890-000-22

; Sequence 22, Application US/10890000

; Publication No. US20040265301A1

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/10/890,000

; CURRENT FILING DATE: 2004-07-12

; PRIOR APPLICATION NUMBER: US/09/580,018

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

; OTHER INFORMATION: peptide)

US-10-890-000-22

Query Match

Best Local Similarity 91.2%; Score 31; DB 5; Length 10;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7

Db 3 KLVFFAE 9

RESULT 41

US-10-890-000-23

; Sequence 23, Application US/10890000

; Publication No. US20040265301A1

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/10/890,000

; CURRENT FILING DATE: 2004-07-12

; PRIOR APPLICATION NUMBER: US/09/580,018

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-000-23

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
Db 2 KLVFFPAE 8
|||||:

RESULT 42
US-10-890-000-24
; Sequence 24, Application US/10890000
; Publication No. US20040265301A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,000
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-000-24

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
Db 1 KLVFFPAE 7
|||||:

RESULT 43
US-10-823-463-21
; Sequence 21, Application US/10823463
; Publication No. US20050019328A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/823,463
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/580,015

; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-823-463-21

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
Db 4 KLVFFPAE 10
|||||:

RESULT 44
US-10-823-463-22
; Sequence 22, Application US/10823463
; Publication No. US20050019328A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/823,463
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-823-463-22

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 3 KLVFFAE 9

RESULT 45

US-10-823-463-23
; Sequence 23, Application US/10823463
; Publication No. US20050019328A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/823,463
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-823-463-23

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 2 KLVFFAE 8

RESULT 46

US-10-823-463-24
; Sequence 24, Application US/10823463
; Publication No. US20050019328A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/823,463
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970

; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-823-463-24

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 1 KLVFFAE 7

RESULT 47

US-10-822-968-21
; Sequence 21, Application US/10822968
; Publication No. US20050059591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/822,968
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-822-968-21

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 4 KLVFFAE 10

RESULT 48

US-10-822-968-22
; Sequence 22, Application US/10822968

```
; Publication No. US20050059591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/822,968
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-822-968-22

Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 3 KLVFFAE 9

RESULT 49
US-10-822-968-23
; Sequence 23, Application US/10822968
; Publication No. US20050059591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/822,968
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-822-968-24

Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 3 KLVFFAE 9

RESULT 49
US-10-822-968-23
; Sequence 23, Application US/10822968
; Publication No. US20050059591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/822,968
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-822-968-24
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-822-968-23

Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 2 KLVFFAE 8

RESULT 50
US-10-822-968-24
; Sequence 24, Application US/10822968
; Publication No. US20050059591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/822,968
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-822-968-24

Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 1 KLVFFAE 7

RESULT 51
US-10-777-792-21
; Sequence 21, Application US/10777792
; Publication No. US20050059802A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/777,792
```


; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-777-792-21

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
|||
Db 4 KLVFFAE 10

RESULT 52
US-10-777-792-22
; Sequence 22, Application US/10777792
; Publication No. US20050059802A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/777,792
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-777-792-22

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
|||
Db 3 KLVFFAE 9

RESULT 53
US-10-777-792-23
; Sequence 23, Application US/10777792
; Publication No. US20050059802A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/10/777,792
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-777-792-23

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
|||
Db 2 KLVFFAE 8

RESULT 54
US-10-777-792-24
; Sequence 24, Application US/10777792
; Publication No. US20050059802A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/777,792
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-777-792-24

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
|||
Db 1 KLVFFAE 7

RESULT 55
US-10-825-958-27
; Sequence 27, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine

```
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-27
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
   |||||:
Db 4 KLVFFAE 10
```

```
RESULT 56
US-10-890-071-21
; Sequence 21, Application US/108900071
; Publication No. US20050123544A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,071
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-071-21
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
   |||||:
Db 4 KLVFFAE 10
```

```
RESULT 57
US-10-890-071-22
; Sequence 22, Application US/108900071
; Publication No. US20050123544A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
```

```
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,071
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-071-22
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
   |||||:
Db 3 KLVFFAE 9
```

```
RESULT 58
US-10-890-071-23
; Sequence 23, Application US/108900071
; Publication No. US20050123544A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,071
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-071-23
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFAQ 7
   |||||:
Db 2 KLVFFAE 8
```

```
RESULT 59
US-10-890-071-24
; Sequence 24, Application US/108900071
; Publication No. US20050123544A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
```

; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,071
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-071-24

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||||:
Db 1 KLVFFPAE 7

RESULT 60
US-10-890-024-21
; Sequence 21, Application US/10890024
; Publication No. US20050158304A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,024
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-024-21

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||||:
Db 4 KLVFFPAE 10

RESULT 61
US-10-890-024-22
; Sequence 22, Application US/10890024
; Publication No. US20050158304A1
; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,024
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-024-22

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||||:
Db 3 KLVFFPAE 9

RESULT 62
US-10-890-024-23
; Sequence 23, Application US/10890024
; Publication No. US20050158304A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,024
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-024-23

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||||:
Db 2 KLVFFPAE 8

RESULT 63
US-10-890-024-24
; Sequence 24, Application US/10890024
; Publication No. US20050158304A1

```
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,024
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-024-24
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFAQ 7
Db      1 KLVFFAE 7
```

```
RESULT 64
US-10-928-926-21
; Sequence 21, Application US/10928926
; Publication No. US20050196399A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/928,926
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-928-926-21
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
```

```
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFAQ 7
Db      4 KLVFFAE 10
```

```
RESULT 65
US-10-928-926-22
; Sequence 22, Application US/10928926
; Publication No. US20050196399A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/928,926
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-928-926-22
```

```
Query Match          91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFAQ 7
Db      3 KLVFFAE 9
```

```
RESULT 66
US-10-928-926-23
; Sequence 23, Application US/10928926
; Publication No. US20050196399A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/928,926
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
```

; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-928-926-23

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||||:
Db 2 KLVFFFAE 8

RESULT 67
US-10-928-926-24
; Sequence 24, Application US/10928926
; Publication No. US20050196399A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/928,926
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-928-926-24

Query Match 91.2%; Score 31; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||||:
Db 1 KLVFFFAE 7

RESULT 68
US-11-058-757-21
; Sequence 21, Application US/11058757
; Publication No. US20050142132A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/11/058,757
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-11-058-757-21

Query Match 91.2%; Score 31; DB 6; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||||:
Db 4 KLVFFFAE 10

RESULT 69
US-11-058-757-22
; Sequence 22, Application US/11058757
; Publication No. US20050142132A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/11/058,757
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-11-058-757-22

Query Match 91.2%; Score 31; DB 6; Length 10;
Best Local Similarity 85.7%; Pred. No. 4.8;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7

Db 3 KLVFFAE 9

RESULT 70

US-11-058-757-23
; Sequence 23, Application US/11058757
; Publication No. US20050142132A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/11/058,757
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-11-058-757-23

Query Match

Best Local Similarity 91.2%; Score 31; DB 6; Length 10;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7

Db 2 KLVFFAE 8

RESULT 71

US-11-058-757-24
; Sequence 24, Application US/11058757
; Publication No. US20050142132A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/11/058,757
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-11-058-757-24

Query Match

Best Local Similarity 91.2%; Score 31; DB 6; Length 10;

Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7

Db 1 KLVFFAE 7

RESULT 72

US-09-988-842-9
; Sequence 9, Application US/09988842
; Patent No. US20020143105A1
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

Query Match

Best Local Similarity 91.2%; Score 31; DB 3; Length 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7

Db 2 KLVFFAE 8

RESULT 73

US-09-988-842-25
; Sequence 25, Application US/09988842
; Patent No. US20020143105A1
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

Query Match

Best Local Similarity 91.2%; Score 31; DB 3; Length 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7

Db 1 KLVFFAE 7

Db 2 KLVFFAE 8

RESULT 74

US-10-235-483-14

; Sequence 14, Application US/10235483

; Publication No. US20030087407A1

; GENERAL INFORMATION:

; APPLICANT: SOTO-JARA, Claudio

; BAUMANN, Marc

; FRANGIONE, Blas

; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL

; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE

; DEPOSITS

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 400

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/235,483

; FILING DATE: 06-Sep-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/766,596

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/630,645

; FILING DATE: 10-APR-1996

; APPLICATION NUMBER: US 08/478,326

; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: YUN, Allen C.

; REGISTRATION NUMBER: 37,971

; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-10-235-483-14

Query Match

Best Local Similarity 91.2%; Score 31; DB 4; Length 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7

Db 2 KLVFFAE 8

RESULT 75

US-10-237-673-20

; Sequence 20, Application US/10237673

; Publication No. US20040121398A1

; GENERAL INFORMATION:

; APPLICANT: FUJITSU LIMITED

; APPLICANT: DAIICHI PHARMACEUTICAL CO., LTD.

; TITLE OF INVENTION: Method for predicting protein-protein interactions

; FILE REFERENCE: GP01-1001PCT

; CURRENT APPLICATION NUMBER: US/10/237,673

; CURRENT FILING DATE: 2002-09-10

; PRIOR APPLICATION NUMBER: JP P2000-72485

; PRIOR FILING DATE: 2000-03-10

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-237-673-20

Query Match

Best Local Similarity 91.2%; Score 31; DB 4; Length 11;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7

Db 1 KLVFFAE 7

Search completed: December 29, 2005, 18:49:49

Job time : 78.3387 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 23.371 Seconds
(without alignments)
24.763 Million cell updates/sec

Title: US-10-009-122-18
Perfect score: 34
Sequence: 1 KLVFQA 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- 1: /cgm2_6/ptodata/1/iaa/5-COMB.pep.*
- 2: /cgm2_6/ptodata/1/iaa/6-COMB.pep.*
- 3: /cgm2_6/ptodata/1/iaa/H-COMB.pep.*
- 4: /cgm2_6/ptodata/1/iaa/PCrUS-COMB.pep.*
- 5: /cgm2_6/ptodata/1/iaa/RE-COMB.pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	7	2	US-09-747-408-18
2	34	100.0	7	2	US-09-747-408-19
3	34	100.0	28	2	US-09-388-890-12
4	34	100.0	28	2	US-09-660-954-12
5	34	100.0	35	2	US-09-623-548A-979
6	34	100.0	35	2	US-09-623-548A-1006
7	34	100.0	35	2	US-09-657-276-979
8	34	100.0	35	2	US-09-657-276-1006
9	34	100.0	40	1	US-08-304-585-8
10	34	100.0	43	2	US-09-573-789-1
11	34	100.0	43	2	US-09-859-261-1
12	34	100.0	63	1	US-08-463-859A-3
13	34	100.0	63	1	US-08-123-659A-3
14	34	100.0	63	1	US-08-464-247A-3
15	34	100.0	63	1	US-08-464-248A-3
16	34	100.0	99	2	US-08-339-708A-6
17	31	91.2	7	1	US-08-127-904-14
18	31	91.2	7	2	US-09-264-709A-13
19	31	91.2	7	4	PCT-US94-10475-14
20	31	91.2	8	1	US-08-630-645-1
21	31	91.2	8	2	US-08-766-596A-1
22	31	91.2	8	2	US-09-668-314C-73
23	31	91.2	8	4	PCT-US96-10220-1
24	31	91.2	9	2	US-08-766-596A-64
25	31	91.2	10	2	US-08-970-833-3
26	31	91.2	10	2	US-09-724-961-21
27	31	91.2	10	2	US-09-724-961-22

28	31	91.2	10	2	US-09-724-961-23	Sequence 23, Appl
29	31	91.2	10	2	US-09-724-961-24	Sequence 24, Appl
30	31	91.2	10	2	US-09-580-018-21	Sequence 21, Appl
31	31	91.2	10	2	US-09-580-018-22	Sequence 22, Appl
32	31	91.2	10	2	US-09-580-018-23	Sequence 23, Appl
33	31	91.2	10	2	US-09-580-018-24	Sequence 24, Appl
34	31	91.2	10	2	US-09-724-551-21	Sequence 21, Appl
35	31	91.2	10	2	US-09-724-551-22	Sequence 22, Appl
36	31	91.2	10	2	US-09-724-551-23	Sequence 23, Appl
37	31	91.2	10	2	US-09-724-551-24	Sequence 24, Appl
38	31	91.2	10	2	US-09-724-940-21	Sequence 21, Appl
39	31	91.2	10	2	US-09-724-940-22	Sequence 22, Appl
40	31	91.2	10	2	US-09-724-940-23	Sequence 23, Appl
41	31	91.2	10	2	US-09-724-940-24	Sequence 24, Appl
42	31	91.2	11	1	US-08-630-645-14	Sequence 14, Appl
43	31	91.2	11	2	US-08-766-596A-14	Sequence 14, Appl
44	31	91.2	11	2	US-09-988-842-9	Sequence 9, Appl
45	31	91.2	11	2	US-09-988-842-25	Sequence 25, Appl
46	31	91.2	11	4	PCT-US96-10220-14	Sequence 14, Appl
47	31	91.2	14	2	US-09-594-366-5	Sequence 5, Appl
48	31	91.2	14	2	US-09-992-800-5	Sequence 5, Appl
49	31	91.2	15	1	US-08-612-785B-14	Sequence 14, Appl
50	31	91.2	15	1	US-08-612-785B-37	Sequence 37, Appl
51	31	91.2	15	2	US-08-617-267C-14	Sequence 14, Appl
52	31	91.2	15	2	US-08-766-596A-56	Sequence 56, Appl
53	31	91.2	15	2	US-08-766-596A-57	Sequence 57, Appl
54	31	91.2	15	2	US-08-766-596A-58	Sequence 58, Appl
55	31	91.2	15	2	US-08-766-596A-61	Sequence 61, Appl
56	31	91.2	15	2	US-08-766-596A-63	Sequence 63, Appl
57	31	91.2	15	2	US-08-766-596A-65	Sequence 65, Appl
58	31	91.2	17	2	US-09-264-709A-2	Sequence 2, Appl
59	31	91.2	17	2	US-09-594-366-3	Sequence 3, Appl
60	31	91.2	17	2	US-09-623-548A-950	Sequence 950, App
61	31	91.2	17	2	US-09-623-548A-983	Sequence 983, App
62	31	91.2	17	2	US-09-932-800-3	Sequence 3, Appl
63	31	91.2	17	2	US-09-657-276-950	Sequence 950, App
64	31	91.2	17	2	US-09-657-276-983	Sequence 983, App
65	31	91.2	19	2	US-08-970-833-11	Sequence 11, Appl
66	31	91.2	19	2	US-09-723-384-5	Sequence 5, Appl
67	31	91.2	19	2	US-09-724-961-75	Sequence 75, Appl
68	31	91.2	19	2	US-09-724-552-5	Sequence 5, Appl
69	31	91.2	19	2	US-09-580-018-75	Sequence 75, Appl
70	31	91.2	19	2	US-09-723-927-5	Sequence 5, Appl
71	31	91.2	19	2	US-09-724-489-5	Sequence 5, Appl
72	31	91.2	19	2	US-09-724-477-5	Sequence 5, Appl
73	31	91.2	19	2	US-09-723-762-5	Sequence 5, Appl
74	31	91.2	19	2	US-09-201-430-5	Sequence 5, Appl
75	31	91.2	19	2	US-09-724-551-75	Sequence 75, Appl
76	31	91.2	19	2	US-10-815-353-5	Sequence 5, Appl
77	31	91.2	19	2	US-10-816-529-5	Sequence 5, Appl
78	31	91.2	19	2	US-10-815-391-5	Sequence 5, Appl
79	31	91.2	19	2	US-10-816-022-5	Sequence 5, Appl
80	31	91.2	19	2	US-09-724-940-75	Sequence 75, Appl
81	31	91.2	19	2	US-10-834-609-5	Sequence 5, Appl
82	31	91.2	19	2	US-10-884-892-5	Sequence 5, Appl
83	31	91.2	20	2	US-08-970-833-10	Sequence 10, Appl
84	31	91.2	20	2	US-09-724-953-33	Sequence 33, Appl
85	31	91.2	20	2	US-09-724-567-33	Sequence 33, Appl
86	31	91.2	20	2	US-09-979-952-33	Sequence 33, Appl
87	31	91.2	20	2	US-09-565-817-33	Sequence 33, Appl
88	31	91.2	26	1	US-08-304-585-7	Sequence 7, Appl
89	31	91.2	28	1	US-08-346-849-4	Sequence 4, Appl
90	31	91.2	28	1	US-08-302-808-7	Sequence 7, Appl
91	31	91.2	28	1	US-08-609-090-2	Sequence 2, Appl
92	31	91.2	28	1	US-08-986-948-7	Sequence 7, Appl
93	31	91.2	28	1	US-08-293-284A-4	Sequence 4, Appl
94	31	91.2	28	1	US-08-461-216-2	Sequence 2, Appl
95	31	91.2	28	2	US-09-388-890-2	Sequence 2, Appl
96	31	91.2	28	2	US-09-388-890-3	Sequence 3, Appl
97	31	91.2	28	2	US-09-388-890-4	Sequence 4, Appl
98	31	91.2	28	2	US-09-388-890-5	Sequence 5, Appl
99	31	91.2	28	2	US-09-388-890-6	Sequence 6, Appl
100	31	91.2	28	2	US-09-388-890-7	Sequence 7, Appl

101	31	91.2	28	2	US-09-388-890-8	Sequence 8, Appli	174	31	91.2	40	2	US-09-861-847A-8	Sequence 8, Appli
102	31	91.2	28	2	US-09-388-890-9	Sequence 9, Appli	175	31	91.2	40	2	US-09-988-842-3	Sequence 3, Appli
103	31	91.2	28	2	US-09-388-890-10	Sequence 10, Appl	176	31	91.2	40	2	US-10-455-218-1	Sequence 1, Appli
104	31	91.2	28	2	US-09-388-890-13	Sequence 13, Appl	177	31	91.2	40	2	US-10-151-614-1	Sequence 1, Appli
105	31	91.2	28	2	US-09-388-890-14	Sequence 14, Appl	178	31	91.2	40	2	US-09-623-548A-956	Sequence 956, App
106	31	91.2	28	2	US-09-264-709A-1	Sequence 1, Appli	179	31	91.2	40	2	US-09-623-548A-962	Sequence 962, App
107	31	91.2	28	2	US-08-723-661B-2	Sequence 2, Appli	180	31	91.2	40	2	US-09-623-548A-968	Sequence 968, App
108	31	91.2	28	2	US-09-660-954-2	Sequence 3, Appli	181	31	91.2	40	2	US-09-623-548A-978	Sequence 978, App
109	31	91.2	28	2	US-09-660-954-3	Sequence 3, Appli	182	31	91.2	40	2	US-09-623-548A-989	Sequence 989, App
110	31	91.2	28	2	US-09-660-954-4	Sequence 4, Appli	183	31	91.2	40	2	US-09-623-548A-995	Sequence 995, App
111	31	91.2	28	2	US-09-660-954-5	Sequence 5, Appli	184	31	91.2	40	2	US-09-623-548A-1005	Sequence 1005, Ap
112	31	91.2	28	2	US-09-660-954-6	Sequence 6, Appli	185	31	91.2	40	2	US-09-657-276-956	Sequence 956, App
113	31	91.2	28	2	US-09-660-954-7	Sequence 7, Appli	186	31	91.2	40	2	US-09-657-276-962	Sequence 962, App
114	31	91.2	28	2	US-09-660-954-8	Sequence 8, Appli	187	31	91.2	40	2	US-09-657-276-968	Sequence 968, App
115	31	91.2	28	2	US-09-660-954-9	Sequence 9, Appli	188	31	91.2	40	2	US-09-657-276-978	Sequence 978, App
116	31	91.2	28	2	US-09-660-954-10	Sequence 10, Appl	189	31	91.2	40	2	US-09-657-276-989	Sequence 989, App
117	31	91.2	28	2	US-09-660-954-13	Sequence 13, Appl	190	31	91.2	40	2	US-09-657-276-995	Sequence 995, App
118	31	91.2	28	2	US-09-660-954-14	Sequence 14, Appl	191	31	91.2	40	2	US-09-657-276-1005	Sequence 1005, Ap
119	31	91.2	28	2	US-08-898-300-4	Sequence 4, Appli	192	31	91.2	40	2	US-09-962-955D-36	Sequence 36, Appl
120	31	91.2	28	2	US-08-824-513-4	Sequence 4, Appli	193	31	91.2	40	4	PCT-US92-06700-1	Sequence 1, Appli
121	31	91.2	28	2	US-09-623-548A-959	Sequence 959, App	194	31	91.2	41	1	US-08-302-808-4	Sequence 4, Appli
122	31	91.2	28	2	US-09-623-548A-965	Sequence 965, App	195	31	91.2	41	1	US-08-682-245A-3	Sequence 3, Appli
123	31	91.2	28	2	US-09-623-548A-976	Sequence 976, App	196	31	91.2	41	1	US-08-986-948-4	Sequence 4, Appli
124	31	91.2	28	2	US-09-623-548A-992	Sequence 992, App	197	31	91.2	42	1	US-07-744-767A-2	Sequence 2, Appli
125	31	91.2	28	2	US-09-623-548A-1003	Sequence 1003, Ap	198	31	91.2	42	1	US-08-179-574-1	Sequence 1, Appli
126	31	91.2	28	2	US-09-657-276-959	Sequence 959, App	199	31	91.2	42	1	US-08-271-162-5	Sequence 5, Appli
127	31	91.2	28	2	US-09-657-276-965	Sequence 965, App	200	31	91.2	42	1	US-08-347-144-1	Sequence 1, Appli
128	31	91.2	28	2	US-09-657-276-976	Sequence 976, App	201	31	91.2	42	1	US-08-463-859A-19	Sequence 19, Appl
129	31	91.2	28	2	US-09-657-276-982	Sequence 982, App	202	31	91.2	42	1	US-08-123-659A-19	Sequence 19, Appl
130	31	91.2	28	2	US-09-657-276-1003	Sequence 1003, Ap	203	31	91.2	42	1	US-08-464-247A-19	Sequence 19, Appl
131	31	91.2	28	2	US-09-865-294A-66	Sequence 66, Appl	204	31	91.2	42	1	US-08-464-248A-19	Sequence 19, Appl
132	31	91.2	30	1	US-08-609-090-3	Sequence 3, Appli	205	31	91.2	42	1	US-08-476-464A-1	Sequence 1, Appli
133	31	91.2	30	1	US-09-861-847A-1	Sequence 1, Appli	206	31	91.2	42	1	US-08-304-585-2	Sequence 2, Appli
134	31	91.2	34	1	US-08-609-090-4	Sequence 4, Appli	207	31	91.2	42	1	US-08-302-808-5	Sequence 5, Appli
135	31	91.2	34	1	US-08-475-579A-4	Sequence 4, Appli	208	31	91.2	42	1	US-08-268-348A-1	Sequence 1, Appli
136	31	91.2	35	1	US-08-304-585-6	Sequence 6, Appli	209	31	91.2	42	1	US-08-268-348A-2	Sequence 2, Appli
137	31	91.2	35	1	US-08-612-785B-16	Sequence 16, Appl	210	31	91.2	42	1	US-08-268-348A-3	Sequence 3, Appli
138	31	91.2	35	1	US-08-612-785B-36	Sequence 36, Appl	211	31	91.2	42	1	US-08-268-348A-4	Sequence 4, Appli
139	31	91.2	35	1	US-08-612-785B-38	Sequence 38, Appl	212	31	91.2	42	1	US-08-268-348A-5	Sequence 5, Appli
140	31	91.2	35	1	US-08-612-785B-40	Sequence 40, Appl	213	31	91.2	42	1	US-08-268-348A-6	Sequence 6, Appli
141	31	91.2	35	2	US-08-617-267C-16	Sequence 16, Appl	214	31	91.2	42	1	US-08-433-734-2	Sequence 2, Appli
142	31	91.2	36	1	US-08-609-090-6	Sequence 6, Appli	215	31	91.2	42	1	US-08-609-090-9	Sequence 9, Appli
143	31	91.2	36	2	US-09-861-847A-6	Sequence 6, Appli	216	31	91.2	42	1	US-07-737-371E-72	Sequence 72, Appl
144	31	91.2	36	2	US-09-861-847A-11	Sequence 11, Appl	217	31	91.2	42	1	US-08-422-333-4	Sequence 4, Appli
145	31	91.2	38	1	US-08-302-808-1	Sequence 1, Appli	218	31	91.2	42	1	US-08-682-245A-4	Sequence 4, Appli
146	31	91.2	38	1	US-07-737-371B-68	Sequence 68, Appl	219	31	91.2	42	1	US-08-986-948-5	Sequence 5, Appli
147	31	91.2	38	1	US-08-986-948-1	Sequence 1, Appli	220	31	91.2	42	2	US-08-717-551A-2	Sequence 2, Appli
148	31	91.2	38	2	US-09-623-548A-975	Sequence 975, App	221	31	91.2	42	2	US-09-388-890-1	Sequence 20, Appl
149	31	91.2	38	2	US-09-623-548A-1002	Sequence 1002, Ap	222	31	91.2	42	2	US-09-005-215-20	Sequence 23, Appl
150	31	91.2	38	2	US-09-657-276-975	Sequence 975, App	223	31	91.2	42	2	US-09-242-724-23	Sequence 23, Appl
151	31	91.2	38	1	US-09-657-276-1002	Sequence 1002, Ap	224	31	91.2	42	2	US-08-923-930-2	Sequence 2, Appli
152	31	91.2	39	1	US-08-304-585-5	Sequence 5, Appli	225	31	91.2	42	2	US-09-660-954-1	Sequence 1, Appli
153	31	91.2	39	1	US-08-302-808-2	Sequence 2, Appli	226	31	91.2	42	2	US-08-923-055-2	Sequence 2, Appli
154	31	91.2	39	1	US-08-609-090-7	Sequence 7, Appli	227	31	91.2	42	2	US-08-922-889-2	Sequence 2, Appli
155	31	91.2	39	1	US-08-682-245A-1	Sequence 1, Appli	228	31	91.2	42	2	US-09-731-460-1	Sequence 1, Appli
156	31	91.2	39	1	US-08-986-948-2	Sequence 2, Appli	229	31	91.2	42	2	US-09-133-866-2	Sequence 2, Appli
157	31	91.2	40	1	US-07-744-767A-1	Sequence 1, Appli	230	31	91.2	42	2	US-09-723-384-1	Sequence 1, Appli
158	31	91.2	40	1	US-08-235-400-2	Sequence 2, Appli	231	31	91.2	42	2	US-09-724-961-42	Sequence 42, Appl
159	31	91.2	40	1	US-08-476-464A-2	Sequence 2, Appli	232	31	91.2	42	2	US-09-724-552-1	Sequence 1, Appli
160	31	91.2	40	1	US-08-304-585-1	Sequence 1, Appli	233	31	91.2	42	2	US-09-580-018-42	Sequence 42, Appl
161	31	91.2	40	1	US-08-302-808-3	Sequence 3, Appli	234	31	91.2	42	2	US-10-455-218-2	Sequence 2, Appli
162	31	91.2	40	1	US-08-433-734-1	Sequence 1, Appli	235	31	91.2	42	2	US-09-723-927-1	Sequence 1, Appli
163	31	91.2	40	1	US-08-609-090-8	Sequence 8, Appli	236	31	91.2	42	2	US-09-724-489-1	Sequence 1, Appli
164	31	91.2	40	1	US-07-737-371B-69	Sequence 69, Appl	237	31	91.2	42	2	US-09-724-477-1	Sequence 1, Appli
165	31	91.2	40	1	US-08-682-245A-2	Sequence 2, Appli	238	31	91.2	42	2	US-09-723-762-1	Sequence 1, Appli
166	31	91.2	40	1	US-08-986-948-3	Sequence 3, Appli	239	31	91.2	42	2	US-09-201-430-1	Sequence 1, Appli
167	31	91.2	40	1	US-08-461-216-1	Sequence 1, Appli	240	31	91.2	42	2	US-09-724-551-42	Sequence 42, Appl
168	31	91.2	40	2	US-08-959-148-1	Sequence 1, Appli	241	31	91.2	42	2	US-10-815-353-1	Sequence 1, Appli
169	31	91.2	40	2	US-09-242-724-22	Sequence 22, Appl	242	31	91.2	42	2	US-10-278-181-1	Sequence 1, Appli
170	31	91.2	40	2	US-08-723-661B-1	Sequence 1, Appli	243	31	91.2	42	2	US-10-816-529-1	Sequence 1, Appli
171	31	91.2	40	2	US-09-062-365-3	Sequence 3, Appli	244	31	91.2	42	2	US-09-623-548A-955	Sequence 955, App
172	31	91.2	40	2	US-09-133-866-1	Sequence 1, Appli	245	31	91.2	42	2	US-09-623-548A-961	Sequence 961, App
173	31	91.2	40	2	US-09-861-847A-7	Sequence 7, Appli	246	31	91.2	42	2	US-09-623-548A-967	Sequence 967, App

247	31	91.2	42	2	US-09-623-548A-98A
248	31	91.2	42	2	US-09-623-548A-99A
249	31	91.2	42	2	US-10-815-391-1
250	31	91.2	42	2	US-10-816-022-1
251	31	91.2	42	2	US-09-724-953-34
252	31	91.2	42	2	US-09-657-276-955
253	31	91.2	42	2	US-09-657-276-961
254	31	91.2	42	2	US-09-657-276-967
255	31	91.2	42	2	US-09-657-276-968
256	31	91.2	42	2	US-09-657-276-994
257	31	91.2	42	2	US-09-724-567-34
258	31	91.2	42	2	US-09-724-940-42
259	31	91.2	42	2	US-09-865-294A-65
260	31	91.2	42	2	US-09-979-953-34
261	31	91.2	42	2	US-09-585-817-34
262	31	91.2	42	2	US-09-962-955D-37
263	31	91.2	42	2	US-09-706-574A-20
264	31	91.2	42	2	US-10-934-609-1
265	31	91.2	42	2	US-10-884-892-1
266	31	91.2	42	4	PCT-US92-06700-2
267	31	91.2	42	4	PCT-US93-00325-1
268	31	91.2	42	4	PCT-US95-08302-5
269	31	91.2	42	6	5220013-12
270	31	91.2	42	6	5220013-14
271	31	91.2	42	6	52203482-12
272	31	91.2	43	1	US-08-235-400-1
273	31	91.2	43	1	US-08-437-067-1
274	31	91.2	43	1	US-08-302-808-6
275	31	91.2	43	1	US-08-079-511-1
276	31	91.2	43	1	US-08-467-607-1
277	31	91.2	43	1	US-08-404-831-1
278	31	91.2	43	1	US-08-602-264A-3
279	31	91.2	43	1	US-08-469-363-1
280	31	91.2	43	1	US-08-612-785B-1
281	31	91.2	43	1	US-08-475-579A-1
282	31	91.2	43	1	US-08-850-392-1
283	31	91.2	43	1	US-07-737-371E-70
284	31	91.2	43	1	US-08-986-948-6
285	31	91.2	43	1	US-08-975-977-1
286	31	91.2	43	1	US-08-817-423-1
287	31	91.2	43	2	US-08-920-162A-1
288	31	91.2	43	2	US-08-461-018A-3
289	31	91.2	43	2	US-08-976-191-1
290	31	91.2	43	2	US-08-976-179-1
291	31	91.2	43	2	US-09-216-958-3
292	31	91.2	43	2	US-09-356-931-1
293	31	91.2	43	2	US-08-733-202-1
294	31	91.2	43	2	US-08-703-675C-1
295	31	91.2	43	2	US-09-390-692-1
296	31	91.2	43	2	US-08-617-267C-1
297	31	91.2	43	2	US-09-303-655-1
298	31	91.2	43	2	US-08-294-819-1
299	31	91.2	43	2	US-09-408-283-1
300	31	91.2	43	2	US-09-280-966-1

ALIGNMENTS

RESULT 1
US-09-747-408-18
; Sequence 18, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23

```

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-18

Query Match      100.0%; Score 34; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
      |||||
DB      1 KLVFFAQ 7

RESULT 2
US-09-747-408-19
; Sequence 19, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-19

Query Match      100.0%; Score 34; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
      |||||
DB      1 KLVFFAQ 7

RESULT 3
US-09-388-890-12
; Sequence 12, Application US/09388890
; Patent No. 6136548
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: /09/388,890
; APPLICATION NUMBER: US/09/388,890
; FILING DATE:
; CLASSIFICATION:

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,959
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; IMMEDIATE SOURCE:
; CLONE: E22Q B(1-28) peptide of amyloid B protein
US-09-388-890-12

Query Match 100.0%; Score 34; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.49; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 KLVFFPAQ 7
Db 16 KLVFFPAQ 22
|||||

RESULT 4
US-09-660-954-12
; Sequence 12, Application US/09660954
; Patent No. 6471960
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/660,954
; APPLICATION NUMBER: US/09/660,954
; FILING DATE: 13-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/388,890
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/686,959
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; IMMEDIATE SOURCE:
; CLONE: E22Q B(1-28) peptide of amyloid B protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-660-954-12

Query Match 100.0%; Score 34; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.49; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 KLVFFPAQ 7
Db 16 KLVFFPAQ 22
|||||

RESULT 5
US-09-623-548A-979
; Sequence 979, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 979
; LENGTH: 35
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-979

Query Match 100.0%; Score 34; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.62; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 KLVFFPAQ 7
Db 11 KLVFFPAQ 17
|||||

RESULT 6
US-09-623-548A-1006
; Sequence 1006, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen

;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
;; TITLE OF INVENTION: COMPONENTS
;; FILE REFERENCE: 2110

;; CURRENT APPLICATION NUMBER: US/09/623,548A

;; CURRENT FILING DATE: 2000-09-05

;; PRIOR APPLICATION NUMBER: 60/134,406

;; PRIOR FILING DATE: 1999-05-17

;; PRIOR APPLICATION NUMBER: 60/153,406

;; PRIOR FILING DATE: 1999-09-10

;; PRIOR APPLICATION NUMBER: 60/159,783

;; PRIOR FILING DATE: 1999-10-18

;; NUMBER OF SEQ ID NOS: 1617

;; SOFTWARE: Patentin Ver. 2.1

;; SEQ ID NO 1006

;; LENGTH: 35

;; TYPE: PRT

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-623-548A-1006

Query Match 100.0%; Score 34; DB 2; Length 35;

Best Local Similarity 100.0%; Pred. No. 0.62; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 KLVFFAQ 7

|||||

Db 11 KLVFFAQ 17

RESULT 7

US-09-657-276-979

;; Sequence 979, Application US/09657276

;; Patent No. 6887470

;; GENERAL INFORMATION:

;; APPLICANT: Conjuchem, Inc.

;; APPLICANT: Bridon, Dominique

;; APPLICANT: Ezrin, Alan

;; APPLICANT: Milner, Peter

;; APPLICANT: Holmes, Darren

;; APPLICANT: Thibaudau, Karen

;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM

;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD

;; TITLE OF INVENTION: COMPONENTS

;; FILE REFERENCE: 2110

;; CURRENT APPLICATION NUMBER: US/09/657,276

;; CURRENT FILING DATE: 2000-09-07

;; PRIOR APPLICATION NUMBER: 60/134,406

;; PRIOR FILING DATE: 1999-05-17

;; PRIOR APPLICATION NUMBER: 60/153,406

;; PRIOR FILING DATE: 1999-09-10

;; PRIOR APPLICATION NUMBER: 60/159,783

;; PRIOR FILING DATE: 1999-10-18

;; NUMBER OF SEQ ID NOS: 1617

;; SOFTWARE: Patentin Ver. 2.1

;; SEQ ID NO 979

;; LENGTH: 35

;; TYPE: PRT

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-657-276-979

Query Match 100.0%; Score 34; DB 2; Length 35;

Best Local Similarity 100.0%; Pred. No. 0.62; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 KLVFFAQ 7

|||||

Db 11 KLVFFAQ 17

RESULT 8

US-09-657-276-1006

;; Sequence 1006, Application US/09657276

;; Patent No. 6887470

;; GENERAL INFORMATION:

;; APPLICANT: Conjuchem, Inc.

;; APPLICANT: Bridon, Dominique

;; APPLICANT: Ezrin, Alan

;; APPLICANT: Milner, Peter

;; APPLICANT: Holmes, Darren

;; APPLICANT: Thibaudau, Karen

;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM

;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD

;; TITLE OF INVENTION: COMPONENTS

;; FILE REFERENCE: 2110

;; CURRENT APPLICATION NUMBER: US/09/657,276

;; CURRENT FILING DATE: 2000-09-07

;; PRIOR APPLICATION NUMBER: 60/134,406

;; PRIOR FILING DATE: 1999-05-17

;; PRIOR APPLICATION NUMBER: 60/153,406

;; PRIOR FILING DATE: 1999-09-10

;; PRIOR APPLICATION NUMBER: 60/159,783

;; PRIOR FILING DATE: 1999-10-18

;; NUMBER OF SEQ ID NOS: 1617

;; SOFTWARE: Patentin Ver. 2.1

;; SEQ ID NO 1006

;; LENGTH: 35

;; TYPE: PRT

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-657-276-1006

Query Match 100.0%; Score 34; DB 2; Length 35;

Best Local Similarity 100.0%; Pred. No. 0.62; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 KLVFFAQ 7

|||||

Db 11 KLVFFAQ 17

RESULT 9

US-08-304-585-8

;; Sequence 8, Application US/08304585

;; Patent No. 5721106

;; GENERAL INFORMATION:

;; APPLICANT: Maggio, John E.

;; APPLICANT: Mantyh, Patrick W.

;; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND

;; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE

;; NUMBER OF SEQUENCES: 12

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.

;; STREET: P.O. Box 581415

;; CITY: Minneapolis

;; STATE: MN

;; COUNTRY: USA

;; ZIP: 55458-1415

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patentin Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/304,585

;; FILING DATE: 12-SEP-1994

;; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Muetting, Ann M.

REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-304-585-8

Query Match 100.0%; Score 34; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.71; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
| | | | |
DB 16 KLVFFPAQ 22

RESULT 10

US-09-573-789-1
Sequence 1, Application US/09573789
Patent No. 6737038
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Pharma Company (formerly DuPont Pharmaceuticals
APPLICANT: Company)
APPLICANT: Zaczek, Robert
APPLICANT: Olson, Richard E.
APPLICANT: Seiffert, Dietmar A.
APPLICANT: Thompson, Lorin A.

TITLE OF INVENTION: USE OF SMALL MOLECULE RADIOLOGANDS TO DISCOVER INHIBITORS OF AMY
TITLE OF INVENTION: PEPTIDE PRODUCTION AND FOR DIAGNOSTIC IMAGING
FILE REFERENCE: PH-7048-A
CURRENT APPLICATION NUMBER: US/09/573,789
CURRENT FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: US 09/438,901
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 60/108,147
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/131,284
PRIOR FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
US-09-573-789-1

Query Match 100.0%; Score 34; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.76; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
| | | | |
DB 16 KLVFFPAQ 22

RESULT 11

US-09-859-261-1
Sequence 1, Application US/09859261
Patent No. 6878363
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Pharma Company (formerly DuPont Pharmaceuticals
APPLICANT: Company)
APPLICANT: Zaczek, Robert
APPLICANT: Olson, Richard E.
APPLICANT: Seiffert, Dietmar A.
APPLICANT: Thompson, Lorin A.

TITLE OF INVENTION: USE OF SMALL MOLECULE RADIOLOGANDS TO DISCOVER INHIBITORS OF AMY
TITLE OF INVENTION: PEPTIDE PRODUCTION AND FOR DIAGNOSTIC IMAGING
FILE REFERENCE: ph-7215
CURRENT APPLICATION NUMBER: US/09/859,261
CURRENT FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 60/204,685
PRIOR FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-261-1

Query Match 100.0%; Score 34; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.76; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
| | | | |
DB 16 KLVFFPAQ 22

RESULT 12

US-08-462-859A-3
Sequence 3, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-3

Query Match 100.0%; Score 34; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.1; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
| | | | |

Db 25 KLVPFAQ 31

RESULT 13

US-08-123-659A-3

; Sequence 3, Application US/08123659A

; Patent No. 5656477

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vitek, M. P.

; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Anne Rosenblum

; STREET: 163 Delaware Avenue, Suite 212

; CITY: Delmar

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 12054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/123.659A

; FILING DATE: 20-SEP-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Rosenblum, Anne M.

; REGISTRATION NUMBER: 30,419

; REFERENCE/DOCKET NUMBER: 31,844-01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (518)475-0611

; TELEFAX: (518)475-0619

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 63 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-123-659A-3

Query Match 100.0%; Score 34; DB 1; Length 63;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFAQ 7

Db 25 KLVPFAQ 31

RESULT 14

US-08-464-247A-3

; Sequence 3, Application US/08464247A

; Patent No. 5693478

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vitek, M. P.

; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Campus Drive

; CITY: Parsippany

; STATE: New Jersey

; COUNTRY: United States

; ZIP: 07054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,247A

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 31,844-03

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-683-2158

; TELEFAX: 201-683-4117

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 63 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-464-247A-3

Query Match 100.0%; Score 34; DB 1; Length 63;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFAQ 7

Db 25 KLVPFAQ 31

RESULT 15

US-08-464-248A-3

; Sequence 3, Application US/08464248A

; Patent No. 5703209

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vitek, M. P.

; TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Cyanamid Plaza

; CITY: Wayne

; STATE: New Jersey

; COUNTRY: United States

; ZIP: 07470-8426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,248A

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 31,844-02

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (201)831-3246

; TELEFAX: (201)831-3305

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 63 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

```
; MOLECULE TYPE: protein
US-08-464-248A-3

Query Match      100.0%; Score 34; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 25 KLVFFAQ 31

RESULT 16
US-08-339-708A-6
; Sequence 6, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-339-708A-6

Query Match      100.0%; Score 34; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 16 KLVFFAQ 22

RESULT 17
US-08-127-904-14
; Sequence 14, Application US/08127904
; Patent No. 5470951
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For Antagonizing
; TITLE OF INVENTION: Amnestic Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving the
; TITLE OF INVENTION: Quality of Life in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4" diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,904
; FILING DATE: 29 September 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: No. 5470951e
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: No. 5470951e
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; TELEX: No. 5470951e
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown
US-08-127-904-14

Query Match      91.2%; Score 31; DB 1; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 1 KLVFFAQ 7

RESULT 18
US-09-264-709A-13
; Sequence 13, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
; APPLICANT: Roberts, Eugene
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
; TITLE OF INVENTION: Improve the Quality of Life
; FILE REFERENCE: 2124-310
; CURRENT APPLICATION NUMBER: US/09/264,709A
; CURRENT FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 08/797,782
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-264-709A-13

Query Match      91.2%; Score 31; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```



```

Qy 1 KLVFFAQ 7
Db 1 KLVFFAE 7

RESULT 19
PCT-US94-10475-14
; Sequence 14, Application PC/TUS9410475
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For
; TITLE OF INVENTION: Antagonizing Amyloid n
; TITLE OF INVENTION: Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving
; TITLE OF INVENTION: the Quality of Life
; TITLE OF INVENTION: in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4"
; MEDIUM TYPE: diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10475
; FILING DATE: 16 September 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA: U. S. Application
; PRIOR APPLICATION DATA: Serial No.
; PRIOR APPLICATION DATA: 08/127,904; filed
; PRIOR APPLICATION DATA: 29 September 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: None
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 626-3564 or 783-6030
; TELEFAX: (202) 783-6031
; TELEX: None
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown
; PCT-US94-10475-14

Query Match 91.2%; Score 31; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 1 KLVFFAE 7

RESULT 20
US-08-630-645-1
; Sequence 1, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

Qy 1 KLVFFAQ 7
Db 1 KLVFFAE 7

RESULT 21
US-08-766-596A-1
; Sequence 1, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

Query Match 91.2%; Score 31; DB 1; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 1 KLVFFAE 7

TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,645
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-630-645-1

```

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/766,596A
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/630,645
;; FILING DATE: 10-APR-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/478,326
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: YUN, Allen C.
;; REGISTRATION NUMBER: 37,971
;; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-766-596A-1

Query Match 91.2%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 1 KLVFFAE 7

RESULT 22
US-09-668-314C-73
;; Sequence 73, Application US/09668314C
;; Patent No. 6844148
;; GENERAL INFORMATION:
;; APPLICANT: Gurney, et al
;; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREOF
;; FILE REFERENCE: 28341/6280NCP
;; CURRENT APPLICATION NUMBER: US/09/668,314C
;; CURRENT FILING DATE: 2000-09-22
;; PRIOR APPLICATION NUMBER: US 60/169,232
;; PRIOR FILING DATE: 1999-12-06
;; PRIOR APPLICATION NUMBER: US 09/416,901
;; PRIOR FILING DATE: 1999-10-13
;; PRIOR APPLICATION NUMBER: US 60/155,493
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: US 09/404,133
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: PCT/US99/20881
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: US 60/101,594
;; PRIOR FILING DATE: 1998-09-24
;; NUMBER OF SEQ ID NOS: 84
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 73
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic peptide
;; US-09-668-314C-73

Query Match 91.2%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7

DB 1 KLVFFAE 7
RESULT 23
PCT-US96-10220-1
;; Sequence 1, Application PC/TUS9610220
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
;; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; STREET: 419 Seventh Street, N.W., Suite 400
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/10220
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/478,326
;; FILING DATE: 06-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/630,645
;; FILING DATE: 10-APR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; PCT-US96-10220-1

Query Match 91.2%; Score 31; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 1 KLVFFAE 7

RESULT 24
US-08-766-596A-64
;; Sequence 64, Application US/08766596A
;; Patent No. 6462171
;; GENERAL INFORMATION:
;; APPLICANT: SOTO-JARA, Claudio
;; APPLICANT: BRAUMANN, Marc
;; APPLICANT: FRANGIONE, Blas
;; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
;; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
;; NUMBER OF SEQUENCES: 69
;; CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-64

Query Match 91.2%; Score 31; DB 2; Length 9;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
Db 2 KLVFFAE 8

RESULT 25
US-08-970-833-3
Sequence 3, Application US/08970833
Patent No. 6022859
GENERAL INFORMATION:
APPLICANT: Kieselring, Laura L.
APPLICANT: Murphy, Regina M.
TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,833
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Jean C.

REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 960296.94291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5709
TELEFAX: (414) 271-3552
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-970-833-3

Query Match 91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
Db 1 KLVFFAE 7

RESULT 26
US-09-724-961-21
Sequence 21, Application US/09724961
Patent No. 6743427
GENERAL INFORMATION:
APPLICANT: Schenk, Dale B.
APPLICANT: Bard, Frederique
APPLICANT: Vasquez, Nicki
APPLICANT: Yednock, Ted
TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
FILE REFERENCE: 15270J-004750UC
CURRENT APPLICATION NUMBER: US/09/724,961
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/580,015
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/322,289
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: US 09/201,430
PRIOR FILING DATE: 1998-11-30
PRIOR APPLICATION NUMBER: WO PCT/US00/14810
PRIOR FILING DATE: 1998-11-30
PRIOR APPLICATION NUMBER: US 60/080,970
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 60/067,740
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 21
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: 10-mer peptide
OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
OTHER INFORMATION: peptide)
US-09-724-961-21

Query Match 91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
Db 4 KLVFFAE 10

RESULT 27
US-09-724-961-22
Sequence 22, Application US/09724961
Patent No. 6743427

```
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-22

Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFPAQ 7
Db      3 KLVFFPAE 9
      |||||:

RESULT 28
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-23

Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFPAQ 7
Db      2 KLVFFPAE 8
      |||||:

RESULT 29
US-09-724-961-24
; Sequence 24, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-24

Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFPAQ 7
Db      1 KLVFFPAE 7
      |||||:

RESULT 30
US-09-580-018-21
; Sequence 21, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
```

```
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-580-018-21
```

```
Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KLVFFPAQ 7
Db 4 KLVFFPAE 10
```

```
RESULT 31
US-09-580-018-22
; Sequence 22, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-580-018-22
```

```
Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KLVFFPAQ 7
Db 3 KLVFFPAE 9
```

```
RESULT 32
US-09-580-018-23
; Sequence 23, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-580-018-23
```

```
Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KLVFFPAQ 7
Db 2 KLVFFPAE 8
```

```
RESULT 33
US-09-580-018-24
; Sequence 24, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-580-018-24
```

```
Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KLVFFPAQ 7
Db 1 KLVFFPAE 7
```

```
RESULT 34
US-09-724-551-21
; Sequence 21, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-21
```

```
Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFPAQ 7
Db 4 KLVFFPAE 10
|||||:
```

```
RESULT 35
```

```
US-09-724-551-22
; Sequence 22, Application US/09724551
; Patent No. 6787637
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Schenk, Dale B.
```

```
; APPLICANT: Bard, Frederique
```

```
; APPLICANT: Vednock, Ted
```

```
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
```

```
; FILE REFERENCE: 15270J-004760US
```

```
; CURRENT APPLICATION NUMBER: US/09/724,551
```

```
; CURRENT FILING DATE: 2000-11-28
```

```
; PRIOR APPLICATION NUMBER: US/09/580,018
```

```
; PRIOR FILING DATE: 2000-05-26
```

```
; PRIOR APPLICATION NUMBER: US 09/322,289
```

```
; PRIOR FILING DATE: 1999-05-28
```

```
; NUMBER OF SEQ ID NOS: 77
```

```
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 22
```

```
; LENGTH: 10
```

```
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
```

```
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
```

```
; OTHER INFORMATION: peptide)
US-09-724-551-22
```

```
Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFPAQ 7
Db 3 KLVFFPAE 9
|||||:
```

```
RESULT 36
```

```
US-09-724-551-23
```

```
; Sequence 23, Application US/09724551
```

```
; Patent No. 6787637
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Schenk, Dale B.
```

```
; APPLICANT: Bard, Frederique
```

```
; APPLICANT: Vednock, Ted
```

```
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
```

```
; FILE REFERENCE: 15270J-004760US
```

```
; CURRENT APPLICATION NUMBER: US/09/724,551
```

```
; CURRENT FILING DATE: 2000-11-28
```

```
; PRIOR APPLICATION NUMBER: US/09/580,018
```

```
; PRIOR FILING DATE: 2000-05-26
```

```
; PRIOR APPLICATION NUMBER: US 09/322,289
```

```
; PRIOR FILING DATE: 1999-05-28
```

```
; NUMBER OF SEQ ID NOS: 77
```

```
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 23
```

```
; LENGTH: 10
```

```
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
```

```
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
```

```
; OTHER INFORMATION: peptide)
US-09-724-551-23
```

```
Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFPAQ 7
Db 2 KLVFFPAE 8
|||||:
```

```
RESULT 37
```

```
US-09-724-551-24
```

```
; Sequence 24, Application US/09724551
```

```
; Patent No. 6787637
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Schenk, Dale B.
```

```
; APPLICANT: Bard, Frederique
```

```
; APPLICANT: Vednock, Ted
```

```
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
```

```
; FILE REFERENCE: 15270J-004760US
```

```
; CURRENT APPLICATION NUMBER: US/09/724,551
```

```
; CURRENT FILING DATE: 2000-11-28
```

```
; PRIOR APPLICATION NUMBER: US/09/580,018
```

```
; PRIOR FILING DATE: 2000-05-26
```

```
; PRIOR APPLICATION NUMBER: US 09/322,289
```

```
; PRIOR FILING DATE: 1999-05-28
```

```
; NUMBER OF SEQ ID NOS: 77
```

```
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 24
```

```
; LENGTH: 10
```

```
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
```

```
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
```

```
; OTHER INFORMATION: peptide)
US-09-724-551-24
```

```
Query Match          91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVFFPAQ 7
Db 1 KLVFFPAE 7
|||||:
```

```
RESULT 38
```

```
US-09-724-940-21
```

```
; Sequence 21, Application US/09724940
```

```
; Patent No. 6905686
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Schenk, Dale B.
```

```
; APPLICANT: Bard, Frederique
```

```
; APPLICANT: Vasquez, Nicki
```

```
; APPLICANT: Vednock, Ted
```

```
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
```

```
; FILE REFERENCE: 15270J-004750UC
```

```
; CURRENT APPLICATION NUMBER: US/09/724,940
```

```
; CURRENT FILING DATE: 2000-11-28
```

```
; PRIOR APPLICATION NUMBER: US/09/580,015
```

```
; PRIOR FILING DATE: 2000-05-26
```

```
; PRIOR APPLICATION NUMBER: US 09/322,289
```

```

, PRIOR FILING DATE: 1999-05-28
, PRIOR APPLICATION NUMBER: US 09/201,430
, PRIOR FILING DATE: 1998-11-30
, PRIOR APPLICATION NUMBER: WO PCT/US00/14810
, PRIOR FILING DATE: 1998-11-30
, PRIOR APPLICATION NUMBER: US 60/080,970
, PRIOR FILING DATE: 1998-04-07
, PRIOR APPLICATION NUMBER: US 60/067,740
, PRIOR FILING DATE: 1997-12-02
, NUMBER OF SEQ ID NOS: 77
, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 21
, LENGTH: 10
, TYPE: PRT
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence
, OTHER INFORMATION: From AN1792 sequence (human)
, OTHER INFORMATION: (peptide)
US-09-724-940-21

```

Query Match	91.2%;	Score 31;	DB 2;	Length 10;
Best Local Similarity	85.7%;	Pred. No. 0.81;		
Matches 6;	Conservative	1;	Mismatches	0;
			Indels	0;
			Gaps	0;

Qy	1	KLVFFAQ	7
		:	
Db	4	KLVFFAE	10

```

RESULT 39
US-09-724-940-22
; Sequence 22, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: I0-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-22

```

Query Match	91.2	Score 31	DB 2	Length 10
Best Local Similarity	95.7	Pred. No. 0.81		
Matches 6	Conservative	1	Mismatches	0
			Indels	0
			Gaps	0

Qy 1 KLVFFAQ 7
|||:

Db 3 KLVFFAE 9

RESULT 40
US-09-724-940-23
; Sequence 23, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vedrock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-23

Query Match	Score 31;	DB 2;	Length 10;
Best Local Similarity	91.2%;		
Matches	85.7%;		
6: Conservative	Pred. No. 0.81;		
	1: Mismatches		
	0: Indels		
	0: Gaps		

Qy	1	KLVFFAQ	7
		:	
D ^b	2	KLVFFAE	8

RESULT 41
US-09-724-940-24
Sequence 24, Application US/09724940
Patent No. 6905686
GENERAL INFORMATION:
APPLICANT: Schenk, Dale B.
APPLICANT: Bard, Frederique
APPLICANT: Vasquez, Nicki
APPLICANT: Vednock, Ted
TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
FILE REFERENCE: 15270J-004750UC
CURRENT APPLICATION NUMBER: US/09/724,940
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US/09/580,015
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/322,289
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: US 09/201,430
PRIOR FILING DATE: 1998-11-30
PRIOR APPLICATION NUMBER: WO PCT/US00/14810
PRIOR FILING DATE: 1998-11-30
PRIOR APPLICATION NUMBER: US 60/080,970
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 60/067,740

; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-24

Query Match 91.2%; Score 31; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
| | | | |
Db 1 KLVFFAE 7

RESULT 42
US-08-630-645-14
; Sequence 14, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,645
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-630-645-14

Query Match 91.2%; Score 31; DB 1; Length 11;
Best Local Similarity 85.7%; Pred. No. 0.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
| | | | |
Db 2 KLVFFAE 8

RESULT 43
US-08-766-596A-14
; Sequence 14, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-14

Query Match 91.2%; Score 31; DB 2; Length 11;
Best Local Similarity 85.7%; Pred. No. 0.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
| | | | |
Db 2 KLVFFAE 8

RESULT 44
US-09-988-842-9
; Sequence 9, Application US/09988842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION


```
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

Query Match          91.2%; Score 31; DB 2; Length 11;
Best Local Similarity 85.7%; Pred. No. 0.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
Db 2 KLVFFFAE 8

RESULT 45
US-09-988-842-25
; Sequence 25, Application US/09988842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISORDANT HELIX STABILIZATION FOR PREVENTION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

Query Match          91.2%; Score 31; DB 2; Length 11;
Best Local Similarity 85.7%; Pred. No. 0.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
Db 2 KLVFFFAE 8

RESULT 46
PCT-US96-10220-14
; Sequence 14, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEROF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
```

```
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10220
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US96-10220-14

Query Match          91.2%; Score 31; DB 4; Length 11;
Best Local Similarity 85.7%; Pred. No. 0.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
Db 2 KLVFFFAE 8

RESULT 47
US-09-594-366-5
; Sequence 5, Application US/09594366
; Patent No. 6582945
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2004
; CURRENT APPLICATION NUMBER: US/09/594,366
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-594-366-5

Query Match          91.2%; Score 31; DB 2; Length 14;
Best Local Similarity 85.7%; Pred. No. 1.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
Db 4 KLVFFFAE 10

RESULT 48
US-09-992-800-5
```

```

; Sequence 5, Application US/09992800
; Patent No. 6872554
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2006
; CURRENT APPLICATION NUMBER: US/09/992,800
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-800-5

Query Match          91.2%; Score 31; DB 2; Length 14;
Best Local Similarity 85.7%; Pred. No. 1.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFPAQ 7
DB      4 KLVFFFAE 10

RESULT 49
US-08-612-785B-14
; Sequence 14, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-612-785B-37

Query Match          91.2%; Score 31; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFPAQ 7
DB      6 KLVFFFAE 12

RESULT 50
US-08-612-785B-37
; Sequence 37, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-612-785B-37

Query Match          91.2%; Score 31; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFPAQ 7
DB      6 KLVFFFAE 12

```

RESULT 51
US-08-617-267C-14
; Sequence 14, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PFI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-617-267C-14

Query Match 91.2%; Score 31; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFAQ 7
Db 1 KLVPFAE 7

RESULT 52
US-08-766-596A-56
; Sequence 56, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:

STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 08-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-56

Query Match 91.2%; Score 31; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFAQ 7
Db 5 KLVPFAE 11

RESULT 53
US-08-766-596A-57
; Sequence 57, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:

```
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/630,645
/ FILING DATE: 10-APR-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/478,326
/ FILING DATE: 06-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: YUN, Allen C.
/ REGISTRATION NUMBER: 37,971
/ REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 57:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-766-596A-57

Query Match          91.2%; Score 31; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      5 KLVFFAE 11
|||||:

RESULT 54
US-08-766-596A-58
; Sequence 58, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
```

```
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 58:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-766-596A-58

Query Match          91.2%; Score 31; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      5 KLVFFAE 11
|||||:

RESULT 55
US-08-766-596A-61
; Sequence 61, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 61:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-766-596A-61

Query Match          91.2%; Score 31; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 KLVPFAQ 7
Db 5 KLVPFAE 11

RESULT 56

US-08-766-596A-63
; Sequence 63, Application US/08766596A
; Patent No. 6462171

GENERAL INFORMATION:

; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc

; APPLICANT: FRANGIONE, Blas

; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL

; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE

; TITLE OF INVENTION: DEPOSITS

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 400

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/766,596A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/630,645

; FILING DATE: 10-APR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/478,326

; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: YUN, Allen C.

; REGISTRATION NUMBER: 37,971

; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 63:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-766-596A-63

Query Match 91.2%; Score 31; DB 2; Length 15;

Best Local Similarity 85.7%; Pred. No. 1.2;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFAQ 7
Db 5 KLVPFAE 11

RESULT 57

US-08-766-596A-65

; Sequence 65, Application US/08766596A

; Patent No. 6462171

GENERAL INFORMATION:

; APPLICANT: SOTO-JARA, Claudio

; APPLICANT: BAUMANN, Marc

; APPLICANT: FRANGIONE, Blas

; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL

; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE

; TITLE OF INVENTION: DEPOSITS

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 400

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/766,596A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/630,645

; FILING DATE: 10-APR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/478,326

; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: YUN, Allen C.

; REGISTRATION NUMBER: 37,971

; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 65:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-766-596A-65

Query Match 91.2%; Score 31; DB 2; Length 15;

Best Local Similarity 85.7%; Pred. No. 1.2;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFAQ 7
Db 5 KLVPFAE 11

RESULT 58

US-09-264-709A-2

; Sequence 2, Application US/09264709A

; Patent No. 6320024

GENERAL INFORMATION:

; APPLICANT: Roberts, Eugene

; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and

; TITLE OF INVENTION: Improve the Quality of Life

; FILE REFERENCE: 2124-310

; CURRENT APPLICATION NUMBER: US/09/264,709A

; CURRENT FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 08/797,782

; PRIOR FILING DATE: 1997-02-07

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 17

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-264-709A-2

Query Match 91.2%; Score 31; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 5 KLVFFAE 11

RESULT 59
US-09-594-366-3
; Sequence 3, Application US/09594366
; Patent No. 6582945
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2004
; CURRENT APPLICATION NUMBER: US/09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-594-366-3

Query Match 91.2%; Score 31; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 8 KLVFFAE 14

RESULT 60
US-09-623-548A-950
; Sequence 950, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 950
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-950

Query Match 91.2%; Score 31; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 5 KLVFFAE 11

RESULT 61
US-09-623-548A-983
; Sequence 983, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 983
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-983

Query Match 91.2%; Score 31; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 5 KLVFFAE 11

RESULT 62
US-09-992-800-3
; Sequence 3, Application US/09992800
; Patent No. 6872554
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2006
; CURRENT APPLICATION NUMBER: US/09/992,800
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-800-3

Query Match 91.2%; Score 31; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 8 KLVFFAE 14

RESULT 63

US-09-657-276-950
; Sequence 950, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 950
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide

US-09-657-276-950

Query Match 91.2%; Score 31; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 5 KLVFFAE 11

RESULT 64

US-09-657-276-983
; Sequence 983, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406

; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 983
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-983

Query Match 91.2%; Score 31; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 5 KLVFFAE 11

RESULT 65

US-08-970-833-11
; Sequence 11, Application US/08970833
; Patent No. 6022859
; GENERAL INFORMATION:
; APPLICANT: Kiessling, Laura L.
; APPLICANT: Murphy, Regina M.
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,833
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 960296.94291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-970-833-11

Query Match 91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 10 KLVFFAE 16

```
RESULT 66
US-09-723-384-5
; Sequence 5, Application US/09723384
; Patent No. 6710226
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/09/723,384
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-723-384-5

Query Match          91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      4 KLVFFAE 10

RESULT 67
US-09-724-961-75
; Sequence 75, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta 13-28
; OTHER INFORMATION: peptide with two Gly residues added and inserted
; OTHER INFORMATION: Cys residue
; NAME/KEY: MOD_RES
```

```
; LOCATION: (1)
; OTHER INFORMATION: Xaa = N-acetyl His
US-09-724-961-75

Query Match          91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      4 KLVFFAE 10

RESULT 68
US-09-724-552-5
; Sequence 5, Application US/09724552
; Patent No. 6750324
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/09/724,552
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,019A
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-724-552-5

Query Match          91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFAQ 7
Db      4 KLVFFAE 10

RESULT 69
US-09-580-018-75
; Sequence 75, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
```


; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta 13-28
; OTHER INFORMATION: peptide with two Gly residues added and inserted
; OTHER INFORMATION: Cys residue
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = N-acetyl His
US-09-580-018-75

Query Match 91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 4 KLVFFAE 10

RESULT 70

US-09-723-927-5
; Sequence 5, Application US/09723927
; Patent No. 6787138
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/723,927
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-723-927-5

Query Match 91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 4 KLVFFAE 10

RESULT 71

US-09-724-489-5
; Sequence 5, Application US/09724489
; Patent No. 6787140
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/724,489
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/201,430
; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-724-489-5

Query Match 91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 4 KLVFFAE 10

RESULT 72

US-09-724-477-5
; Sequence 5, Application US/09724477
; Patent No. 6787143
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/724,477
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-724-477-5

Query Match 91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 4 KLVFFAE 10

RESULT 73

US-09-723-762-5
; Sequence 5, Application US/09723762

```
; Patent No. 6787144
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/723,762
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-723-762-5

Query Match          91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
Db      4 KLVFFAE 10
|||||:

RESULT 74
US-09-201-430-5
; Sequence 5, Application US/09201430
; Patent No. 6787523
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/201,430
; CURRENT FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-201-430-5

Query Match          91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
Db      4 KLVFFAE 10
|||||:

RESULT 75
US-09-724-551-75
; Sequence 75, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta 13-28
; OTHER INFORMATION: peptide with two Gly residues added and inserted
; OTHER INFORMATION: Cys residue
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = N-acetyl His
US-09-724-551-75

Query Match          91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
Db      4 KLVFFAE 10
|||||:

Search completed: December 29, 2005, 17:52:40
Job time : 24.471 secs
```

```
; Patent No. 6787144
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/723,762
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-723-762-5

Query Match          91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
Db      4 KLVFFAE 10
|||||:

RESULT 74
US-09-201-430-5
; Sequence 5, Application US/09201430
; Patent No. 6787523
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/201,430
; CURRENT FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-201-430-5

Query Match          91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
Db      4 KLVFFAE 10
|||||:

RESULT 75
US-09-724-551-75
; Sequence 75, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta 13-28
; OTHER INFORMATION: peptide with two Gly residues added and inserted
; OTHER INFORMATION: Cys residue
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = N-acetyl His
US-09-724-551-75

Query Match          91.2%; Score 31; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFAQ 7
Db      4 KLVFFAE 10
|||||:

Search completed: December 29, 2005, 17:52:40
Job time : 24.471 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 95.4032 Seconds
(without alignments)
32.238 Million cell updates/sec

Title: US-10-009-122-18
Perfect score: 34
Sequence: 1 KLVFFQAQ 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	7	4	AAB48492
2	34	100.0	7	4	AAB48491
3	34	100.0	7	4	AAB82640
4	34	100.0	7	4	AAB82639
5	34	100.0	7	5	AAU96827
6	34	100.0	7	5	AAU96828
7	34	100.0	7	5	AAU11665
8	34	100.0	7	5	AAU11666
9	34	100.0	7	8	ADQ37330
10	34	100.0	7	8	ADQ37331
11	34	100.0	7	9	ADY37938
12	34	100.0	7	9	ADY37937
13	34	100.0	9	2	AAR45239
14	34	100.0	10	4	AAB82641
15	34	100.0	10	5	AAU96829
16	34	100.0	10	9	ADY37939
17	34	100.0	15	7	ADK82697
18	34	100.0	28	2	AAW01414
19	34	100.0	28	6	AAB35600
20	34	100.0	28	6	ABG72244
21	34	100.0	35	4	AAB91830
22	34	100.0	35	4	AAB91803
23	34	100.0	40	2	AAW47232
24	34	100.0	42	6	ABP97887

25	34	100.0	42	9	ADV42360	Human amy
26	34	100.0	42	9	ADZ88256	Anyloid b
27	34	100.0	42	9	AEA37375	Human amy
28	34	100.0	53	2	AAR55697	Sequence
29	34	100.0	63	2	AAW26391	Anyloid p
30	34	100.0	63	2	AAW26511	Anyloid p
31	34	100.0	63	2	AAW42975	Beta-amy1
32	34	100.0	63	2	AAW44746	APP-RFP 7
33	34	100.0	99	2	AAR74695	Beta-amy1
34	34	100.0	100	5	AAE14377	Anyloid p
35	34	100.0	108	5	AAE14385	Gamma-sec
36	31	91.2	7	2	AAR88300	Non-amnes
37	31	91.2	7	2	AAR87921	Test pept
38	31	91.2	7	4	AAB67281	Residues
39	31	91.2	7	5	ABB04920	Human amy
40	31	91.2	7	6	ABB82630	Abeta fib
41	31	91.2	7	6	AAE35454	Abeta pep
42	31	91.2	7	6	AAE35453	Abeta pep
43	31	91.2	7	7	ADP20746	Human bet
44	31	91.2	7	7	ADP50855	Human cal
45	31	91.2	7	8	ADP64922	Beta-amy1
46	31	91.2	7	8	ADQ37278	Vaccine a
47	31	91.2	8	2	ADQ37279	Vaccine a
48	31	91.2	8	2	AAW32551	Anyloidog
49	31	91.2	8	4	AAE10663	Human amy
50	31	91.2	8	4	AAE02615	Human amy
51	31	91.2	8	5	ABB78624	Human alp
52	31	91.2	8	6	ABU09765	Anyloidog
53	31	91.2	8	6	ABR61959	Human amy
54	31	91.2	8	7	ABW00134	Beta-amy1
55	31	91.2	8	8	ADQ37385	Antifibri
56	31	91.2	8	9	ADZ08900	Human bet
57	31	91.2	8	9	AEA51423	C-Abeta 1
58	31	91.2	8	9	AEA51420	A 16-22-C
59	31	91.2	8	9	AEA62831	Immuocon
60	31	91.2	8	9	AEA62834	Immuocon
61	31	91.2	9	6	ABU79063	Aggregati
62	31	91.2	9	7	ABW00197	Peptide #
63	31	91.2	9	8	AD136003	Anyloid b
64	31	91.2	9	8	AD135849	Anyloid b
65	31	91.2	9	8	AD135871	Anyloid b
66	31	91.2	9	8	AD135903	Anyloid b
67	31	91.2	9	9	AEA51414	A 16-23-C
68	31	91.2	9	9	AEA51417	C-A 16-23
69	31	91.2	9	9	AEA62825	Immuocon
70	31	91.2	10	3	AEA62828	Immuocon
71	31	91.2	10	3	AAV79938	Beta-amy1
72	31	91.2	10	4	AAB46226	Human APP
73	31	91.2	10	4	AAB46225	Human APP
74	31	91.2	10	4	AAB46227	Human APP
75	31	91.2	10	4	AAB46227	Human APP
76	31	91.2	10	6	AAE35455	Abeta pep
77	31	91.2	10	8	ADQ37280	Vaccine a
78	31	91.2	10	8	ADQ37371	Anyloid-b
79	31	91.2	11	2	AAW32560	Anti-amy1
80	31	91.2	11	4	AAU52586	Peptide #
81	31	91.2	11	5	AAU99431	Human amy
82	31	91.2	11	5	AAE29504	Anyloid b
83	31	91.2	11	6	ABU79013	Anyloidog
84	31	91.2	11	7	ABW00147	Anyloid-b
85	31	91.2	12	6	AAE35466	Abeta pep
86	31	91.2	12	8	ADQ37289	Vaccine a
87	31	91.2	12	9	ADZ08892	Human bet
88	31	91.2	13	6	AAE35465	Abeta pep
89	31	91.2	13	6	AAE35467	Abeta pep
90	31	91.2	13	6	ADA37467	Human amy
91	31	91.2	13	8	ADJ71477	N-termina
92	31	91.2	13	8	ADQ37408	Anyloid-b
93	31	91.2	13	8	ADQ37290	Vaccine a
94	31	91.2	14	6	ADA89887	Beta-A4 s
95	31	91.2	14	8	ADJ71465	N-termina
96	31	91.2	14	8	ADJ71478	N-termina
97	31	91.2	14	9	ADZ08889	Human bet

98	31	91.2	15	2	AAW02334	Aaw02334 Beta-amyl	171	31	91.2	28	4	AAAB35594	Aab35594 Human c1o
99	31	91.2	15	2	AAW89358	Aaw89358 Beta-amyl	172	31	91.2	28	4	AAAB35592	Aab35592 Human c1o
100	31	91.2	15	2	AAW89354	Aaw89354 Beta-amyl	173	31	91.2	28	4	AAAB35593	Aab35593 Human c1o
101	31	91.2	15	5	ABG71014	Abg71014 Long form	174	31	91.2	28	4	AAAB35597	Aab35597 Human c1o
102	31	91.2	15	5	ABW05162	Abw05162 Beta amyl	175	31	91.2	28	4	AAAB35596	Aab35596 Human c1o
103	31	91.2	15	5	ABW05162	Abw05162 Beta amyl	176	31	91.2	28	4	AAAB35598	Aab35598 Human c1o
104	31	91.2	15	6	ABU79057	Abu79057 Aggregati	177	31	91.2	28	4	AAAB35598	Aab35598 Human c1o
105	31	91.2	15	6	ABU79064	Abu79064 Aggregati	178	31	91.2	28	4	AAAB36202	Aab36202 Human c1o
106	31	91.2	15	6	ABU79060	Abu79060 Aggregati	179	31	91.2	28	4	AAAB35590	Aab35590 Human c1o
107	31	91.2	15	6	ABU79055	Abu79055 Aggregati	180	31	91.2	28	4	AAAB36201	Aab36201 Human c1o
108	31	91.2	15	6	ABU79056	Abu79056 Aggregati	181	31	91.2	28	4	AAAB36201	Aab36201 Human c1o
109	31	91.2	15	6	ABU79056	Abu79056 Aggregati	182	31	91.2	28	4	AAAB91816	Aab91816 Amyloid b
110	31	91.2	15	6	ABU79062	Abu79062 Aggregati	183	31	91.2	28	4	AAAB91789	Aab91789 Amyloid b
111	31	91.2	15	7	ABW00190	Abw00190 Peptide #	184	31	91.2	28	4	AAAB91827	Aab91827 Amyloid b
112	31	91.2	15	7	ABW00198	Abw00198 Peptide #	185	31	91.2	28	4	AAAB91783	Aab91783 Amyloid b
113	31	91.2	15	7	ABW00189	Abw00189 Peptide #	186	31	91.2	28	4	AAAB91800	Aab91800 Amyloid b
114	31	91.2	15	7	ABW00191	Abw00191 Peptide #	187	31	91.2	28	4	AAAB91800	Aab91800 Amyloid b
115	31	91.2	15	7	ABW00196	Abw00196 Peptide #	188	31	91.2	28	5	AAAB91816	Aab91816 Amyloid b
116	31	91.2	15	7	ABW00194	Abw00194 Peptide #	189	31	91.2	28	5	AAAB91789	Aab91789 Amyloid b
117	31	91.2	15	7	ADK82695	Adk82695 Beta-amyl	190	31	91.2	28	5	AAAB91827	Aab91827 Amyloid b
118	31	91.2	15	7	ADK82700	Adk82700 Beta-amyl	191	31	91.2	28	5	AAAB91783	Aab91783 Amyloid b
119	31	91.2	15	8	ADJ71466	Adj71466 N-termina	192	31	91.2	28	5	AAAB91800	Aab91800 Amyloid b
120	31	91.2	15	8	ADJ71453	Adj71453 N-termina	193	31	91.2	28	5	AAAB91816	Aab91816 Amyloid b
121	31	91.2	15	8	ADJ71479	Adj71479 N-termina	194	31	91.2	28	5	AAAB91789	Aab91789 Amyloid b
122	31	91.2	15	8	ADJ71467	Adj71467 N-termina	195	31	91.2	28	5	AAAB91827	Aab91827 Amyloid b
123	31	91.2	16	5	AAE26330	Aae26330 Human bet	196	31	91.2	28	6	AAAB91783	Aab91783 Amyloid b
124	31	91.2	16	8	ADJ71454	Adj71454 N-termina	197	31	91.2	28	6	AAAB91800	Aab91800 Amyloid b
125	31	91.2	16	8	ADJ71480	Adj71480 N-termina	198	31	91.2	28	6	AAAB91816	Aab91816 Amyloid b
126	31	91.2	16	8	ADJ71441	Adj71441 N-termina	199	31	91.2	28	6	AAAB91789	Aab91789 Amyloid b
127	31	91.2	17	2	AAE54703	Aae54703 Beta-amyl	200	31	91.2	28	6	AAAB91827	Aab91827 Amyloid b
128	31	91.2	17	2	AAW18880	Aaw18880 Beta-amyl	201	31	91.2	28	6	AAAB91783	Aab91783 Amyloid b
129	31	91.2	17	4	AAE911774	Aae911774 Amyloid b	202	31	91.2	28	6	AAAB91800	Aab91800 Amyloid b
130	31	91.2	17	4	AAE911807	Aae911807 Amyloid b	203	31	91.2	28	6	AAAB91816	Aab91816 Amyloid b
131	31	91.2	17	4	AAE911807	Aae911807 Amyloid b	204	31	91.2	28	6	AAAB91789	Aab91789 Amyloid b
132	31	91.2	17	5	AAE48346	Aae48346 Beta-amyl	205	31	91.2	28	6	AAAB91827	Aab91827 Amyloid b
133	31	91.2	17	5	AAE904911	Aae904911 Human amy	206	31	91.2	28	6	AAAB91783	Aab91783 Amyloid b
134	31	91.2	17	6	ABE99611	Abes99611 Peptide d	207	31	91.2	28	6	AAAB91800	Aab91800 Amyloid b
135	31	91.2	17	8	ADG93165	Adg93165 Novel exp	208	31	91.2	28	6	AAAB91816	Aab91816 Amyloid b
136	31	91.2	17	8	ADJ65843	Adj65843 Amyloid B	209	31	91.2	28	6	AAAB91827	Aab91827 Amyloid b
137	31	91.2	17	8	ADN02827	Adn02827 Mammalian	210	31	91.2	28	6	AAAB91783	Aab91783 Amyloid b
138	31	91.2	17	8	ADN02827	Adn02827 Mammalian	211	31	91.2	28	6	AAAB91800	Aab91800 Amyloid b
139	31	91.2	18	3	AAE10963	Aae10963 Beta-amyl	212	31	91.2	28	6	AAAB91816	Aab91816 Amyloid b
140	31	91.2	19	2	AAW18882	Aaw18882 ADANS-be	213	31	91.2	28	6	AAAB91827	Aab91827 Amyloid b
141	31	91.2	19	3	AAW18881	Aaw18881 Trp-Beta-	214	31	91.2	28	6	AAAB91783	Aab91783 Amyloid b
142	31	91.2	19	3	AAW18882	Aaw18882 Trp-Beta-	215	31	91.2	28	6	AAAB91800	Aab91800 Amyloid b
143	31	91.2	19	4	AAE49097	Aae49097 Human amy	216	31	91.2	28	6	AAAB91816	Aab91816 Amyloid b
144	31	91.2	19	4	AAE49097	Aae49097 Human amy	217	31	91.2	28	6	AAAB91827	Aab91827 Amyloid b
145	31	91.2	20	3	AAE46201	Aae46201 Human APP	218	31	91.2	28	6	AAAB91783	Aab91783 Amyloid b
146	31	91.2	20	3	AAE46201	Aae46201 Human APP	219	31	91.2	28	6	AAAB91800	Aab91800 Amyloid b
147	31	91.2	20	3	AAE46201	Aae46201 Human APP	220	31	91.2	28	6	AAAB91816	Aab91816 Amyloid b
148	31	91.2	20	3	AAE46201	Aae46201 Human APP	221	31	91.2	28	6	AAAB91827	Aab91827 Amyloid b
149	31	91.2	20	3	AAE46201	Aae46201 Human APP	222	31	91.2	28	6	AAAB91783	Aab91783 Amyloid b
150	31	91.2	20	3	AAE46201	Aae46201 Human APP	223	31	91.2	28	6	AAAB91800	Aab91800 Amyloid b
151	31	91.2	20	3	AAE46201	Aae46201 Human APP	224	31	91.2	28	6	AAAB91816	Aab91816 Amyloid b
152	31	91.2	20	3	AAE46201	Aae46201 Human APP	225	31	91.2	28	6	AAAB91827	Aab91827 Amyloid b
153	31	91.2	20	3	AAE46201	Aae46201 Human APP	226	31	91.2	28	6	AAAB91783	Aab91783 Amyloid b
154	31	91.2	20	3	AAE46201	Aae46201 Human APP	227	31	91.2	28	6	AAAB91800	Aab91800 Amyloid b
155	31	91.2	20	3	AAE46201	Aae46201 Human APP	228	31	91.2	28	6	AAAB91816	Aab91816 Amyloid b
156	31	91.2	20	3	AAE46201	Aae46201 Human APP	229	31	91.2	28	6	AAAB91827	Aab91827 Amyloid b
157	31	91.2	20	3	AAE46201	Aae46201 Human APP	230	31	91.2	28	6	AAAB91783	Aab91783 Amyloid b
158	31	91.2	20	3	AAE46201	Aae46201 Human APP	231	31	91.2	28	6	AAAB91800	Aab91800 Amyloid b
159	31	91.2	20	3	AAE46201	Aae46201 Human APP	232	31	91.2	28	6	AAAB91816	Aab91816 Amyloid b
160	31	91.2	20	3	AAE46201	Aae46201 Human APP	233	31	91.2	28	6	AAAB91827	Aab91827 Amyloid b
161	31	91.2	20	3	AAE46201	Aae46201 Human APP	234	31	91.2	28	6	AAAB91783	Aab91783 Amyloid b
162	31	91.2	20	3	AAE46201	Aae46201 Human APP	235	31	91.2	28	6	AAAB91800	Aab91800 Amyloid b
163	31	91.2	20	3	AAE46201	Aae46201 Human APP	236	31	91.2	28	6	AAAB91816	Aab91816 Amyloid b
164	31	91.2	20	3	AAE46201	Aae46201 Human APP	237	31	91.2	28	6	AAAB91827	Aab91827 Amyloid b
165	31	91.2	20	3	AAE46201	Aae46201 Human APP	238	31	91.2	28	6	AAAB91783	Aab91783 Amyloid b
166	31	91.2	20	3	AAE46201	Aae46201 Human APP	239	31	91.2	28	6	AAAB91800	Aab91800 Amyloid b
167	31	91.2	20	3	AAE46201	Aae46201 Human APP	240	31	91.2	28	6	AAAB91816	Aab91816 Amyloid b
168	31	91.2	20	3	AAE46201	Aae46201 Human APP	241	31	91.2	28	6	AAAB91827	Aab91827 Amyloid b
169	31	91.2	20	3	AAE46201	Aae46201 Human APP	242	31	91.2	28	6	AAAB91783	Aab91783 Amyloid b
170	31	91.2	20	3	AAE46201	Aae46201 Human APP	243	31	91.2	28	6	AAAB91800	Aab91800 Amyloid b

244	31	91.2	35	5	ABG71016	Abg71016	Long form
245	31	91.2	35	5	ABB05164	ABB05164	EVVVHHHQ
246	31	91.2	35	6	AAE35430	AAE35430	ABeta pep
247	31	91.2	35	8	ADJ64067	ADJ64067	Human bet
248	31	91.2	35	8	ADG37254	ADG37254	Vaccine a
249	31	91.2	36	5	AAW81471	AAW81471	Synthetic
250	31	91.2	36	5	AAU11776	AAU11776	Synthetic
251	31	91.2	36	5	AAU11771	AAU11771	Synthetic
252	31	91.2	36	6	ABR42779	ABr42779	Amyloid b
253	31	91.2	36	6	ABR42774	ABr42774	Amyloid b
254	31	91.2	36	8	ADM97743	Adm97743	Amyloid b
255	31	91.2	36	8	ADP73823	Adp73823	Loop insee
256	31	91.2	37	8	ADM97744	Adm97744	Amyloid b
257	31	91.2	38	2	AAE60362	Aar60362	Beta-amyl
258	31	91.2	38	2	AAW52722	AAw52722	Human cac
259	31	91.2	38	4	AAE91826	AAe91826	Amyloid b
260	31	91.2	38	4	AAE91799	AAe91799	Amyloid b
261	31	91.2	38	8	ADU24436	Adu24436	Novel glu
262	31	91.2	38	8	ADU24441	Adu24441	Novel glu
263	31	91.2	38	8	ADU46715	Adu46715	Gln3 amyl
264	31	91.2	38	8	ADU46710	Adu46710	Amyloid b
265	31	91.2	38	9	ADY81762	Ady81762	Human bet
266	31	91.2	38	9	ADZ71362	Adz71362	Human bet
267	31	91.2	38	9	ADZ71367	Adz71367	Human bet
268	31	91.2	38	9	AEA35400	Aea35400	Novel QC
269	31	91.2	38	9	AEA35395	Aea35395	Novel QC
270	31	91.2	38	9	AE925868	Aeb92586	Glutaminy
271	31	91.2	38	9	AE925733	Aeb92573	Glutaminy
272	31	91.2	39	2	AAE60363	Aar60363	Beta-amyl
273	31	91.2	39	2	AAW81472	AAw81472	Synthetic
274	31	91.2	39	2	AAW25134	AAw25134	Human amyl
275	31	91.2	39	3	AAW52132	AAw52132	Human Rec
276	31	91.2	39	3	ABU08509	Abu08509	Human amyl
277	31	91.2	39	6	ABP96148	Abp96148	Human Abe
278	31	91.2	39	9	ADY81763	Ady81763	Human bet
279	31	91.2	40	2	AAE33191	AAe33191	Beta-amyl
280	31	91.2	40	2	AAE60364	Aar60364	Beta-amyl
281	31	91.2	40	2	ADD11651	Add11651	Human bet
282	31	91.2	40	2	AAW23335	AAw23335	Amyloid b
283	31	91.2	40	2	AAW37507	AAw37507	Amyloid b
284	31	91.2	40	2	AAW47226	AAw47226	Beta-amyl
285	31	91.2	40	2	AAE14099	AAe14099	Human bet
286	31	91.2	40	2	AAE39804	AAe39804	Beta-amyl
287	31	91.2	40	2	AAW99584	AAw99584	Wild type
288	31	91.2	40	2	AAW81473	AAw81473	Synthetic
289	31	91.2	40	2	AAE39339	AAe39339	Beta-amyl
290	31	91.2	40	2	AAE25135	AAe25135	Human amyl
291	31	91.2	40	2	AAW52723	AAw52723	Human cac
292	31	91.2	40	2	AAW52723	AAw52723	Partial s
293	31	91.2	40	4	AAE84426	AAe84426	Partial s
294	31	91.2	40	4	AAE84429	AAe84429	Partial s
295	31	91.2	40	4	AAE91786	AAe91786	Amyloid b
296	31	91.2	40	4	AAE91813	AAe91813	Amyloid b
297	31	91.2	40	4	AAE91819	AAe91819	Amyloid b
298	31	91.2	40	4	AAE91780	AAe91780	Amyloid b
299	31	91.2	40	4	AAE91792	AAe91792	Amyloid b
300	31	91.2	40	4	AA		

ALIGNMENTS

RESULT 1	
AA84892	
ID	AA84892 standard; peptide; 7 AA.
XX	
XX	AA84892;
XX	
DT	02-MAR-2001 (first entry)
XX	
DE	Antifibrillogenic peptide #19.
XX	
KW	Nootropic; neuroprotective; anti-

KW	cytoprotection; amyloid deposit degradation; amyloidosis disorder;
KX	Alzheimer's disease.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 7
PT	/note= "C-terminal amide"
XX	
XX	WO200068263-A2.
XX	
PD	16-NOV-2000.
XX	
PF	04-MAY-2000; 2000WO-CA000515.
XX	
PR	05-MAY-1999; 99US-0132592P.
XX	(NEUR-) NEUROCHEM INC.
PA	
XX	
PI	Challifour R, Gervais F, Gupta A;
XX	
DR	WPI; 2001-031852/04.
XX	
PT	Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
PT	cytoprotection for treating amyloidosis disorders, comprises a peptide,
PT	its isomer or peptidomimetic.
XX	
PS	Claim 7; Page 25; 46pp; English.
XX	
CC	Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
CC	for inhibiting amyloidosis and/or for cytoprotection. The peptides of
CC	AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
CC	useful for treating amyloidosis disorders such as Alzheimer's disease.
CC	Peptides AAB48474-B48496 were identified from the glycosaminoglycan
CC	binding region and the prot-prot interaction region of the human amyloid
CC	protein
XX	
SQ	Sequence 7 AA;
	Query Match 100.0%; Score 34; DB 4; Length 7;
	Best Local Similarity 100.0%; Pred No. 2e+06;
	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 KLVFFAQ 7
Dd	1 KLVFFAQ 7
RESULT 2	
AAB48491	ID AAB48491 standard; peptide; 7 AA.
XX	
AC	AAB48491;
XX	
DT	02-MAR-2001 (first entry)
XX	
DE	Antifibrillogenic peptide #18.
XX	
KW	Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
KW	cytoprotection; amyloid deposit degradation; amyloidosis disorder;
KW	Alzheimer's disease.
XX	
OS	Homo sapiens.
XX	
FN	WO200068263-A2.
XX	
PD	16-NOV-2000.
XX	
PF	04-MAY-2000; 2000WO-CA000515.
XX	
PR	05-MAY-1999; 99US-0132592P.
XX	(NEUR-) NEUROCHEM INC.
PA	

XX Chalifour R, Gervais F, Gupta A;
 XX WPI; 2001-031852/04.
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 XX Claim 7; Page 25; 46pp; English.
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 XX Sequence 7 AA;
 Query Match 100.0%; Score 34; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFAQ 7
 Db 1 KLVFFAQ 7
 AAB82640
 ID AAB82640 standard; peptide; 7 AA.
 XX AAB82640;
 XX 02-OCT-2001 (first entry)
 XX All-D peptide used in Alzheimer's disease vaccine.
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 1..7 /note= "all D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT WO200139796-A2.
 XX 07-JUN-2001.
 XX 29-NOV-2000; 2000WO-CA001413.
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 PA Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.
 XX Disclosure; Page 11; 31pp; English.

CC The present sequence is that of an all-D peptide suitable for use in
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX Sequence 7 AA;
 Query Match 100.0%; Score 34; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFAQ 7
 Db 1 KLVFFAQ 7
 AAB82639
 ID AAB82639 standard; peptide; 7 AA.
 XX AAB82639;
 XX 02-OCT-2001 (first entry)
 XX All-D peptide used in Alzheimer's disease vaccine.
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 1..7 /note= "all D-form residues"
 FT WO200139796-A2.
 XX 07-JUN-2001.
 XX 29-NOV-2000; 2000WO-CA001413.
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 PA Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,

PT which elicits production of antibodies to prevent fibrillogenesis and
 XX associated cellular toxicity.

XX Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use in
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see A882622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self',
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in A882623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||
 Db 1 KLVFFPAQ 7

RESULT 5
 AAU96827
 ID AAU96827 standard; peptide; 7 AA.

XX AAU96827;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #17.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1. 7 /note= "Preferably D-form residue"

XX WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

PR 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.
 XX (NEUR-) NEUROCHEM INC.
 XX Gervais F, Kong X, Chalifour R, Migneault D;
 XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 PT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 22; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A-t-(A-l)n-k-z-A-l-a-b (I) where z = 0-1;
 CC A-t = an amyloid targeting moiety; A-l-n-k = a linker moiety; and A-l-a-b
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (I) to the patient, and ultrasound imaging (I) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||

Db 1 KLVFFPAQ 7

RESULT 6
 AAU96828
 ID AAU96828 standard; peptide; 7 AA.

XX AAU96828;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #18.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1. 7

```

FT FT /note= "Preferably D-form residue"
FT Modified-site 7
XX /note= "Gln is amidated"
XX
PN WO200207781-A2.
XX
PD 31-JAN-2002.
XX
XX 25-JUL-2001; 2001WO-CA001071.
XX PF
XX 25-JUL-2000; 2000US-0220808P.
XX PR
XX 24-JUL-2001; 2001US-00915092.
XX PA
XX (NEUR-) NEUROCHEM INC.
XX PI
XX Gervais F, Kong X, Chalifour R, Migneault D;
XX WPI; 2002-371447/40.
XX DR
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
XX plaques and/or for the treatment of amyloidosis disorders.
XX PS
XX Claim 49; Page 22; 57pp; English.
XX
XX The invention relates to an amyloid-targeting imaging agent comprising an
XX amyloid targeting moiety, a linker moiety and a labelling moiety. The
XX agent is of general formula A1-L1-N1-K1-Z-A1-L1-a1-b1 (I) where z = 0 - 1;
XX A1 = an amyloid targeting moiety; L1-N1-K1 = a linker moiety; and A1-L1-a1-b1
XX = a labelling moiety. Also included are imaging amyloid deposition or
XX diagnosing an amyloid-related condition in a patient involving
XX administering (I) to the patient, and ultrasound imaging (I) in the
XX patient to determine the presence of amyloid or amyloid-related condition
XX ; and a kit for preparing a radiopharmaceutical preparation comprising
XX (I), a reducing agent, a buffering agent, a transchelating agent, and
XX instructions for the preparation and use of the radiopharmaceutical in
XX the imaging of amyloid or an amyloid-related condition. The agents are
XX used for imaging amyloid deposition and for diagnosing an amyloid related
XX condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
XX cerebral amyloidosis (transmissible virus dementia), familial CJD,
XX scrapie, transmissible mink encephalopathy, bovine spongiform
XX encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
XX primary amyloidosis, feline spongiform encephalopathy, non-transmissible
XX cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
XX dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
XX amyloid angiopathy. The agents are capable of crossing the blood-brain
XX barrier and are capable of binding specifically to amyloid plaques. The
XX present sequence is a peptide forming the amyloid targeting moiety of the
XX agent of the invention
XX
XX Query Match 100.0%; Score 34; DB 5; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KLVFFPAQ 7
XX Db 1 KLVFFPAQ 7
XX
XX RESULT 7
XX AAU11665
XX ID AAU11665 standard; peptide; 7 AA.
XX AC AAU11665;
XX DT 09-APR-2002 (first entry)
XX DE Peptide #18, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 7 /note= "C-terminal amide"
XX FT
XX XX WO200185093-A2.
XX PN
XX 15-NOV-2001.
XX PD
XX 22-DEC-2000; 2000WO-IB002078.
XX PF
XX 23-DEC-1999; 99US-0171877P.
XX PR
XX (NEUR-) NEUROCHEM INC.
XX PA
XX Green AM, Gervais F;
XX PI WPI; 2002-075222/10.
XX DR
XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
XX PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
XX PT inhibitor.
XX PS
XX Disclosure; Page 10; 68pp; English.
XX
XX The present invention relates to a new method of inhibiting cerebral
XX amyloid angiopathy. The new method of the invention involves contacting a
XX blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
XX can be used for treating disease states characterised by cerebral amyloid
XX angiopathy, particularly Alzheimer's disease, hereditary cerebral
XX haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
XX The present sequence represents one of a group of peptides (AAU11648-
XX AAU11669, AAU11910 & AAU11911) that were used in the invention as a
XX carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
XX was used in the invention to treat a disease state characterised by
XX cerebral amyloid angiopathy (CAA)
XX
XX Sequence 7 AA;
XX
XX Query Match 100.0%; Score 34; DB 5; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KLVFFPAQ 7
XX Db 1 KLVFFPAQ 7
XX
XX RESULT 8
XX AAU11666
XX ID AAU11666 standard; peptide; 7 AA.
XX AC AAU11666;
XX DT 09-APR-2002 (first entry)
XX DE Peptide #19, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 7 /note= "C-terminal amide"
XX FT
XX XX WO200185093-A2.
XX PN
XX 15-NOV-2001.
XX PD
XX 22-DEC-2000; 2000WO-IB002078.
XX PF
XX 23-DEC-1999; 99US-0171877P.
XX PR

```


XX PA (NEUR-) NEUROCHEM INC.
 XX PI Green AM, Gervais F;
 XX DR WPI; 2002-075222/10.
 XX PT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.
 XX XX
 XX PS Disclosure; Page 10; 68pp; English.
 XX CC The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 34; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVPFFAQ 7
 |||||
 Db 1 KLVPFFAQ 7
 RESULT 9
 ADQ37330
 ID ADQ37330 standard; peptide; 7 AA.
 AC ADQ37330;
 XX 07-OCT-2004 (first entry)
 XX Antifibrillogenic amyloidosis inhibiting peptide.
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiac; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX OS Synthetic.
 XX WO2004058239-A1.
 XX 15-JUL-2004.
 XX 24-DEC-2003; 2003WO-CA002021.
 XX 24-DEC-2002; 2002US-0436379P.
 XX 23-JUN-2003; 2003US-0482214P.
 XX

PA (NEUR-) NEUROCHEM INT LTD.
 XX Gervais F, Bellini F;
 XX WPI; 2004-543342/52.
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX PS Disclosure; Page 70; 143pp; English.
 XX CC The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiac, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.
 XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 34; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVPFFAQ 7
 |||||
 Db 1 KLVPFFAQ 7
 RESULT 10
 ADQ37331
 ID ADQ37331 standard; peptide; 7 AA.
 XX AC ADQ37331;
 XX 07-OCT-2004 (first entry)
 XX Antifibrillogenic amyloidosis inhibiting peptide.
 KW amyloid-beta; amyloid-beta related disease;
 KW

amyloid-beta fibril formation; immune response; nootropic;
 neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 cardiant; antidepressant; endocrine; hypnotic;
 amyloid-beta fibril formation modulator; immune system modulator;
 Alzheimer's disease; mild cognitive impairment;
 mild-to-moderate cognitive impairment; vascular
 cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 senile dementia; Down's syndrome; inclusion body myositis;
 age-related macular degeneration; hypothyroidism;
 cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 behavioural dysfunction; neurological condition; psychological condition;
 vaccine antigen.
 Synthetic.
 OS
 XX
 XX
 XX
 FT Key Location/Qualifiers
 FT Modified-site 7
 FT /note= "amidated"
 XX
 XX
 PN WO2004058239-A1.
 XX
 PD 15-JUL-2004.
 XX
 XX 24-DEC-2003; 2003WO-CA002021.
 XX
 PF 24-DEC-2002; 2002US-0436379P.
 PR 23-JUN-2003; 2003US-0482214P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 PA
 PI Gervais F, Bellini F;
 XX
 XX WPI; 2004-543342/52.
 DR
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 XX Disclosure; Page 70; 143pp; English.
 PS
 XX
 XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep

CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 34; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFPAQ 7
 Db 1 KLVFFPAQ 7
 RESULT 11
 ADV37938
 ID ADV37938 standard; peptide; 7 AA.
 XX
 AC ADV37938;
 XX
 DT 19-MAY-2005 (first entry)
 XX
 DE Amyloid-targeting peptide, SEQ ID NO:18, for use in imaging agent.
 XX
 KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
 KW transmissible spongiform encephalopathy; scrapie; BSE;
 KW Alheimers disease; neurological disease; amyloidosis;
 KW non-insulin dependent diabetes; metabolic disorder.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 7 /note= "C-terminal amide"
 FT
 XX
 PN US2005048000-A1.
 XX
 PD 03-MAR-2005.
 XX
 XX 03-DEC-2003; 2003US-00728028.
 XX
 PR 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.
 PR 29-JAN-2003; 2003US-0443291P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 PA
 PI Gervais F, Kong X, Chalifour R, Migneault D;
 XX
 XX WPI; 2005-212201/22.
 XX
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
 PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.
 XX
 XX Disclosure; SEQ ID NO 18; 34pp; English.
 XX
 XX The invention relates to an amyloid-targeting imaging agent. The imaging
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
 CC a labeling moiety via a linking moiety, and is preferably able to cross
 CC the blood-brain barrier. The invention also relates to a kit for
 CC preparing a radiopharmaceutical preparation from the imaging agent of the
 CC invention, a method for imaging amyloid deposition in a patient and a
 CC method for diagnosing an amyloid-related condition in a patient. The
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
 CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
 CC transmissible cerebral amyloidosis (also known as transmissible virus
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,

CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
 CC mediated diseases, dialysis-related amyloidosis, light chain-related
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
 CC patient. The agent does not exhibit excessive toxicity or irritation,
 CC does not induce an allergic response, and permits an earlier diagnosis of
 CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
 |||||
 Db 1 KLVFFAQ 7

RESULT 12

ADY37937
 ID ADY37937 standard; peptide; 7 AA.

XX AC ADY37937;

XX DT 19-MAY-2005 (first entry)

XX DE Amyloid-targeting peptide, SEQ ID NO:17, for use in imaging agent.

XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
 KW transmissible spongiform encephalopathy; scrapie; BSE;
 KW Alzheimers disease; neurological disease; amyloidosis;
 KW non-insulin dependent diabetes; metabolic disorder.

XX OS Synthetic.

XX PN US2005048000-A1.

XX PD 03-MAR-2005.

XX PF 03-DEC-2003; 2003US-00728028.

XX PR 25-JUL-2000; 2000US-0220808P.

XX PR 24-JUL-2001; 2001US-00915092.

XX PR 29-JAN-2003; 2003US-0443291P.

XX PA (NEUR-) NEUROCHEM INT LTD.

XX PI Gervais F, Kong X, Chalifour R, Migneault D;

XX DR WPI; 2005-212201/22.

XX PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
 PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.

XX PS Disclosure; SEQ ID NO 17; 34pp; English.

XX CC The invention relates to an amyloid-targeting imaging agent. The imaging
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
 CC a labeling moiety via a linking moiety, and is preferably able to cross
 CC the blood-brain barrier. The invention also relates to a kit for
 CC preparing a radiopharmaceutical preparation from the imaging agent of the
 CC invention, a method for imaging amyloid deposition in a patient and a
 CC method for diagnosing an amyloid-related condition in a patient. The
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
 CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
 CC transmissible cerebral amyloidosis (also known as transmissible virus
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,

CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
 CC mediated diseases, dialysis-related amyloidosis, light chain-related
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
 CC patient. The agent does not exhibit excessive toxicity or irritation,
 CC does not induce an allergic response, and permits an earlier diagnosis of
 CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
 |||||
 Db 1 KLVFFAQ 7

RESULT 13

AAR45239
 ID AAR45239 standard; peptide; 9 AA.

XX AC AAR45239;

XX DT 20-JUN-1994 (first entry)

XX DE Mutant amyloid precursor protein fragment.

XX KW Amyloid precursor protein; APP; beta amyloid protein; BAP; detection;
 KW Alzheimer's disease; Down's syndrome.

XX OS Homo sapiens.

XX PN AU9338358-A.

XX PD 04-NOV-1993.

XX PF 03-MAY-1993; 93AU-00038358.

XX PR 01-MAY-1992; 92US-00877675.

XX PA (AMCY) AMERICAN CYANAMID CO.

XX PI Vitek MP, Jacobsen JS;

XX DR WPI; 1993-406194/51.

XX DR N-PSDB; AAQ54267.

XX PT New mutant forms of amyloid precursor protein - for detecting cpds. that
 PT modify activity of enzymes involved in precursor cleavage, also new
 PT nucleic acid encoding them.

XX PS Disclosure; Page 35; 66pp; English.

XX CC Recombinant polypeptides produced using the coding sequences of mutant
 CC forms of amyloid precursor proteins comprising from the 5' to the 3' end
 CC a sequence encoding a marker and either (1) a sequence encoding the N-
 CC terminus of an amyloid precursor protein (APP) up to, but not including,
 CC the nucleotides encoding the beta amyloid protein (BAP) domain or (2) the
 CC BAP domain; or the two ligated together, can be used to detect drugs or
 CC compounds that inhibit/augment the activity of proteolytic enzymes which
 CC cleave APP to generate BAP fragments (deposition of which occurs in
 CC patients with Alzheimers disease and Down's syndrome). This is a fragment
 CC of amyloid precursor protein containing a mutation which is associated
 CC with diseases involving BAP deposition

XX Sequence 9 AA;

Query Match 100.0%; Score 34; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||
 Db 2 KLVFFPAQ 8

RESULT 14
 AAB82641
 ID AAB82641 standard; peptide; 10 AA.
 XX AAB82641;
 AC
 XX 02-OCT-2001 (first entry)
 XX
 XX All-D peptide used in Alzheimer's disease vaccine.
 XX
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 1..10 /note= "all D-form residues"
 FT
 XX WO2001139796-A2.
 XX
 XX 07-JUN-2001.
 XX
 XX 29-NOV-2000; 2000WO-CA001413.
 XX
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX
 XX (NEUR-) NEUROCHEM INC.
 XX
 XX Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 XX
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 FT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 FT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.
 PT
 XX Disclosure; Page 11; 31pp; English.
 XX

CC The present sequence is that of an all-D peptide suitable for use in
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self',
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC Creutzfeldt-Jakob disease, scrapie, bovine spongiform encephalitis,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.

CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX Sequence 10 AA;
 Query Match 100.0%; Score 34; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||
 Db 4 KLVFFPAQ 10

RESULT 15
 AAU96829
 ID AAU96829 standard; peptide; 10 AA.
 XX
 AC AAU96829;
 XX
 XX 30-JUL-2002 (first entry)
 XX
 XX Amyloid targeting peptide #19.
 XX
 XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 1..10 /note= "Preferably D-form residue"
 FT
 XX WO200207781-A2.
 XX
 XX 31-JAN-2002.
 XX
 XX 25-JUL-2001; 2001WO-CA001071.
 PF
 XX 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.
 XX
 XX (NEUR-) NEUROCHEM INC.
 XX
 XX Gervais F, Kong X, Chalifour R, Migneault D;
 XX WPI; 2002-371447/40.
 XX
 XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 PT plaques and/or for the treatment of amyloidosis disorders.
 PT
 XX Claim 49; Page 22; 57pp; English.
 XX

CC The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A_t-(A_l)_n_k-z-A_l_a_b (1) where z = 0 - 1;
 CC A_t = an amyloid targeting moiety; A_l_n_k = a linker moiety; and A_l_a_b
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (1) to the patient, and ultrasound imaging (1) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (1), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible

CC cerebral amyloidoses (transmissible virus dementias), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC dialysis-related amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC cerebral amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiodysplasia. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 34; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
 |||||
 Db 4 KLVFFAQ 10

RESULT 16
 ADY37939
 ID ADY37939 standard; peptide; 10 AA.
 XX
 AC ADY37939;
 XX
 DT 19-MAY-2005 (first entry)
 XX
 DE Amyloid-targeting peptide, SEQ ID NO:19, for use in imaging agent.

XX
 KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
 KW transmissible spongiform encephalopathy; scrapie; BSE;
 KW Alzheimer's disease; neurological disease; amyloidosis;
 KW non-insulin dependent diabetes; metabolic disorder.

XX Synthetic.

XX US2005048000-A1.

XX 03-MAR-2005.

XX 03-DEC-2003; 2003US-00728028.

XX 25-JUL-2000; 2000US-0220808P.

XX 24-JUL-2001; 2001US-00915092.

XX 29-JAN-2003; 2003US-0443231P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2005-212201/22.

XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
 related condition, e.g. Creutzfeldt-Jakob disease, bovine spongiform
 encephalopathy, primary amyloidosis or Alzheimer's disease.

XX Disclosure; SEQ ID NO 19; 34pp; English.

XX The invention relates to an amyloid-targeting imaging agent. The imaging
 agent comprises an amyloid targeting moiety (such as a peptide) joined to
 a labeling moiety via a linking moiety, and is preferably able to cross
 the blood-brain barrier. The invention also relates to a kit for
 preparing a radiopharmaceutical preparation from the imaging agent of the
 invention, a method for imaging amyloid deposition in a patient and a
 method for diagnosing an amyloid-related condition in a patient. The
 amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
 related conditions such as Creutzfeldt-Jakob disease (CJD), Kuru,
 transmissible cerebral amyloidosis (also known as transmissible virus
 dementias), familial CJD, scrapie, transmissible mink encephalopathy,
 bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,

CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
 mediated diseases, dialysis-related amyloidosis, light chain-related
 CC amyloidosis, cerebral amyloid angiodysplasia or Alzheimer's disease in a
 CC patient. The agent does not exhibit excessive toxicity or irritation,
 CC does not induce an allergic response, and permits an earlier diagnosis of
 CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 34; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
 |||||
 Db 4 KLVFFAQ 10

RESULT 17
 ADX82697
 ID ADX82697 standard; peptide; 15 AA.
 XX
 AC ADX82697;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Beta-amyloid peptide #3 recognised by antibody to treat senile dementia.

XX fusion antibody; senile dementia; beta-amyloid peptide; fibre;
 KW immunocell.

XX Homo sapiens.

XX CN1396183-A.

XX 12-FEB-2003.

XX 13-JUL-2001; 2001CN-00120278.

XX 13-JUL-2001; 2001CN-00120278.

XX (ZHAN/) ZHANG X.

XX Zhang X, Zhang J;

XX WPI; 2003-442233/42.

XX Human fusion antibody for reducing cerebral amyloid fibers associated
 with senile dementia.

XX Claim 1; Page 2; 26pp; Chinese.

XX The invention relates to a human fusion antibody for preventing and
 treating senile dementia. The antibody recognises and binds the beta-
 amyloid peptide and the fibres generated by it. The human antibody Pc
 segment recognized by human immunocells are sequentially contained by its
 terminals from N to C. The fusion gene coding for the antibody is also
 disclosed. This sequence represents a beta-amyloid peptide recognised by
 the antibody.

XX Sequence 15 AA;

Query Match 100.0%; Score 34; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.97;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
 |||||
 Db 1 KLVFFAQ 7

```

RESULT 18
AAW01414
ID AAW01414 standard; protein; 28 AA.
AC AAW01414;
XX
XX 20-JAN-1997 (first entry)
XX
XX Beta/A4-amyloid peptide residues 1-28 Dutch.
XX
XX Beta/A4-amyloid peptide; tissue plasminogen activator; Dutch;
KW Alzheimer's disease; stimulation; investigation; pathogenesis;
KW hereditary cerebral haemorrhage with amyloidosis-Dutch type; control;
KW cerebral amyloid angiopathy; cerebral; haemorrhage; haemorrhage.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 22
FT /notes= "wild type Glu substd. with Gln"
XX
XX W09615799-Al.
XX
XX 30-MAY-1996.
XX
XX 22-NOV-1995; 95WO-US015007.
XX
XX 22-NOV-1994; 94US-00347144.
XX
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Anderson S;
XX
XX WPI; 1996-268332/27.
XX
XX Use of agents which bind beta-amyloid peptide - for diagnosis, prevention
PT and treatment of vascular damage caused by amyloid deposits, partic. in
PT haemorrhaging and Alzheimer's disease.
XX
XX Example 1; Fig 1; 52pp; English.
XX
XX To investigate the effects of beta-amyloid peptide (BAP) on tissue
CC plasminogen activator (t-PA) 3 synthetic peptides were used. One peptide
CC contained 42 amino acids and corresp. to the full length BAP (AAR95248).
CC The other 2 peptides (AAR95249 and 50) contained the 28 N-terminal
CC residues of the BAP found in Alzheimer's disease and hereditary cerebral
CC haemorrhage with amyloidosis-Dutch type (HCHWA-D), respectively. In an
CC assay to determine the effect of the peptides on t-PA activation, each
CC peptide (AAR95248, 49 and 50) gave 1st order rate constant of activation
CC (k(app)) values of 13.4, 13.9 and 14.5, respectively, compared to 1.7 and
CC 7.8 for null and fibrinogen controls. The results demonstrate that the
CC BAP are able to stimulate t-PA activity in vitro, which is significant in
CC that it provides a means for investigating and controlling the
CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid
CC angiopathy related cerebral haemorrhage
XX
XX Sequence 28 AA;
XX
XX Query Match 100.0%; Score 34; DB 2; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 1.8;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KLVFFPAQ 7
XX |||||
XX Db 16 KLVFFPAQ 22
XX
XX RESULT 19
XX AAB35600
XX ID AAB35600 standard; peptide; 28 AA.
XX

```

```

AC AAB35600;
XX
XX 15-FEB-2001 (first entry)
XX
XX Human clone E22Q B(1-28) amyloid B peptide.
XX
XX Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KW acute cardiovascular disease; therapy.
XX
XX Homo sapiens.
XX
XX US6136548-A.
XX
XX 24-OCT-2000.
XX
XX 02-SEP-1999; 99US-00388890.
XX
XX 22-NOV-1994; 94US-00347144.
XX 22-NOV-1995; 95WO-US015007.
XX 26-JUL-1996; 96US-00686959.
XX
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Anderson S;
XX
XX WPI; 2001-030939/04.
XX
XX Identifying mutant tissue-type plasminogen activator (t-PA) for improving
PT thrombolytic therapy or treating vascular hemorrhaging, by determining
PT whether t-PA binds to fibrin but not to a beta amyloid peptide.
XX
XX Example 3; Col 26; 23pp; English.
XX
XX The present invention describes a method for identifying mutant
CC derivatives of tissue-type plasminogen activator, which involves
CC determining whether or not they bind to beta-amyloid peptides and fibrin.
CC Mutants will only bind to the latter. These mutants are useful in
CC improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC and in the treatment of acute cardiovascular disease, which may be caused
CC by myocardial infarction, stroke, ischaemia and pulmonary embolism
XX
XX Sequence 28 AA;
XX
XX Query Match 100.0%; Score 34; DB 4; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 1.8;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KLVFFPAQ 7
XX |||||
XX Db 16 KLVFFPAQ 22
XX
XX RESULT 20
XX ABG72244
XX ID ABG72244 standard; peptide; 28 AA.
XX
XX AC ABG72244;
XX
XX 27-FEB-2003 (first entry)
XX
XX Mutant E22Q of human beta(1-28) peptide of amyloid beta peptide.
XX
XX Plasmin-mediated proteolysis; beta-amyloid peptide; brain cell;
KW brain tissue; tissue plasminogen activator; t-PA; Alzheimer's disease;
KW vascular haemorrhaging; thrombolytic therapy; neurological disorder;
KW nerve cell; neuroprotective; nootropic; beta(1-28) peptide;
KW amyloid beta peptide; mutant; mutein.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 22
FT

```


PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX WPI; 2001-112059/12.
 XX
 CC Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 514; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 XX Sequence 35 AA;
 SQ
 Query Match 100.0%; Score 34; DB 4; Length 35;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFPAQ 7
 Db 11 KLVFFPAQ 17
 |||||
 |||||
 RESULT 23
 AAW47232
 ID AAW47232 standard; peptide; 40 AA.
 XX
 AC AAW47232;
 XX
 XX 22-MAY-1998 (first entry)
 DT
 DE Beta-amyloid peptide fragment.
 XX
 XX Screening assay; beta-amyloid peptide; treatment; amyloidosis disease;
 KW Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 XX US5721106-A.
 PN
 XX 24-FEB-1998.
 PD
 XX 12-SEP-1994; 94US-00304585.
 PF
 XX 13-AUG-1991; 91US-00744767.
 PR
 XX (MINU) UNIV MINNESOTA.
 PA (HARD) HARVARD COLLEGE.
 XX
 XX Mantyh PW, Maggio JE;
 PI
 XX WPI; 1998-168404/15.
 DR
 XX New in vitro screening assay for Alzheimer's disease drugs - comprises
 PT assessing binding of labelled beta-amyloid peptide to silk sample.
 PT
 XX Disclosure; Col 31-32; 36pp; English.
 PS
 XX

CC The present sequence was used in the development of a novel in vitro
 CC screening assay for agents capable of affecting the deposition of beta-
 CC amyloid peptide (BAP) on tissue. The method comprises contacting a silk
 CC sample with labelled BAP, optionally in the presence of a test agent,
 CC detecting the amount of label bound to the silk and assessing the effect
 CC of the agent on the deposition of BAP. Agents that inhibit binding of BAP
 CC to silk are potentially useful for treating amyloidosis diseases,
 CC especially Alzheimer's disease
 XX
 XX Sequence 40 AA;
 SQ
 Query Match 100.0%; Score 34; DB 2; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFPAQ 7
 Db 16 KLVFFPAQ 22
 |||||
 |||||
 RESULT 24
 ABP97887
 ID ABP97887 standard; peptide; 42 AA.
 XX
 AC ABP97887;
 XX
 XX 03-JUN-2003 (first entry)
 DT
 XX Amino acid sequence of human 22Q-A-beta1-42 (Dutch) mutant peptide.
 DE
 XX Amyloid precursor protein; A-beta peptide; angiogenesis; psoriasis;
 KW angiogenesis-mediated disease; cancer; arthritis; atherosclerosis;
 KW macular degeneration; diabetic retinopathy; Alzheimer's disease;
 KW cerebral amyloid angiopathy; cerebrovascular disease; brain injury.
 XX
 OS Homo sapiens.
 XX
 XX WO2003014329-A2.
 PN
 XX 20-FEB-2003.
 PD
 XX 12-AUG-2002; 2002WO-US027040.
 PF
 XX 10-AUG-2001; 2001US-0311656P.
 PR (USF-) UNIV SOUTH FLORIDA.
 PA
 XX Paris D, Mullan M;
 PI
 XX WPI; 2003-256578/25.
 DR
 XX Inhibiting angiogenesis, and preventing or alleviating the symptoms of an
 XX angiogenesis-mediated disease, e.g. cancer, arthritis or atherosclerosis,
 XX comprises increasing in vivo concentrations of an A-beta peptide in the
 XX patient.
 PT
 XX Claim 3; Page 42; 85pp; English.
 PS
 XX The present sequence represents a peptide derived from amyloid precursor
 CC protein, and designated 22Q-A-beta1-42 (Dutch) mutant peptide. A-beta
 CC peptides are used in the method of the invention. The specification
 CC describes a method of inhibiting angiogenesis, and preventing or
 CC alleviating the symptoms of an angiogenesis-mediated disease in a
 CC patient. The method comprises increasing in vivo concentrations of an A-
 CC beta peptide within the patient. The A-beta peptides are useful for
 CC preventing or alleviating angiogenesis-mediated diseases such as cancer,
 CC arthritis, atherosclerosis, psoriasis, macular degeneration and diabetic
 CC retinopathy. A-beta peptide antagonists may be used to treat Alzheimer's
 CC disease, cerebral amyloid angiopathy, cerebrovascular disease in the
 CC presence of Alzheimer's disease, or traumatic brain injury
 XX
 XX Sequence 42 AA;
 SQ

Query Match 100.0%; Score 34; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
DB 16 KLVFFPAQ 22

RESULT 25

ADV42360
ID ADV42360 standard; peptide; 42 AA.

XX AC ADV42360;

XX DT 24-FEB-2005 (first entry)

XX DE Human amyloid-beta peptide 42 (Dutch mutation), seq id 1.

XX KW Neuroprotective; gene therapy; transgenic animal; beta-amyloid;
KW amyloid-beta 42 Dutch; neurodegenerative disease.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 22 /note= "wild-type Glu replaced by Gln"

XX PN US2004250302-A1.

XX XX

XX PD 09-DEC-2004.

XX PF 25-MAY-2004; 2004US-00853593.

XX PR 21-OCT-2003; 2003US-0512972P.

XX PA (ENVI-) ENVIVO PHARM INC.

XX PI Lowe DA, Koenig G, Cummings CJ;

XX DR WPI; 2005-020614/02.

XX DR N-PSDB; ADV42361.

XX PT New transgenic fly expressing the Dutch mutation of the amyloid-beta
PT peptide 42, useful in identifying an agent for treating neurodegenerative
PT disease, e.g. Alzheimer's disease.

XX PS Claim 1; SEQ ID NO 1; 25pp; English.

XX CC The invention relates to a transgenic fly having a genome comprising a
CC DNA sequence encoding a polypeptide having the amyloid-beta peptide 42
CC containing the Dutch mutation of the 42-amino acid sequence. Further
CC disclosed is a method for identifying an agent active in
CC neurodegenerative disease. The transgenic fly is a transgenic Drosophila.
CC The transgenic fly comprises embryonic, larval, pupal or adult stage. The
CC DNA sequence is operatively linked to a tissue specific expression
CC control sequence or is fused to a sequence encoding a signal peptide,
CC which is the wingless (wg) signal peptide or the Argos (aos) signal
CC peptide. The method also comprises providing a transgenic fly and a
CC control wild-type fly, contacting the first transgenic fly and the
CC control wild-type fly with a candidate agent, and observing a difference
CC in phenotype between the first transgenic fly and the control fly, where
CC a difference in phenotype of the first transgenic fly relative to the
CC control fly indicates an agent active in neurodegenerative disease. The
CC transgenic fly is useful in identifying an agent active in
CC neurodegenerative disease for preparing a composition for treating
CC neurodegenerative disease, e.g. Alzheimer's disease. The current sequence
CC represents the human amyloid-beta peptide 42 containing the E22Q (Dutch
CC mutation).

XX SQ Sequence 42 AA;

Query Match 100.0%; Score 34; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
DB 16 KLVFFPAQ 22

RESULT 26

ADZ88256
ID ADZ88256 standard; protein; 42 AA.

XX AC ADZ88256;

XX DT 14-JUL-2005 (first entry)

XX DE Amyloid beta 42 (Dutch).

XX KW mutant; amyloid-beta 42; Abeta42; transgenic; Iowa; Dutch; Flemish;
KW Italian; Arctic; Tau; neurodegenerative disorder; Alzheimers disease;
KW Drosophila; wingless; wg; signal peptide; Argos; aos.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 22 /label= Glu22Gln

XX PN WO2005041650-A1.

XX XX

XX PD 12-MAY-2005.

XX PF 21-OCT-2004; 2004WO-US034838.

XX PR 21-OCT-2003; 2003US-0512913P.

XX PR 21-OCT-2003; 2003US-0512970P.

XX PR 21-OCT-2003; 2003US-0512972P.

XX PR 21-OCT-2003; 2003US-0513149P.

XX PR 21-OCT-2003; 2003US-0513152P.

XX PR 25-MAY-2004; 2004US-00852892.

XX PR 25-MAY-2004; 2004US-00852951.

XX PR 25-MAY-2004; 2004US-00852973.

XX PR 25-MAY-2004; 2004US-00852974.

XX PR 25-MAY-2004; 2004US-00853593.

XX PA (ENVI-) ENVIVO PHARM INC.

XX PI Lowe DA, Cummings CJ, Koenig G;

XX DR WPI; 2005-366469/37.

XX DR N-PSDB; ADZ88261.

XX PT New transgenic flies that express the human amyloid-beta 42 peptide
PT containing a pathogenic (e.g. Iowa, Dutch, Flemish, Italian or Arctic)
PT mutation, and optionally, a Tau protein, useful as models of
PT neurodegenerative disorders.

XX PS Claim 1; SEQ ID NO 2; 85pp; English.

XX CC This sequence represents a mutant amyloid-beta 42 (Abeta42) protein. This
CC sequence specifically represents Abeta42(Dutch). In this mutant protein
CC Glu22 is mutated to Gln. The mutant coding sequence is used in the
CC generation of a transgenic fly expressing a mutant Abeta42. The
CC transgenic fly comprises a genome comprising: a DNA sequence encoding a
CC polypeptide comprising the Abeta42 peptide containing the Iowa, Dutch,
CC Flemish or Italian mutation; or a first DNA sequence that encodes a human
CC Abeta42 peptide containing the Arctic mutation, and a second DNA sequence
CC that encodes a Tau. The transgenic fly is useful as a model of
CC neurodegenerative disorders, such as Alzheimer's disease. It may be used
CC for identifying genetic modifiers or for identifying therapeutic
CC compounds that may treat neurodegenerative disorders. The transgenic fly
CC is a Drosophila. The DNA sequence(s) is/are operatively linked to an

expression control sequence. The expression control sequence is a tissue specific expression control sequence. The DNA sequence is fused to a sequence encoding a signal peptide. Identifying an agent active in neurodegenerative disease comprises providing a first transgenic fly with an observable phenotype; contacting it with a candidate agent; and observing a phenotype of the first transgenic fly relative to the phenotype of a control fly, where an observable difference in the phenotype of the first transgenic fly relative to the control fly is indicative of an agent active in neurodegenerative disease. The transgenic fly is an adult fly or is in its larval stage. The expression control sequence is a tissue specific expression control sequence or comprises a UAS control element. The first DNA sequence is fused to a sequence encoding a signal peptide. The signal peptide is the wingless (wg) signal peptide or the Argos (aos) signal peptide. The observable phenotype is selected from rough eye, concave wing, a behavioral phenotype, and locomotor dysfunction. Alternatively, identifying an agent active in neurodegenerative disease comprises providing the above transgenic fly and a control wild-type fly; contacting the first transgenic fly and the control wild-type fly with a candidate agent; and observing a difference in phenotype between the transgenic fly and the control fly, where a difference in phenotype is indicative of an agent active in neurodegenerative disease.

SQ Sequence 42 AA;

Query Match 100.0%; Score 34; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||
16 KLVFFPAQ 22

RESULT 27

AEA37375
ID AEA37375 standard; peptide; 42 AA.

AC AEA37375;

DT 25-AUG-2005 (first entry)

DE Human amyloid-beta peptide 42 comprising Dutch mutation, SEQ ID 1.

XX Nootropic; Neuroprotective; CNS-Gen.; Antiinflammatory; Dermatological;
KW Immunosuppressive; Cytostatic; Antiparkinsonian; Cerebroprotective;
KW Muscular-Gen.; transgenic insect; Alzheimers disease;
KW neurodegenerative disease; motor neuron disease; dementia;
KW Guillain Barre syndrome; lupus; brain tumor; spinal cord tumor;
KW Down syndrome; parkinsons disease; Pick's disease;
KW restless legs syndrome; Sydenham's chorea; beta-amyloid.

XX Homo sapiens.

XX Key Location/Qualifiers
FH Key
FT Misc-difference 22

FT /note= "Wild-type Glu substituted with Gln"

XX US2005132424-A1.

XX 16-JUN-2005.

PD 21-OCT-2004; 2004US-00969898.

XX 21-OCT-2003; 2003US-0512972P.

PR 25-MAY-2004; 2004US-00853593.

XX (ENVI-) ENVIVO PHARM INC.

XX Lowe DA, Koenig G, Cummings CJ;

XX WPI; 2005-424631/43.

DR N-PSDB; AEA37376.

XX New transgenic fly comprising a human amyloid-beta peptide 42 containing
PT a Dutch mutation and a Tau protein, useful for identifying agents to
PT treat neurodegenerative disorders.

XX Claim 1; SEQ ID NO 1; 26pp; English.

XX The present invention relates to a transgenic fly whose genome comprises
CC a first DNA sequence that encodes a human amyloid-beta (Abeta) peptide 42
CC of amyloid precursor protein (APP) containing the Dutch mutation
CC (AEA37375), and a second DNA sequence that encodes a human Tau protein.
CC The Dutch mutation, Glu22Gln, is associated with Alzheimer's disease. The
CC DNA sequence is also fused to a signal sequence. Also claimed is a method
CC of identifying an agent active in neurodegenerative disease. The
CC transgenic flies of the invention are useful for identifying genetic
CC modifiers and therapeutic compounds for treating neurodegenerative
CC disorders such as Alzheimer's disease, amyotrophic lateral sclerosis,
CC dementia, Guillain-Barre syndrome, lupus, brain and spinal tumors, Down's
CC syndrome, Parkinson's disease, Pick's disease, restless leg syndrome and
CC Sydenham's chorea.

XX Sequence 42 AA;

Query Match 100.0%; Score 34; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||
16 KLVFFPAQ 22

RESULT 28

AAR55697

ID AAR55697 standard; protein; 53 AA.

XX AAR55697;

XX 25-MAR-2003 (revised)

DT 29-DEC-1994 (first entry)

XX Sequence of unidentified protein sequence ID number 22.

XX Amyloid precursor protein; APP; plaque; beta/A4; Alzheimers; transgene;
KW ss.

XX Synthetic.

XX WO9412627-A1.

XX 09-JUN-1994.

XX 24-NOV-1993; 93WO-US011480.

XX 25-NOV-1992; 92US-00989850.

PR 09-NOV-1993; 93US-00149222.

XX (CEPH-) CEPHALON INC.

XX Scott RW, Howland DS;

XX WPI; 1994-200256/24.

XX Transgenic animal model for Alzheimer's disease - contains transgene
PT encoding amyloid protein under transcriptional control of synapsin gene
PT promoter.

XX Example; Page 55; 94pp; English.

XX There was no apparent reference to sequence ID numbers 20, 21 or 22 in
CC the specification. The specification describes a transgenic animal model
CC for Alzheimer's disease. A transgenic animal harbouring a transgene
CC coding for an amyloid protein under the control of a promoter is claimed.

CC The amyloid protein can be APP695, APP751 or APP770. The coding sequence
 CC may contain a mutation, including the hereditary cerebral haemorrhage
 CC with amyloidosis - Dutch type (HCHWA-DT) and familial Alzheimer's disease
 CC (FAD). Perhaps SQ IDs 20-22 corresp. to wt, HCHWA-DT and FAD? (Updated on
 CC 25-MAR-2003 to correct PN field.)
 XX Sequence 53 AA;

Query Match 100.0%; Score 34; DB 2; Length 53;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFFAQ 7
 |||||
 Db 20 KLVFFFAQ 26

RESULT 29
 AAW26391
 ID AAW26391 standard; peptide; 63 AA.
 XX AC AAW26391;

XX 25-MAR-2003 (revised)
 DT 15-DEC-1997 (first entry)
 XX

DE Amyloid precursor protein fragment APP-REP 751 (BAP E22Q).

XX Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
 KW mutin; secretase; Alzheimer's disease;
 KW hereditary cerebral haemorrhage with amyloidosis; human.
 XX Homo sapiens.

Key	Location/Qualifiers
Peptide	10..51
	/label= BAP(E22Q)
	/note= "beta-amyloid protein E22Q mutant"
Cleavage-site	25..26
	/note= "secretase cleavage site"
Domain	38..61
	/label= Transmembrane

US5652092-A.
 29-JUL-1997.
 05-JUN-1995; 95US-00462859.
 01-MAY-1992; 92US-00877675.
 20-SEP-1993; 93US-00123659.

(AMCY) AMERICAN CYANAMID CO.

Jacobsen JS, Vitek MP;

WPI; 1997-392937/36.

Screening for compounds which reduce beta-amyloid protein formation -
 using cells which express a construct encoding a marker and an amyloid
 precursor mutin derived from APP isoforms.

Disclosure; Fig 5A; 84pp; English.

CC This peptide sequence shows the region of amyloid precursor protein (APP)
 CC that includes a beta-amyloid protein (BAP) carrying a point mutation (BAP
 CC E22Q) found in patients with hereditary cerebral haemorrhage with
 CC amyloidosis of Dutch origin (HCHWA-D). In an attempt to engineer an APP
 CC non-cleavable substrate for secretase, an APP-reporter (APP-REP) protein
 CC that carries the E22Q mutation has been expressed in recombinant host
 CC cells. This resulted in the secretion of an N-terminal fragment
 CC indistinguishable from that of APP-REP 751 (see AAW26393-94). Non-
 CC cleavable APP substrates can be used to detect other putative abnormal

CC APP processing events. They can also be used to investigate cellular post
 CC -translational modifications to APP in order to determine the potential
 CC influence on normal secretase and abnormal BAP 'clipping' activities.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX Sequence 63 AA;

Query Match 100.0%; Score 34; DB 2; Length 63;
 Best Local Similarity 100.0%; Pred. No. 4.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFFAQ 7
 |||||
 Db 25 KLVFFFAQ 31

RESULT 30
 AAW26511
 ID AAW26511 standard; peptide; 63 AA.
 XX AC AAW26511;

XX 25-MAR-2003 (revised)
 DT 06-JAN-1998 (first entry)
 XX

DE Amyloid precursor protein fragment APP-REP 751 (BAP E22Q).

XX Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
 KW mutin; secretase; Alzheimer's disease;
 KW hereditary cerebral haemorrhage with amyloidosis; human.
 XX Homo sapiens.

Key	Location/Qualifiers
Peptide	10..51
	/label= BAP(E22Q)
	/note= "beta-amyloid protein E22Q mutant"
Cleavage-site	25..26
	/note= "secretase cleavage site"
Domain	38..61
	/label= Transmembrane

US5656477-A.
 12-AUG-1997.
 20-SEP-1993; 93US-00123659.
 01-MAY-1992; 92US-00877675.

(AMCY) AMERICAN CYANAMID CO.

Jacobsen JS, Vitek MP;

WPI; 1997-414594/38.

Nucleic acid encoding amyloid precursor mutin(s) - comprising reporter
 gene and coding sequence, for identifying compounds which modify the
 activity of proteolytic enzymes which cleave APP.

Disclosure; Fig 5A; 84pp; English.

CC This peptide sequence shows the region of amyloid precursor protein (APP)
 CC that includes a beta-amyloid protein (BAP) carrying a point mutation (BAP
 CC E22Q) found in patients with hereditary cerebral haemorrhage with
 CC amyloidosis of Dutch origin (HCHWA-D). In an attempt to engineer an APP
 CC non-cleavable substrate for secretase, an APP-reporter (APP-REP) protein
 CC that carries the E22Q mutation has been expressed in recombinant host
 CC cells. This resulted in the secretion of an N-terminal fragment
 CC indistinguishable from that of APP-REP 751 (see AAW26393-94). Non-
 CC cleavable APP substrates can be used to detect other putative abnormal
 CC APP processing events. They can also be used to investigate cellular post
 CC -translational modifications to APP in order to determine the potential

CC influence on normal secretase and abnormal BAP 'clipping' activities.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 63 AA;

Query Match 100.0%; Score 34; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
Db 25 KLVFFPAQ 31
|||||
25 KLVFFPAQ 31

RESULT 31
AAW42975
ID AAW42975 standard; peptide; 63 AA.
XX
AC AAW42975;
XX
XX 09-SEP-2004 (revised)
DT 01-MAY-1998 (first entry)
XX
DE Beta-amyloid peptide (BAP) E22Q.
XX
KW Beta-amyloid peptide; BAP; extracellular BAP plaque; amyloidosis;
KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;
KW Dutch origin; amyloid precursor protein; APP; secretase; BAP aggregation;
KW abnormal proteolytic cleavage; hereditary cerebral haemorrhage.
XX
OS Homo sapiens.
OS Unidentified.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 22 /label= E22Q
FT /note= "wild type Glu replaced with Gln"
FT Domain 38..61
FT /note= "putative transmembrane domain"
XX
XX
PN US5703209-A.
XX
XX 30-DEC-1997.
XX
XX 05-JUN-1995; 95US-00464248.
XX
PR 01-MAY-1992; 92US-00877675.
PR 20-SEP-1993; 93US-00123659.
XX
XX (AMCY) AMERICAN CYANAMID CO.
XX
XX Jacobsen JS, Vitek MP;
XX
XX WPI; 1998-076482/07.
XX
XX Amyloid precursor protein fusion polypeptides - comprising APP fragment
XX and marker, useful for research and drug screening.
XX
XX Disclosure; Fig 5A; 84pp; English.
XX
XX The present sequence represents a beta-amyloid peptide (BAP) with a E22Q
XX mutation. Abnormal accumulation of extracellular BAP in plaques and
XX cerebrovascular deposits is characteristic in brains of individuals
XX suffering from Alzheimers disease and Downs syndrome. BAP is a poorly
XX soluble, self-aggregating protein which is derived from a larger amyloid
XX precursor protein (APP). APP is expressed as an integral membrane
XX protein, and is cleaved by secretase, between BAP 16Lys and 17Leu.
XX Cleavage at this site precludes amyloidogenesis and results in the
XX release of the amino-terminal APP fragment. The E22Q mutation in BAP is
XX found within the APP of patients with hereditary cerebral haemorrhage
XX with amyloidosis of Dutch origin, and may be due to an alteration in the
XX rate of BAP aggregation. APP can be used as a substrate for studying
XX abnormal proteolytic cleavage which results in the release of BAP, and

CC also to screen for drugs that will inhibit such cleavage
CC Revised record issued on 09-SEP-2004 : Correction to feature table key
XX
SQ Sequence 63 AA;

Query Match 100.0%; Score 34; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
Db 25 KLVFFPAQ 31
|||||
25 KLVFFPAQ 31

RESULT 32
AAW44746
ID AAW44746 standard; protein; 63 AA.
XX
AC AAW44746;
XX
XX 01-JUN-1998 (first entry)
DT
XX
DE APP-REP 751 [BAP E22Q] peptide.
XX
KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
KW Alzheimer's disease; cleavage.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Cleavage-site 25..26
FT /note= "secretase cleavage site"
FT Misc-difference 31
FT /note= "Glu to Gln change from wild type sequence"
XX
XX US5693478-A.
XX
XX 02-DEC-1997.
XX
XX 05-JUN-1995; 95US-00464247.
XX
PR 01-MAY-1992; 92US-00877675.
PR 20-SEP-1993; 93US-00123659.
XX
XX (AMCY) AMERICAN CYANAMID CO.
XX
XX Jacobsen JS, Vitek MP;
XX
XX WPI; 1998-031744/03.
XX
XX Amyloid precursor muten reporter molecule assay containing antibody
XX recognised marker - used to study pathways associated with Alzheimer's
XX disease.
XX
XX Disclosure; Fig 5A; 84pp; English.
XX
XX This sequence represent the beta-amyloid protein sequence from the
XX construct APP-REP751 [BAP E22Q]. The mutant sequence can be used in a
XX method to study secretase and beta-amyloid protein (BAP)-generating
XX pathways associated with Alzheimer's disease by studying proteolytic
XX cleavage of the reporter polypeptides (e.g. AAW44744 and AAW44745)
XX
SQ Sequence 63 AA;

Query Match 100.0%; Score 34; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
Db 25 KLVFFPAQ 31
|||||
25 KLVFFPAQ 31

Db 25 KLVFFPAQ 31

RESULT 33
 AAR74695
 ID AAR74695 standard; peptide; 99 AA.
 XX
 AC AAR74695;
 XX
 XX 25-MAR-2003 (revised)
 DT 11-NOV-1995 (first entry)
 XX
 XX Beta-amyloid precursor protein mutant C-terminal peptide.
 DE
 XX Human; beta-amyloid precursor protein mutant; C-terminal peptide;
 KW gene transfer; transgenic animal; Alzheimer disease model; gene therapy.
 KW
 XX Homo sapiens.
 OS
 XX EP653154-A2.
 PN
 XX 17-MAY-1995.
 PD
 XX 07-NOV-1994; 94EP-00117512.
 PP
 XX 12-NOV-1993; 93JP-00306026.
 PR
 XX (PARH) HOECHST JAPAN LTD.
 PA
 XX Sato M, Kobayashi T, Tada N, Shoji M, Kawarabayashi T;
 PI WPI; 1995-180492/24.
 XX N-PSDB; AAQ88697.
 DR
 XX Transgenic animal model for Alzheimer's disease - contains DNA encoding
 PT part of beta-amyloid precursor protein in a gene construct designed for
 FT over-expression in various cell types.
 PT
 XX Claim 2; Page 13; 32pp; English.
 PS
 XX The sequence represents a human brain beta-amyloid precursor protein
 CC (APP) C-terminal peptide. The peptide is a Gln-22 mutant of AAR74694. DNA
 CC encoding the peptide may be transferred, along with a signal peptide
 CC (e.g. AAR74693) gene into somatic and germ cells of a non-human mammal,
 CC and the resulting transgenic animal may be used as a model for Alzheimer
 CC disease (AD). The animal model exhibits symptoms similar to AD, producing
 CC large quantities of APP C-terminal peptide, death of neuron cells in
 CC pyramidal cells at cerebral amyloid regions, increases in glial cells and
 CC deposition of abnormally phosphorylated tau protein. The animal model may
 CC be used to develop new therapies for AD, including gene therapy
 CC strategies. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 99 AA;

Query Match 100.0%; Score 34; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||
 DB 16 KLVFFPAQ 22

RESULT 34
 AAE14377
 ID AAE14377 standard; peptide; 100 AA.
 XX
 AC AAE14377;
 XX
 XX 12-MAR-2002 (first entry)
 DT
 XX Amyloid precursor protein beta-CTF domain #7.
 DE
 XX

Gamma-secretase substrate; beta-CTF domain; amyloid precursor protein;
 APP; beta-secretase; Alzheimer's disease.
 Unidentified.
 WO200183811-A1.
 PN
 XX 08-NOV-2001.
 PD
 XX 25-APR-2001; 2001WO-US013332.
 PF
 XX 01-MAY-2000; 2000US-0201053P.
 PR
 XX (MERI) MERCK & CO INC.
 PA
 XX Li Y, Xu M, Huang Q, Gardell S;
 PI WPI; 2002-066536/09.
 XX
 DR Novel gamma secretase substrate for assaying gamma secretase activity and
 XX identifying compounds that regulate gamma secretase activity, e.g.
 FT inhibitors of gamma secretase useful for treating Alzheimer's disease.
 PT
 XX Claim 3; Page 6; 36pp; English.
 PS
 XX The invention relates to gamma-secretase substrates containing a
 CC hydrophilic polypeptide moiety covalently joined to the carboxyl terminus
 CC of a beta-CTF domain. A beta-CTF domain is a polypeptide that can be
 CC cleaved by gamma-secretase, and that approximates the C-terminal fragment
 CC (amino acids 596-695) of amyloid precursor protein (APP) produced after
 CC cleavage of APP by beta-secretase. The hydrophilic polypeptide moiety
 CC increases the solubility of the substrate in a zwitterionic detergent.
 CC The gamma-secretase substrate is used in in vitro assays employing
 CC zwitterionic detergent for measuring gamma-secretase activity. The assay
 CC methods are useful for purifying and characterising the enzyme, to screen
 CC for compounds that modulate gamma-secretase activity, and to test the
 CC ability of a particular compound that affect gamma-secretase activity.
 CC The compounds that modulate gamma-secretase activity include gamma-
 CC secretase inhibitors which are useful in the treatment of Alzheimer's
 CC disease, and in the characterisation of the biological importance of
 CC gamma-secretase. The present sequence is a beta-CTF domain used in the
 CC invention
 XX
 SQ Sequence 100 AA;

Query Match 100.0%; Score 34; DB 5; Length 100;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||
 DB 17 KLVFFPAQ 23

RESULT 35
 AAE14385
 ID AAE14385 standard; protein; 108 AA.
 XX
 AC AAE14385;
 XX
 XX 12-MAR-2002 (first entry)
 DT
 XX Gamma-secretase substrate #7.
 DE
 XX Gamma-secretase substrate; beta-CTF domain; amyloid precursor protein;
 KW APP; beta-secretase; Alzheimer's disease; fusion protein.
 XX
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 FH 1..100
 FT Region /label= Beta-CTF_domain
 FT Region 101..108

```

FT XX /note= "Hydrophilic moiety"
PN XX WO200183811-A1.
XX XX
PD XX 08-NOV-2001.
XX XX
PF XX 25-APR-2001; 2001WO-US013332.
XX XX
PR XX 01-MAY-2000; 2000US-0201053P.
XX XX
PA XX (MERI ) MERCK & CO INC.
XX XX
PI XX Li Y, Xu M, Huang Q, Gardell S;
XX XX WPI; 2002-066536/09.
XX XX
PT Novel gamma secretase substrate for assaying gamma secretase activity and
PT identifying compounds that regulate gamma secretase activity, e.g.
PT inhibitors of gamma secretase useful for treating Alzheimer's disease.
XX XX
PS Claim 8; Page 9; 36pp; English.
XX XX
CC The invention relates to gamma-secretase substrates containing a
CC hydrophilic polypeptide moiety covalently joined to the carboxyl terminus
CC of a beta-CTF domain. A beta-CTF domain is a polypeptide that can be
CC cleaved by gamma-secretase, and that approximates the C-terminal fragment
CC (amino acids 596-695) of amyloid precursor protein (APP) produced after
CC cleavage of APP by beta-secretase. The hydrophilic polypeptide moiety
CC increases the solubility of the substrate in a zwitterionic detergent.
CC The gamma-secretase substrate is used in in vitro assays employing
CC zwitterionic detergent for measuring gamma-secretase activity. The assay
CC methods are useful for purifying and characterising the enzyme, to screen
CC for compounds that modulate gamma-secretase activity, and to test the
CC ability of a particular compound that affect gamma-secretase activity.
CC The compounds that modulate gamma-secretase activity include gamma-
CC secretase inhibitors which are useful in the treatment of Alzheimer's
CC disease, and in the characterisation of the biological importance of
CC gamma-secretase. The present sequence is an example of gamma-secretase
CC substrate of the invention. The substrate is a fusion protein containing
CC APP beta-CTF domain and a hydrophilic moiety
XX XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 34; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFFAQ 7
DB 17 KLVFFFAQ 23

RESULT 36
AAR88300
ID AAR88300 standard; peptide; 7 AA.
XX XX
AC AAR88300;
XX XX
DT 23-FEB-1996 (first entry)
XX XX
DE Non-amnestic peptide Beta-A4 (16-22).
XX XX
KW memory; enhancer; topographic model; amnestic peptide binding site;
KW beta-A4.
XX XX
OS Synthetic.
XX XX
PN WO9507093-A1.
XX XX
PD 16-MAR-1995.
XX XX
PF 08-SEP-1994; 94WO-US010083.
XX XX

PR 08-SEP-1993; 93US-00117927.
XX XX
PA (CITY ) CITY OF HOPE.
XX XX
PI Roberts E;
XX XX
XX WPI; 1995-123235/16.
XX XX
PT Topographic model for amnestic peptide binding - used to design cpds.
PT which enhance memory; and new peptide(s) so designed.
XX XX
PS Disclosure; Page 28; 51pp; English.
XX XX
CC The peptide AAR88300 corresponds to residues 16-22 of beta-A4 was
CC designed as a potential memory enhancing peptide but was found not to be
CC amnestic. (Amnestic peptides are memory-enhancing at lower concentrations
CC than those at which they cause amnesia)
XX XX
SQ Sequence 7 AA;

Query Match 91.2%; Score 31; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 2e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFFAQ 7
DB 1 KLVFFFAE 7

RESULT 37
AAR87921
ID AAR87921 standard; peptide; 7 AA.
XX XX
AC AAR87921;
XX XX
DT 01-MAR-1996 (first entry)
XX XX
DE Test peptide used in study of antagonism of amyloid beta protein.
XX XX
KW amnesia; amyloid beta; Alzheimer's disease.
XX XX
OS Synthetic.
XX XX
PN WO9508999-A1.
XX XX
PD 06-APR-1995.
XX XX
PF 16-SEP-1994; 94WO-US010475.
XX XX
PR 29-SEP-1993; 93US-00127904.
XX XX
PA (CITY ) CITY OF HOPE.
XX XX
PI Roberts E;
XX XX
XX WPI; 1995-147244/19.
XX XX
PT New peptide(s) which block binding of amyloid beta protein - used for
PT antagonising the amnestic effects of amyloid beta protein, partic. in
PT Alzheimer's disease.
XX XX
PS Disclosure; Page 9; 27pp; English.
XX XX
CC The invention relates to three new peptides which block the amnestic
CC effects of amyloid beta protein and which can be used to ameliorate
CC amnesia and other neurotoxicity in Alzheimer's disease caused by
CC deposition of this protein. The peptides themselves are not amnestic or
CC memory-enhancing. The new peptides are described in AAR87912, AAR87913
CC and AAR87914. The present sequence is an additional peptide tested in the
CC process but found not to be active
XX XX
SQ Sequence 7 AA;

```

Query Match 91.2%; Score 31; DB 2; Length 7;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
 |||||:
 Db 1 KLVFFAE 7

RESULT 38

AAB67281
 ID AAB67281 standard; peptide; 7 AA.

XX AC AAB67281;
 XX DT 20-APR-2001 (first entry)

XX DE Residues 16-22 of Alzheimer's Abeta peptide.
 XX KW Alzheimer's; Abeta; beta-strand.

XX OS Homo sapiens.

XX PN WO200107473-A1.
 XX PD 01-FEB-2001.

XX PF 28-JUL-2000; 2000WO-GB002901.
 XX PR 28-JUL-1999; 99GB-00017724.

XX PA (STOT/) STOTT K.
 XX PI Stott K;
 XX DR WPI; 2001-182777/18.

XX PT Novel chemical compound or composition useful for preventing beta-strand
 PT association, comprises peptides containing N-alpha substituted L-amino
 PT acids.
 XX PS Claim 17; Page 46; 77pp; English.

XX CC The present invention relates to a chemical compound or composition
 CC comprising a peptide with a beta strand forming section and associates
 CC with a target beta-strand formed by a separate peptide-containing
 CC molecule. The invention is useful for inhibiting or reversing the
 CC association of target beta-strand, formed by Alzheimer's Abeta peptide
 CC into a beta-sheet or beta-fibre and the aggregation of proteins or
 CC peptides

XX SQ Sequence 7 AA;

Query Match 91.2%; Score 31; DB 4; Length 7;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
 |||||:
 Db 1 KLVFFAE 7

RESULT 39

ABB04920
 ID ABB04920 standard; peptide; 7 AA.

XX AC ABB04920;
 XX DT 14-MAR-2002 (first entry)

XX DE Human amyloid beta protein (beta-A4) peptide 16-22 SEQ ID NO:13.
 XX KW Human; amyloid beta protein; beta-A4; memory enhancement; learning.

XX OS Homo sapiens.
 XX PN US6320024-B1.
 XX PD 20-NOV-2001.
 XX PF 09-MAR-1999; 99US-00264709.
 XX PR 07-FEB-1997; 97US-00797782.
 XX PA (ROBE/) ROBERTS E.
 XX PI Roberts E;
 XX DR WPI; 2002-096566/13.
 XX PT New peptide compound useful for design of substances that enhance memory.
 XX PS Disclosure; Col 6; 30pp; English.

XX CC The present invention describes a novel peptide compound comprising Lys-
 CC His-Tyr-beta-alanine, which has a memory modulating effect. The peptide
 CC has nootropic activity. The peptide can be used for the development of
 CC topographic models useful to design and synthesise memory-enhancing and
 CC life-quality improving substances. The peptide compound restores the
 CC balance between excitatory and inhibitory systems in the brain, which is
 CC required for optimal acquisition and retention of learning and helps to
 CC correct defects in the balance that arise as a result of aging,
 CC infections and injury. The substances exert reyeberneticising effects on
 CC nervous system function and has more prolonged desired effects at lower
 CC doses than the peptide structures. The substances mimic the action of
 CC active peptides without having a peptide structure and do not subject to
 CC degradation of peptide-splitting enzymes in the gut or other tissues. The
 CC present sequence represents a human amyloid beta protein (beta-A4)
 CC peptide which is not amnesic, and is used in the exemplification of the
 CC present invention

XX SQ Sequence 7 AA;

Query Match 91.2%; Score 31; DB 5; Length 7;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
 |||||:
 Db 1 KLVFFAE 7

RESULT 40

ABB82630
 ID ABB82630 standard; peptide; 7 AA.

XX AC ABB82630;
 XX DT 04-FEB-2003 (first entry)

XX DE Abeta fibrillogenesis inhibitor peptide Abeta16-22.
 XX KW Abeta; beta-amyloid; fibrillogenesis; fibril; nootropic; neuroprotective;
 KW cerebroprotective; haemostatic; antipyretic; nephrotropic; vasotropic;
 KW dermatological; auditory; antidiabetic; cytostatic; antiinflammatory;
 KW antimicrobial; anticonvulsant; antidiabetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX Modified-site 3..6
 FT /note= "can be methylated; both the methylated and non-
 FT methylated versions of this peptide are poor
 FT fibrillogenesis inhibitor"
 FT Modified-site 7
 FT /note= "C-terminal CONH2"

XX WO200274931-A2.
 XX 26-SEP-2002.
 XX 20-MAR-2002; 2002WO-US008803.
 XX 20-MAR-2001; 2001US-0277477P.
 XX (UYCH-) UNIV CHICAGO.
 XX Gordon DJ, Meredith SC;
 XX WPI; 2003-040553/03.
 XX Novel peptide for inhibiting fibrillogenesis, and for screening
 PT fibrillogenesis inhibitors, has beta-strand with one face having hydrogen
 PT bonds and other face blocking propagation of hydrogen bonding between
 PT beta-strands.
 XX Disclosure; Page 7; 151pp; English.
 XX The invention relates to a peptide (I) inhibiting fibrillogenesis, that
 CC comprises a beta-strand with two faces, where the first face has hydrogen
 CC bonds, and the second face blocks or disrupts propagation of hydrogen
 CC bonding between beta-strands needed to form fibrils. (I) is useful for
 CC inhibiting fibrillogenesis, for detecting fibrils in a subject and for
 CC screening candidate fibrillogenesis inhibitors. A pharmaceutical
 CC composition comprising (I) is useful for inhibiting or disassembling
 CC fibrils associated with pathological states such as Alzheimer's disease,
 CC Down's syndrome, Dutch-type hereditary cerebral haemorrhage amyloidosis,
 CC reactive amyloidosis, familial Mediterranean fever, familial amyloid
 CC nephropathy with utricaria and deafness, Muckle-Wells syndrome,
 CC idiopathic myeloma, macroglobulinemia-associated myeloma, familial
 CC amyloid polynuropathy, familial amyloid cardiomyopathy, isolated cardiac
 CC amyloid, systemic senile amyloidosis, adult onset diabetes, insulinoma,
 CC isolated atrial amyloid, medullary carcinoma of the thyroid, familial
 CC amyloidosis, hereditary cerebral haemorrhage with amyloidosis, familial
 CC amyloidotic polynuropathy, scrapie, Creutzfeldt-Jakob disease, Gerstmann
 CC -Strausler-Scheinker syndrome, bovine spongiform encephalitis, prion-
 CC mediated diseases, or Huntington's disease. (I) is useful for treating
 CC disease associated with fibrillogenesis or for creating and/or diagnosing
 CC a subject which is a mammal, preferably human, having protein aggregation
 CC disease or protein misfolding disease. The composition is useful in both
 CC preventive and curative therapies of fibril based pathologies mentioned
 CC above. The present sequence represents a peptide which can comprise
 CC consecutive N-methylation, but is a weak inhibitor of Abeta
 CC fibrillogenesis
 XX
 XX Sequence 7 AA;
 SQ

Query Match 91.2%; Score 31; DB 6; Length 7;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFAQ 7
 |||||:
 Db 1 KLVFFAE 7

RESULT 41
 AAE35454
 ID AAE35454 standard; peptide; 7 AA.
 XX AAE35454;
 AC AAE35454;
 XX 17-JUN-2003 (first entry)
 DT
 XX Abeta peptide #25.
 DE
 XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;

KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotrophic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 1..7
 FT /note= "D-form residues"
 FT Modified-site 7
 FT /note= "C-terminal amide"
 XX WO200296937-A2.
 XX 05-DEC-2002.
 XX 29-MAY-2002; 2002WO-CA000763.
 XX 29-MAY-2001; 2001US-00857847.
 XX (NEUR-) NEUROCHEM INC.
 XX Gervais F, Hebert L, Chalifour RJ, Kong X;
 XX WPI; 2003-201269/19.
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX Claim 1; Page 59; 44pp; English.
 CC The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX
 XX Sequence 7 AA;
 SQ

Query Match 91.2%; Score 31; DB 6; Length 7;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFAQ 7
 |||||:
 Db 1 KLVFFAE 7

RESULT 42
 AAE35453
 ID AAE35453 standard; peptide; 7 AA.
 XX AAE35453;
 AC AAE35453;
 XX 17-JUN-2003 (first entry)
 DT
 XX Abeta peptide #24.
 DE
 XX

KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Behcet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.

XX Unidentified.

XX Key Location/Qualifiers
 PH Misc-difference 1..7 /note= "D-form residues"
 FT

XX WO200296937-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-CA000763.

XX 29-MAY-2001; 2001US-00867847.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.

XX Prevention and/or treatment of an amyloid-related disease e.g.

XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.

XX Claim 1; Page 59; 44pp; English.

XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D-
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Behcet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention

XX Sequence 7 AA;

Query Match 91.2%; Score 31; DB 6; Length 7;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
 Db 1 KLVFFAE 7

RESULT 43

ID ADD20746
 AC ADD20746 standard; peptide; 7 AA.

XX ADD20746;

XX 15-JAN-2004 (first entry)

XX Human beta-amyloid 16-22 amino acid sequence.

XX self-assembly; peptide-based structure; beta-amyloid;
 KW self-assembling structure; molecular-level probing; human.
 XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminally modified with CH3CO-"
 FT Modified-site 6 /label= amidated

XX WO2003082900-A2.

XX 09-OCT-2003.

XX 24-MAR-2003; 2003WO-US009229.

XX 22-MAR-2002; 2002US-0368826P.

XX 23-OCT-2002; 2002US-0420746P.

XX 21-MAR-2003; 2003US-0456641P.

XX (UYEW-) UNIV EMORY.

XX Lynn D, Conticello V, Morgan DA, Dong J;

XX WPI; 2003-804023/75.

XX Controlling self-assembly of peptide-based structures (e.g. nanotubes)
 PT comprises providing a controlled environment and placing segments of beta
 FT -amyloids in the controlled environment to generate a self-assembling
 PT structure.

XX Disclosure; Page 10; 46pp; English.

XX The present invention describes a method (M1) for controlling self-
 CC assembly of self-assembling peptide-based structures by providing a
 CC controlled environment and placing segments of beta-amyloids in the
 CC controlled environment to generate a self-assembling structure. Also
 CC described: (1) a method (M1a) for controlling self-assembly of peptide-
 CC based structures comprising providing a controlled environment adapted to
 CC redirect a self-assembly process, and generating a self-assembling
 CC peptide-based structure by placing the self-assembling peptide in the
 CC controlled environment; and (2) a self-assembling peptide-based structure
 CC comprising beta-amyloid segments, optionally with a conservative amino
 CC acid substitution; and hydrogen bonds formed between the segments of the
 CC beta-amyloid. The method is useful in controlling the self-assembly of
 CC self-assembling peptide-based structures. The self-assembling peptide
 CC structures may be used in generating devices at a molecular level to
 CC permit molecular-level probing. The present sequence represents a human
 CC beta-amyloid 16-22 amino acid sequence, which is used in the
 CC exemplification of the present invention.

XX Sequence 7 AA;

Query Match 91.2%; Score 31; DB 7; Length 7;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
 Db 1 KLVFFAE 7

RESULT 44

ID ADF50855
 AC ADF50855 standard; peptide; 7 AA.

XX ADF50855;

XX 12-FEB-2004 (first entry)

XX Human calcitonin derived peptide fragment 2.

XX human; calcitonin; multiple myeloma; medullary carcinoma;
 KW aortic medical carcinoma; antidiabetic; nootropic; neuroprotective;
 KW antiparkinsonian; fibril; type-II diabetes mellitus; amyloidosis;
 KW self-aggregating peptide; amyloid-associated disease;
 KW Alzheimer's disease; SAA amyloidosis; hereditary Icelandic syndrome.
 XX

OS Homo sapiens.

XX WO2003063760-A2.

XX 07-AUG-2003.

XX 30-JAN-2003; 2003WO-IL000079.

XX 31-JAN-2002; 2002US-0352578P.

XX 01-JUL-2002; 2002US-0392266P.

XX 06-SEP-2002; 2002US-00235852.

XX 27-DEC-2002; 2002US-0436453P.

XX (UYRA-) UNIV RAMOT AT TEL AVIV LTD.

XX Gazit E;

XX WPI; 2003-689501/65.

XX New self-aggregating peptide useful for treating amyloid-associated
 PT diseases e.g., Alzheimer's disease, Parkinson's disease, hereditary
 PT Icelandic syndrome, multiple myeloma, medullary carcinoma.

XX Example 21; Fig 1; 138pp; English.

XX This invention relates to novel self-aggregating peptides that can be
 CC used for the diagnosis and treatment of amyloid-associated diseases.
 CC Specifically, it refers to peptides, and antibodies directed
 CC thereagainst, which can prevent or reduce fibril formation and
 CC disaggregate formed aggregates by competitive destabilisation.
 CC Accordingly, these compositions can be used directly to inhibit the
 CC production of islet amyloid polypeptides (IAPPs) and for the inhibition
 CC of amyloidosis. As such they are useful for treating a variety of
 CC unrelated pathological conditions including type-II diabetes mellitus,
 CC Alzheimer's disease, SAA amyloidosis, hereditary Icelandic syndrome,
 CC multiple myeloma, medullary carcinoma, aortic medical carcinoma.
 CC Additionally, they can be described as exhibiting activities such as
 CC antidiabetic, nootropic, neuroprotective and antiparkinsonian. This
 CC peptide sequence is a human medin peptide fragment (also known as milk
 CC fat globule-EGF factor 8 protein, which is the main constituent of aortic
 CC medial amyloid deposits). This peptide sequence is a human calcitonin-
 CC derived peptide fragment 2 used to show self-assembly and hydrophobicity
 CC of amyloid proteins in an exemplification of the invention.

XX Sequence 7 AA;

Query Match 91.2%; Score 31; DB 7; Length 7;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFFAQ 7

Db 1 KLVFFFAE 7

RESULT 45

ADP64922

XX ADP64922 standard; protein; 7 AA.

XX ADP64922;

XX 09-SEP-2004 (first entry)

XX Beta-amyloid central core structure amino acid sequence.

XX spherical nanostructure; tubular nanostructure; field emitter device;

KW nanoscale environment; electron emission lithography; memory cell;
 KW mechanical transmission device; electronic inverter;
 KW heat transfer device; electron emission; beta-amyloid;
 KW central aromatic core structure; nanotube self-assembly;
 KW Alzheimer's disease; beta-amyloid core recognition element.

XX Synthetic.

XX WO2004052773-A2.

XX 24-JUN-2004.

XX 09-DEC-2003; 2003WO-IL001045.

XX 09-DEC-2002; 2002US-0431709P.

XX 31-MAR-2003; 2003US-0458378P.

XX (UYRA-) UNIV RAMOT AT TEL AVIV LTD.

XX Reches M, Gazit E;

XX WPI; 2004-480855/45.

XX Tubular of spherical nanostructure for e.g. use in obtaining information
 PT from nanoscale environment, is composed of peptides including aromatic or
 PT polyaromatic amino acids.

XX Example 1; Fig 9a; 94pp; English.

XX The present invention describes a tubular of spherical nanostructure
 CC composed of peptides including no more than 4 aromatic or polyaromatic
 CC amino acids. Also described: (1) a method of generating a tubular or
 CC spherical nanostructure; (2) a field emitter device; (3) a device for
 CC obtaining information from a nanoscale environment; (4) an apparatus for
 CC electron emission lithography; (5) a memory cell; (6) a mechanical
 CC transmission device; (7) an electronic inverter having a first switching
 CC device and a second switching device; (8) a composition; (9) a heat
 CC transfer device; (10) a method of emitting electrons; and (11) a method
 CC of obtaining information from a nanoscale environment. The nanostructure
 CC can be used in a field emitter device, a device for obtaining information
 CC from a nanoscale environment, an apparatus for electron emission
 CC lithography, a memory cell, a mechanical transmission device, an
 CC electronic inverter, and a matrix-containing composition. It is used in
 CC emitting electrons, in obtaining information from a nanoscale
 CC environment, in recording binary information, in transmitting mechanical
 CC motion, grabbing and/or in manipulating nanoscale objects, and
 CC transferring heat. The nanostructure is highly robust under extreme pH
 CC and temperatures. It enhances electromagnetic fields near ultra small
 CC metal objects. The use of nanostructure as gates in electronic device
 CC allows operation at low gate voltage and enables the switching of several
 CC individual devices on the same substrates. The present sequence
 CC represents a beta-amyloid central aromatic core structure amino acid
 CC sequence, which is used in an example from the present invention for the
 CC nanotube self-assembly of Alzheimer's beta-amyloid core recognition
 CC element.

XX Sequence 7 AA;

Query Match 91.2%; Score 31; DB 8; Length 7;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFFAQ 7

Db 1 KLVFFFAE 7

RESULT 46

ADQ37278

XX ADQ37278 standard; peptide; 7 AA.

XX ADQ37278;

DT XX 07-OCT-2004 (first entry)
DE XX Vaccine antigen amyloid-beta related amino acid sequence.
XX
KW amyloid-beta; amyloid-beta related disease;
KW amyloid-beta fibril formation; immune response; neurotropic;
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
KW cardiant; antidepressant; endocrine; hypnotic;
KW amyloid-beta fibril formation modulator; immune system modulator;
KW Alzheimer's disease; mild cognitive impairment;
KW mild-to-moderate cognitive impairment; vascular dementia;
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
KW senile dementia; Down's syndrome; inclusion body myositis;
KW age-related macular degeneration; hypothyroidism;
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
KW behavioural dysfunction; neurological condition; psychological condition;
KW vaccine antigen.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1..7 /note= "D-form residues"
XX FT
XX FN WO2004058239-A1.
XX XX 15-JUL-2004.
XX XX 24-DEC-2003; 2003WO-CA002021.
XX XX 24-DEC-2002; 2002US-0436379P.
XX XX 23-JUN-2003; 2003US-0482214P.
XX XX (NEUR-) NEUROCHEM INT LTD.
XX XX Gervais F, Bellini F;
XX XX WPI; 2004-543342/52.
XX
XX Composition for treating e.g. Alzheimer's disease comprises first agent
XX that prevents or treats amyloid-beta related disease and second agent
XX that is either a peptide or peptidomimetic or an immune system modulator.
XX
XX Disclosure; Page 67; 143pp; English.
XX
XX The present invention describes compositions (C) comprising: (a) a first
XX agent (a1) that prevents or treats amyloid-beta related disease; and (b)
XX a second agent (a2) that is: (i) a peptide or peptidomimetic that
XX modulates amyloid-beta fibril formation or induces a prophylactic or
XX therapeutic immune response against amyloid-beta fibril formation; or
XX (ii) an immune system modulator that prevents or inhibits amyloid-beta
XX fibril formation. Also described is a kit comprising (C). (C) have
XX neurotropic, neuroprotective, cerebroprotective, haemostatic,
XX ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
XX uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
XX neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
XX and can be used as amyloid-beta fibril formation modulators, and as
XX immune system modulators. (C) can be used for preventing or treating an
XX amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
XX (non-hereditary) or familial (hereditary)), mild cognitive impairment,
XX mild-to-moderate cognitive impairment, vascular dementia, cerebral
XX amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
XX Down's syndrome, inclusion body myositis, age-related macular
XX degeneration, or a condition associated with Alzheimer's disease
XX (including hypothyroidism, cerebrovascular disease, cardiovascular
XX disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
XX aggression, or incontinence), a neurological condition (e.g. Huntington's
XX disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
XX Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
XX with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
XX field deficits, incoordination, gait disturbance, transient ischaemic

CC attack or stroke, transient alertness, attention deficit, frequent falls,
CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
CC damage), or a psychological condition (e.g. depression, delusions,
CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
CC having amyloid-beta deposits. The present sequence represents a peptide
CC that can be used as a vaccine antigen in the exemplification of the
CC present invention.
XX XX Sequence 7 AA;
XX
XX Query Match 91.2%; Score 31; DB 8; Length 7;
XX Best Local Similarity 85.7%; Pred. No. 2e+06;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KLVFFPAQ 7
XX DB 1 KLVFFPAE 7
XX
XX RESULT 47
XX ADQ37279
XX ID ADQ37279 standard; peptide; 7 AA.
XX XX
XX AC ADQ37279;
XX XX
XX DT 07-OCT-2004 (first entry)
XX XX
XX DE Vaccine antigen amyloid-beta related amino acid sequence.
XX XX
XX KW amyloid-beta; amyloid-beta related disease;
XX amyloid-beta fibril formation; immune response; neurotropic;
XX neuroprotective; cerebroprotective; haemostatic; ophthalmological;
XX antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
XX anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
XX cardiant; antidepressant; endocrine; hypnotic;
XX amyloid-beta fibril formation modulator; immune system modulator;
XX Alzheimer's disease; mild cognitive impairment;
XX mild-to-moderate cognitive impairment; vascular dementia;
XX cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
XX senile dementia; Down's syndrome; inclusion body myositis;
XX age-related macular degeneration; hypothyroidism;
XX cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
XX behavioural dysfunction; neurological condition; psychological condition;
XX vaccine antigen.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1..7 /note= "D-form residues"
XX FT
XX FN WO2004058239-A1.
XX XX 15-JUL-2004.
XX XX 24-DEC-2003; 2003WO-CA002021.
XX XX 24-DEC-2002; 2002US-0436379P.
XX XX 23-JUN-2003; 2003US-0482214P.
XX XX (NEUR-) NEUROCHEM INT LTD.
XX XX Gervais F, Bellini F;
XX XX WPI; 2004-543342/52.
XX
XX Composition for treating e.g. Alzheimer's disease comprises first agent
XX that prevents or treats amyloid-beta related disease and second agent
XX that is either a peptide or peptidomimetic or an immune system modulator.
XX
XX Disclosure; Page 67; 143pp; English.
XX
XX The present invention describes compositions (C) comprising: (a) a first
XX agent (a1) that prevents or treats amyloid-beta related disease; and (b)
XX a second agent (a2) that is: (i) a peptide or peptidomimetic that
XX modulates amyloid-beta fibril formation or induces a prophylactic or
XX therapeutic immune response against amyloid-beta fibril formation; or
XX (ii) an immune system modulator that prevents or inhibits amyloid-beta
XX fibril formation. Also described is a kit comprising (C). (C) have
XX neurotropic, neuroprotective, cerebroprotective, haemostatic,
XX ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
XX uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
XX neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
XX and can be used as amyloid-beta fibril formation modulators, and as
XX immune system modulators. (C) can be used for preventing or treating an
XX amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
XX (non-hereditary) or familial (hereditary)), mild cognitive impairment,
XX mild-to-moderate cognitive impairment, vascular dementia, cerebral
XX amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
XX Down's syndrome, inclusion body myositis, age-related macular
XX degeneration, or a condition associated with Alzheimer's disease
XX (including hypothyroidism, cerebrovascular disease, cardiovascular
XX disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
XX aggression, or incontinence), a neurological condition (e.g. Huntington's
XX disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
XX Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
XX with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
XX field deficits, incoordination, gait disturbance, transient ischaemic

PT Composition for treating e.g. Alzheimer's disease comprises first agent
PT that prevents or treats amyloid-beta related disease and second agent
PT that is either a peptide or peptidomimetic or an immune system modulator.

XX Disclosure; Page 67; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
CC modulates amyloid-beta fibril formation or induces a prophylactic or
CC therapeutic immune response against amyloid-beta fibril formation; or
CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
CC fibril formation. Also described is a kit comprising (C). (C) have
CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,
CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
CC and can be used as amyloid-beta fibril formation modulators, and as
CC immune system modulators. (C) can be used for preventing or treating an
CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
CC Down's syndrome, inclusion body myositis, age-related macular
CC degeneration, or a condition associated with Alzheimer's disease
CC (including hypothyroidism, cerebrovascular disease, cardiovascular
CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
CC aggression, or incontinence), a neurological condition (e.g. Huntington's
CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
CC field deficits, incoordination, gait disturbance, transient ischaemic
CC attack or stroke, transient alertness, attention deficit, frequent falls,
CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
CC damage), or a psychological condition (e.g. depression, delusions,
CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
CC having amyloid-beta deposits. The present sequence represents a peptide
CC that can be used as a vaccine antigen in the exemplification of the
CC present invention.

XX Sequence 7 AA;

Query Match 91.2%; Score 31; DB 8; Length 7;
Best Local Similarity 85.7%; Pred. No. 2e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
|||
Db 1 KLVFFAE 7

RESULT 48

AAW32551
ID AAW32551 standard; peptide; 8 AA.
XX
XX
AC AAW32551;

21-JAN-1998 (first entry)

XX Amyloidogenic sequence amyloid beta-peptide.

XX Anti-amyloid peptide; ibeta; abnormal protein folding inhibitor;
KW Alzheimer's disease; dementia; Down's syndrome; amyloidosis disorder;
KW human prion disease; Kuru; Creutzfeldt-Jakob disease;
KW Gerstmann-Straussler-Scheinker Syndrome; animal prion disease;
KW prion associated human neurodegenerative disease; scrapie;
KW spongiform encephalopathy; transmissible mink encephalopathy;
KW Chronic wasting disease; mule; deer; elk; human.

XX Homo sapiens.
OS Synthetic.

XX WO9639834-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US010220.

XX 07-JUN-1995; 95US-00478326.

XX 10-APR-1996; 96US-00630645.

XX (UWNY) UNIV NEW YORK STATE.

XX Soto-Jara C, Baumann MH, Frangione B;

XX WPI; 1997-051637/05.

XX New inhibitors of fibrillogenesis proteins or peptides - used for
PT preventing, treating or detecting amyloidosis disorders such as
PT Alzheimer's disease.

XX Disclosure; Fig 1A; 63pp; English.

XX A method has been developed for the prevention or treatment of a disorder
CC or disease associated with the formation of amyloid or amyloid-like
CC deposits, involving the abnormal folding of a protein or peptide. The
CC method involves administering an inhibitory peptide which prevents the
CC abnormal folding or which dissolves existing amyloid or amyloid-like
CC deposits, where the peptide comprises a sequence of 3-15 amino acid
CC residues and has a hydrophobic cluster of at least 3 amino acids, where
CC at least one of the 3 amino acids is a beta-sheet blocking amino acid
CC residue selected from Pro, Gly, Asn and His. The present sequence
CC represents an amyloidogenic sequence, amyloid beta-peptide, which is
CC involved in the formation of several amyloid deposits. The inhibitory
CC peptide is capable of associating with a structural determinant on the
CC protein or peptide to structurally block and inhibit the abnormal folding
CC into amyloid or amyloid-like deposits. The method can be used for
CC preventing, treating or detecting e.g. Alzheimer's dementia or disease,
CC Down's syndrome, other amyloidosis disorders, human prion diseases such
CC as Kuru, Creutzfeldt-Jakob disease, Gerstmann-Straussler-Scheinker
CC Syndrome, prion associated human neurodegenerative diseases or animal
CC prion diseases such as scrapie, spongiform encephalopathy, transmissible
CC mink encephalopathy and chronic wasting disease of mule deer and elk

XX Sequence 8 AA;

Query Match 91.2%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 2e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
|||
Db 1 KLVFFAE 7

RESULT 49

AAE10663
ID AAE10663 standard; peptide; 8 AA.

XX AAE10663;

XX 10-DEC-2001 (first entry)

XX Human amyloid precursor protein substrate alpha-secretase peptide #2.
XX Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; neurotropic; neuroprotective;
KW alpha-secretase.
XX Homo sapiens.

```

XX FH Key Key Location/Qualifiers
XX FT Cleavage-site 4. .5
XX FN GB2357767-A.
XX PD 04-JUL-2001.
XX XX
XX PF 22-SEP-2000; 2000GB-00023315.
XX PR 23-SEP-1999; 99US-00404133.
XX PR 23-SEP-1999; 99US-0155493P.
XX PR 23-SEP-1999; 99WO-US020881.
XX PR 13-OCT-1999; 99US-00416901.
XX PR 06-DEC-1999; 99US-0169232P.
XX PA (PHAA ) PHARMACIA & UPJOHN CO.
XX PI
XX PI Bienkowski MJ;
XX DR WPI; 2001-444208/48.
XX XX
XX FT Polypeptide comprising fragments of human aspartyl protease with amyloid
XX PT precursor protein processing activity and alpha-secretase activity, for
XX PT identifying modulators useful in treating Alzheimer's disease.
XX PS Claim 10; Page 163; 187pp; English.
XX CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
XX CC proteins which lack transmembrane domain or amino terminal domain or
XX CC cytoplasmic domain and retains alpha-secretase activity and amyloid
XX CC protein precursor (APP) processing activity. The proteins of the
XX CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
XX CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
XX CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
XX CC are useful for treating Alzheimer's disease (AD) which causes progressive
XX CC dementia with consequent formation of amyloid plaques, neurofibrillary
XX CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
XX CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
XX CC with the substrate under acidic conditions and determining the level of
XX CC hu-Asp1 proteolytic activity. The present sequence is human amyloid
XX CC precursor protein (APP) substrate alpha-secretase peptide which is used
XX CC for determining the enzymatic activity of Asp-1 protein lacking
XX CC transmembrane domain (TM) and containing a (His)6 tag
XX SQ Sequence 8 AA;

Query Match 91.2%; Score 31; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;

Qy 1 KLVFFPAQ 7
Db |||||:
1 KLVFFPAE 7

RESULT 50
AAE02615
ID AAE02615 standard; peptide; 8 AA.
XX
XX AC AAE02615;
XX
XX DT 10-AUG-2001 (first entry)
XX
XX DE Human amyloid precursor protein substrate alpha-secretase peptide #2.
XX
XX KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
XX KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp1;
XX KW beta-secretase.
XX
XX OS Homo sapiens.
XX
XX FH Key Key Location/Qualifiers

```

```

FT Cleavage-site 4. .5
XX WO200123533-A2.
XX
XX PD 05-APR-2001.
XX
XX PF 22-SEP-2000; 2000WO-US026080.
XX
XX PR 23-SEP-1999; 99US-0155493P.
XX PR 23-SEP-1999; 99WO-US020881.
XX PR 13-OCT-1999; 99US-00416901.
XX PR 06-DEC-1999; 99US-0169232P.
XX
XX PA (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX PI Gurney M, Bienkowski MJ;
XX PI WPI; 2001-290516/30.
XX
XX FT Enzymes that cleave the alpha-secretase site of the amyloid precursor
XX PT protein, useful for the treatment of Alzheimer's disease.
XX PS Claim 10; Page 98; 189pp; English.
XX
XX CC The present invention relates to enzymes for cleaving the alpha-
XX CC secretase site of the amyloid precursor protein (APP) and methods of
XX CC identifying those enzymes. The methods may be used to identify enzymes
XX CC that may be used to cleave the alpha-secretase cleavage site of the APP
XX CC protein. The enzymes may be used to treat or modulate the progress of
XX CC Alzheimer's disease. The present sequence is human amyloid precursor
XX CC protein (APP) substrate alpha-secretase peptide which is used for
XX CC determining the enzymatic activity of Asp-1 deltam (His)6 protein
XX SQ Sequence 8 AA;

Query Match 91.2%; Score 31; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;

Qy 1 KLVFFPAQ 7
Db |||||:
1 KLVFFPAE 7

RESULT 51
ABB78624
ID ABB78624 standard; peptide; 8 AA.
XX
XX AC ABB78624;
XX
XX DT 16-JUL-2002 (first entry)
XX
XX DE Human alpha secretase (Abeta12-28) peptide SEQ ID NO:73.
XX
XX KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic.
XX
XX OS Homo sapiens.
XX
XX PN GB2367060-A.
XX
XX PD 27-MAR-2002.
XX
XX PF 29-OCT-2001; 2001GB-00025934.
XX
XX PR 23-SEP-1999; 99US-00404133.
XX PR 23-SEP-1999; 99US-0155493P.
XX PR 23-SEP-1999; 99WO-US020881.
XX PR 13-OCT-1999; 99US-00416901.
XX PR 06-DEC-1999; 99US-0169232P.
XX PR 22-SEP-2000; 2000GB-00023315.
XX
XX PA (PHAA ) PHARMACIA & UPJOHN CO.
XX

```


XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PA (UNII) UNIV ILLINOIS FOUND.
 XX
 XX Ghosh AK, Tang J, Bilcer G, Chang W, Hong L, Koelsch G, Loy J;
 PI Turner RT;
 XX WPI; 2003-541410/51.
 DR
 XX
 XX New peptide compounds are memapsin beta secretase inhibitors used for
 PT treating Alzheimer's disease.
 PT
 XX Example 2; Page 156; 407pp; English.
 PS
 XX The invention relates to peptide compounds of specified formula. The
 CC compounds exhibit memapsin 2-beta secretase inhibitory activity relative
 CC to memapsin 1-beta secretase and reduce the accumulation of beta-amyloid
 CC protein. The compounds can be used for treating Alzheimer's disease. The
 CC present sequence represents a human amyloid precursor protein (APP)
 CC fragment where hydrolysis by memapsin takes place
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 91.2%; Score 31; DB 6; Length 8;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFPAQ 7
 Db 1 KLVFFPAE 7
 RESULT 54
 ABW00134
 ID ABW00134 standard; peptide; 8 AA.
 XX
 AC ABW00134;
 XX
 XX 15-JAN-2004 (first entry)
 DT
 XX Beta-amyloid peptide.
 DE
 XX Amyloid-like fibril deposit; prion related encephalopathy; gene therapy;
 KW Alzheimer's disease; beta-amyloid.
 KW
 XX Unidentified.
 OS
 XX US2003087407-A1.
 PN
 XX 08-MAY-2003.
 PD
 XX 06-SEP-2002; 2002US-00235483.
 PF
 XX 07-JUN-1995; 95US-00478326.
 PR 10-APR-1996; 96US-00630645.
 PR 12-DEC-1996; 96US-00766596.
 XX
 XX (UTNY) UNIV NEW YORK STATE.
 PA
 XX Soto-Jara C, Baumann MH, Frangione B;
 PI
 XX WPI; 2003-616149/58.
 DR
 XX New inhibitory peptide, useful for preparing a composition for
 PT diagnosing, preventing or treating disorders associated with amyloid-like
 PT fibril deposits, e.g. Alzheimer's disease, or prion related
 PT encephalopathies.
 XX
 XX Example 1; Fig 1A; 52pp; English.
 PS
 XX The invention relates to inhibitory peptide comprising a portion of at
 CC least three amino acid residues and a sequence predicted not to adopt a
 CC beta-sheet structure that associates with a hydrophobic beta-sheet

CC cluster on a protein or peptide involved in the abnormal folding into a
 CC beta-sheet structure, to structurally block the abnormal folding of the
 CC protein or peptide. The inhibitory peptide is useful for preparing a
 CC composition for preventing, treating or detecting disorders or disease and
 CC associated with amyloid-like fibril deposits e.g. Alzheimer's disease and
 CC prion related encephalopathies. The invention is also useful in gene
 CC therapy. The present sequence is beta-amyloid peptide. This peptide is
 CC involved in the formation of several amyloid deposits
 XX
 SQ Sequence 8 AA;
 Query Match 91.2%; Score 31; DB 7; Length 8;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFPAQ 7
 Db 1 KLVFFPAE 7
 RESULT 55
 ADQ37385
 ID ADQ37385 standard; peptide; 8 AA.
 XX
 AC ADQ37385;
 XX
 XX 07-OCT-2004 (first entry)
 DT
 XX Antifibrillogenic peptide.
 DE
 XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 XX Synthetic.
 OS
 XX WO2004058239-A1.
 PN
 XX 15-JUL-2004.
 PD
 XX 24-DEC-2003; 2003WO-CA002021.
 PF
 XX 24-DEC-2002; 2002US-0436379P.
 PR 23-JUN-2003; 2003US-0482214P.
 PR
 XX (NEUR-) NEUROCHEM INT LTD.
 PA
 XX Gervais P, Bellini F;
 PI
 XX WPI; 2004-543342/52.
 DR
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 PT
 XX Disclosure; Page 95; 143pp; English.
 PS
 XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or

CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiac, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents an
 CC anti-fibrillogenic peptide which is used in the exemplification of the
 CC present invention.

XX Sequence 8 AA;

Query Match 91.2%; Score 31; DB 8; Length 8;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLVPFAQ 7
 |||||:
 Db 1 KLVPFAE 7

RESULT 56

ADZ08900
 ID ADZ08900 standard; peptide; 8 AA.

AC ADZ08900;

XX 16-JUN-2005 (first entry)

DE Human beta-amyloid peptide (SEQ ID No:125) probed with anti-amyloid IgG.

XX amyloid; antibody engineering; antibody production;
 KW amyloid-associated disorder; Alzheimers disease; cancer; allergy;
 KW autoimmune disease; Parkinsons disease;
 KW acquired immune deficiency syndrome; multiple sclerosis; migraine;
 KW dementia; infection; neurotropic; neuroprotective; cytostatic;
 KW antiallergic; immunosuppressive; antiparkinsonian; antimigraine;
 KW antimicrobial; anti-HIV; beta-amyloid.

XX Homo sapiens.

OS
 XX WO2005028511-A2.

XX 31-MAR-2005.

XX 26-MAR-2004; 2004WO-US009522.

XX 28-MAR-2003; 2003US-0458469P.

PR 28-MAR-2003; 2003US-0458474P.
 PR 28-MAR-2003; 2003US-0458509P.
 PR 28-MAR-2003; 2003US-0458510P.
 XX (CENZ) CENTOCOR INC.
 PA (MERC/) MERCKEN M.
 PA (BENS/) BENSON J M.
 XX Mercken M, Benson JM;
 XX WPI; 2005-242565/25.
 XX New isolated mammalian anti-amyloid antibodies useful for treating
 PT amyloid-associated disorders, such as Alzheimer's disease, cancer,
 PT allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,
 PT migraine and dementia.
 XX Example 4; SEQ ID NO 125; 306pp; English.

XX The invention relates to at least one isolated mammalian amyloid antibody
 CC comprising at least one variable region comprising at least one heavy
 CC chain and at least one light chain. Of a fully defined sequence of SEQ ID
 CC NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are:
 CC (i) at least one isolated mammalian amyloid antibody that binds to the
 CC same region of an amyloid polypeptide as an antibody comprising at least
 CC one heavy chain or light chain complementarity determining region (CDR)
 CC having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii)
 CC at least one isolated mammalian amyloid antibody, comprising at least one
 CC human CDR, where the antibody specifically binds at least one epitope
 CC selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined
 CC sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic
 CC acid encoding at least one of any of the isolated mammalian amyloid
 CC antibodies mentioned and having at least one human CDR of a fully defined
 CC sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an
 CC isolated nucleic acid vector comprising an isolated nucleic acid encoding
 CC an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising
 CC an isolated nucleic acid encoding an amyloid antibody, (vi) a method of
 CC producing at least one amyloid antibody, (vii) a composition comprising
 CC at least one of any of the isolated mammalian amyloid antibodies
 CC mentioned, and at least one pharmaceutical carrier or diluent, (viii) an
 CC anti-idiotypic antibody or fragment that specifically binds at least one
 CC of the amyloid antibodies mentioned, (ix) a method of diagnosing or
 CC treating an amyloid related condition in a cell, tissue, organ or animal,
 CC comprising contacting or administering a composition comprising at least
 CC one of the antibodies mentioned, with, or to, the cell, tissue, organ or
 CC animal, (x) a medical device comprising at least one amyloid antibody
 CC mentioned, where the device is suitable for contacting or administering
 CC at least one amyloid antibody, (xi) an article of manufacture for human
 CC pharmaceutical or diagnostic use, comprising packaging material and a
 CC container comprising a solution or a lyophilized form of at least one of
 CC the amyloid antibodies mentioned, and (xii) a method of producing at
 CC least one of the isolated mammalian amyloid antibodies, comprising
 CC providing a host cell or transgenic animal or transgenic plant or plant
 CC cell capable of expressing the antibody in recoverable amounts. The
 CC methods and compositions of the present invention are useful for
 CC producing therapeutic compositions and devices for treating amyloid-
 CC associated disorders, such as Alzheimer's disease, cancer, allergies,
 CC autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis,
 CC migraine, dementia and infections. This sequence represents a peptide
 CC from human beta-amyloid probed with anti-beta-amyloid IgG antibodies.

Sequence 8 AA;

Query Match 91.2%; Score 31; DB 9; Length 8;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLVPFAQ 7
 |||||:
 Db 1 KLVPFAE 7

RESULT 57


```

AEA51423
ID AEA51423 standard; peptide; 8 AA.
XX AC AEA51423;
XX DT 08-SEP-2005 (first entry)
XX KW C-Abeta 16-22 peptide immunogen, SEQ ID NO: 54.
XX DE immunoconjugate; immunostimulant; neuroprotective; nontropic; virucide;
XX KW cytostatic; amyloidosis; Alzheimers disease; Down's syndrome;
XX KW viral infection; cancer.
XX OS Unidentified.
XX PN WO2005058941-A2.
XX PD 30-JUN-2005.
XX PF 17-DEC-2004; 2004WO-US044093.
XX PR 17-DEC-2003; 2003US-0530481P.
XX PP (ELAN-) ELAN PHARM INC.
XX PA (AMHP ) WYETH.
XX PI Arumugham RG, Prasad AK;
XX PT WPI; 2005-467099/47.
XX PS Conjugating peptide immunogen by reacting derivatized protein/polypeptide
XX PT carrier with a reactive group of an amino acid of the peptide immunogen
XX PT so that the peptide immunogen is conjugated to derivatized
XX PT protein/polypeptide carrier.
XX PS Example 10; SEQ ID NO 54; 150pp; English.
XX CC The present invention relates to methods of producing an immunogenic
XX CC conjugate of a peptide immunogen comprising Abeta peptide or fragments of
XX CC Abeta or analogs with a protein/polypeptide carrier. Given is a method of
XX CC conjugating a peptide immunogen, Abeta peptide, via a reactive group of a
XX CC residue to a protein/polypeptide carrier. The method comprises reacting a
XX CC derivatized protein/polypeptide carrier with a reactive group of an amino
XX CC acid of the Abeta peptide. In conjugating a peptide immunogen, the
XX CC keyhole limpet hemocyanin (KLH), immunoglobulin molecules, thyroglobulin,
XX CC and growth factors or hormones and preferably contains a T-cell epitope,
XX CC or is a bacterial toxoid. The growth factor or hormone is selected from
XX CC IL-1, IL-2, gamma-interferon, IL-10, GM-CSF, MIP-1alpha, MIP-1beta, or
XX CC RANTES. Described is a method of inducing an immune response in a
XX CC mammalian subject by administering an amount of the immunogenic
XX CC composition to the subject. The conjugate is useful in the manufacture of
XX CC a medicament for use in the treatment, prophylaxis, or amelioration of an
XX CC amyloidogenic disease. The disease is Alzheimer's disease or Down's
XX CC syndrome. It is also useful for treating viral infection or cancers. The
XX CC present sequence is the C-Abeta 16-22 peptide immunogen, SEQ ID NO: 54.
XX SQ Sequence 8 AA;
XX Query Match 91.2%; Score 31; DB 9; Length 8;
XX Best Local Similarity 85.7%; Pred. No. 2e+06;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 KLVPFAQ 7
XX Db |||||:
XX 2 KLVPFAE 8
XX RESULT 58
XX AEA51420
XX ID AEA51420 standard; peptide; 8 AA.
XX AC AEA51420;

```

```

XX DT 08-SEP-2005 (first entry)
XX DE A 16-22-C peptide immunogen, SEQ ID NO: 51.
XX KW immunoconjugate; immunostimulant; neuroprotective; nontropic; virucide;
XX KW cytostatic; amyloidosis; Alzheimers disease; Down's syndrome;
XX KW viral infection; cancer.
XX OS Unidentified.
XX PN WO2005058941-A2.
XX PD 30-JUN-2005.
XX PF 17-DEC-2004; 2004WO-US044093.
XX PR 17-DEC-2003; 2003US-0530481P.
XX PP (ELAN-) ELAN PHARM INC.
XX PA (AMHP ) WYETH.
XX PI Arumugham RG, Prasad AK;
XX PT WPI; 2005-467099/47.
XX PS Conjugating peptide immunogen by reacting derivatized protein/polypeptide
XX PT carrier with a reactive group of an amino acid of the peptide immunogen
XX PT so that the peptide immunogen is conjugated to derivatized
XX PT protein/polypeptide carrier.
XX PS Example 10; SEQ ID NO 51; 150pp; English.
XX CC The present invention relates to methods of producing an immunogenic
XX CC conjugate of a peptide immunogen comprising Abeta peptide or fragments of
XX CC Abeta or analogs with a protein/polypeptide carrier. Given is a method of
XX CC conjugating a peptide immunogen, Abeta peptide, via a reactive group of a
XX CC residue to a protein/polypeptide carrier. The method comprises reacting a
XX CC derivatized protein/polypeptide carrier with a reactive group of an amino
XX CC acid of the Abeta peptide. In conjugating a peptide immunogen, the
XX CC keyhole limpet hemocyanin (KLH), immunoglobulin molecules, thyroglobulin,
XX CC and growth factors or hormones and preferably contains a T-cell epitope,
XX CC or is a bacterial toxoid. The growth factor or hormone is selected from
XX CC IL-1, IL-2, gamma-interferon, IL-10, GM-CSF, MIP-1alpha, MIP-1beta, or
XX CC RANTES. Described is a method of inducing an immune response in a
XX CC mammalian subject by administering an amount of the immunogenic
XX CC composition to the subject. The conjugate is useful in the manufacture of
XX CC a medicament for use in the treatment, prophylaxis, or amelioration of an
XX CC amyloidogenic disease. The disease is Alzheimer's disease or Down's
XX CC syndrome. It is also useful for treating viral infection or cancers. The
XX CC present sequence is the A 16-22-C peptide immunogen, SEQ ID NO: 51.
XX SQ Sequence 8 AA;
XX Query Match 91.2%; Score 31; DB 9; Length 8;
XX Best Local Similarity 85.7%; Pred. No. 2e+06;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 KLVPFAQ 7
XX Db |||||:
XX 1 KLVPFAE 7
XX RESULT 59
XX AEA62831
XX ID AEA62831 standard; peptide; 8 AA.
XX AC AEA62831;
XX DT 08-SEP-2005 (first entry)
XX DE Immunoconjugate Abeta peptide, SEQ ID NO 51.

```

XX Immunoconjugate; immunotherapy; immunotoxin; tumor-associated antigen;
 KW antigen; antibacterial; virucide; fungicide; antiparasitic;
 KW neuroprotective; nootropic; cytostatic; immunotherapy; immunostimulant;
 KW Alzheimer's disease; cancer.

OS Homo sapiens.

XX WO2005058940-A2.

XX 30-JUN-2005.

XX 17-DEC-2004; 2004WO-US042701.

XX 17-DEC-2003; 2003US-0530480P.

XX (AMHP) WYETH.

XX Arumugham RG, Prasad AK;

XX WPI; 2005-488538/49.

XX Conjugating peptide immunogen, by derivatizing functional groups of
 PT protein or polypeptide carrier, reacting reactive group of amino acid
 PT residue of peptide immunogen with carrier having functional groups, to
 PT produce conjugate.

XX Example 10; SEQ ID NO 51; 155pp; English.

XX The present invention relates to producing an immunogenic conjugate of a
 CC peptide immunogen with a protein or polypeptide carrier. Specifically,
 CC conjugating (M1) the peptide immunogen through a reactive group of an
 CC amino acid residue to a protein/polypeptide carrier (PC) having
 CC functional groups, by derivatizing functional groups of PC, reacting
 CC derivatized PC with a peptide immunogen to produce the conjugate,
 CC reacting the conjugate with a capping reagent to produce the conjugate,
 CC unreacted functional groups, so that the conjugate elicits immune
 CC responses against peptide immunogen. In (M1), the carrier is chosen from
 CC for example, human serum albumin, keyhole limpet hemocyanin (KLH), and
 CC immunoglobulin molecules, hepatitis B surface antigen (HBsAg19.23), and
 CC cholera toxin. The carrier contains a T-cell epitope. The carrier is a
 CC bacterial or viral protein such as influenza hemagglutinin, and malaria
 CC circumsporozoite (CS) protein. Preferably, the carrier is C.pneumoniae ORF
 CC T858. The peptide immunogen can also be an antigen from a malignant
 CC tumor. Antibacterial; Virucide; Fungicide; Antiparasitic; Neuroprotective
 CC ; Nootropic; Cytostatic.Immunotherapy. The method is useful for inducing
 CC an immune response against pathogens, in a mammalian subject, and
 CC Alzheimer's disease and cancer. The present sequence is a Abeta16-22-C
 CC peptide.

XX Sequence 8 AA;

Query Match 91.2%; Score 31; DB 9; Length 8;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLVFFAQ 7

DB 1 KLVFFAE 7

RESULT 60

AEA62834

ID AEA62834 standard; peptide; 8 AA.

XX AEA62834;

XX 08-SEP-2005 (first entry)

XX Immunoconjugate Abeta peptide, SEQ ID NO 54.

XX Immunoconjugate; immunotherapy; immunotoxin; tumor-associated antigen;
 KW antigen; antibacterial; virucide; fungicide; antiparasitic;

KW neuroprotective; nootropic; cytostatic; immunotherapy; immunostimulant;
 KW Alzheimer's disease; cancer.

OS Homo sapiens.

XX WO2005058940-A2.

XX 30-JUN-2005.

XX 17-DEC-2004; 2004WO-US042701.

XX 17-DEC-2003; 2003US-0530480P.

XX (AMHP) WYETH.

XX Arumugham RG, Prasad AK;

XX WPI; 2005-488538/49.

XX Conjugating peptide immunogen, by derivatizing functional groups of
 PT protein or polypeptide carrier, reacting reactive group of amino acid
 PT residue of peptide immunogen with carrier having functional groups, to
 PT produce conjugate.

XX Example 10; SEQ ID NO 54; 155pp; English.

XX The present invention relates to producing an immunogenic conjugate of a
 CC peptide immunogen with a protein or polypeptide carrier. Specifically,
 CC conjugating (M1) the peptide immunogen through a reactive group of an
 CC amino acid residue to a protein/polypeptide carrier (PC) having
 CC functional groups, by derivatizing functional groups of PC, reacting
 CC derivatized PC with a peptide immunogen to produce the conjugate,
 CC reacting the conjugate with a capping reagent to produce the conjugate,
 CC unreacted functional groups, so that the conjugate elicits immune
 CC responses against peptide immunogen. In (M1), the carrier is chosen from
 CC for example, human serum albumin, keyhole limpet hemocyanin (KLH), and
 CC immunoglobulin molecules, hepatitis B surface antigen (HBsAg19.23), and
 CC cholera toxin. The carrier contains a T-cell epitope. The carrier is a
 CC bacterial or viral protein such as influenza hemagglutinin, and malaria
 CC circumsporozoite (CS) protein. Preferably, the carrier is C.pneumoniae ORF
 CC T858. The peptide immunogen can also be an antigen from a malignant
 CC tumor. Antibacterial; Virucide; Fungicide; Antiparasitic; Neuroprotective
 CC ; Nootropic; Cytostatic.Immunotherapy. The method is useful for inducing
 CC an immune response against pathogens, in a mammalian subject, and
 CC Alzheimer's disease and cancer. The present sequence is a C-Abeta16-22-C
 CC peptide.

XX Sequence 8 AA;

Query Match 91.2%; Score 31; DB 9; Length 8;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLVFFAQ 7

DB 2 KLVFFAE 8

RESULT 61

ABU79063

ID ABU79063 standard; peptide; 9 AA.

XX ABU79063;

XX 17-JUN-2003 (first entry)

XX Aggregation blocking peptide #15.

XX Amyloid formation; amyloid-like deposit; Alzheimer's disease;
 KW pathological beta-sheet-rich conformation; Down's syndrome;
 KW amyloidosis disorder; human prion disease; kuru; CJD;
 KW Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; GSS;
 KW prion associated human neurodegenerative disease; animal prion disease;

KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;
 KW chronic wasting disease.

OS Unidentified.

XX US6462171-B1.

XX 08-OCT-2002.

XX 12-DEC-1996; 96US-00766596.

XX 07-JUN-1995; 95US-00478326.

PR 10-APR-1996; 96US-00630645.

XX (UYNV) UNIV NEW YORK STATE.

XX Soto-Jara C, Baumann MH, Frangione B;

XX WPI; 2003-379012/36.

XX Novel inhibitory peptides which inhibit and structurally block abnormal
 PT folding of protein into amyloid or amyloid-like deposit and into
 PT pathological beta-sheet rich conformation, useful for treating
 PT Alzheimer's disease.

XX Disclosure; Col 51-52; 51pp; English.

CC The invention describes an isolated inhibitory peptide (I) which
 CC interacts with a hydrophobic beta-sheet forming cluster of amino acid
 CC residues on a protein or peptide for amyloid or amyloid-like deposit
 CC formation, and inhibits or structurally blocks the abnormal folding of
 CC proteins and peptides into amyloid or amyloid-like deposits and into
 CC pathological beta-sheet rich conformation. (I) is useful for disorders or
 CC diseases associated with abnormal protein folding into amyloid or amyloid
 CC -like deposits or into pathological beta-sheet-rich precursors of such
 CC deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis
 CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease
 CC (CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated
 CC human neurodegenerative diseases as well as animal prion diseases such as
 CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and
 CC chronic wasting disease of mule deer and elk. (I) is also useful for
 CC detecting and diagnosing the presence or absence of amyloid or amyloid-
 CC like deposits in vivo and its precursors. This is the amino acid sequence
 CC of peptide associated with the inhibition of amyloid or amyloid like
 CC deposits

XX Sequence 9 AA;

Query Match 91.2%; Score 31; DB 6; Length 9;

Best Local Similarity 85.7%; Pred. No. 2e+06;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7

Db 2 KLVFFAE 8

RESULT 62

ABW00197

ID ABW00197 standard; peptide; 9 AA.

XX AC

XX ABW00197;

XX 15-JAN-2004 (first entry)

XX Peptide #15 used in the invention.

XX Amyloid-like fibril deposit; prion related encephalopathy; gene therapy;
 KW Alzheimer's disease.

XX Unidentified.

XX US2003087407-A1.

XX 08-MAY-2003.

XX 06-SEP-2002; 2002US-00235483.

XX 07-JUN-1995; 95US-00478326.

PR 10-APR-1996; 96US-00630645.

PR 12-DEC-1996; 96US-00766596.

XX (UYNV) UNIV NEW YORK STATE.

XX Soto-Jara C, Baumann MH, Frangione B;

XX WPI; 2003-616149/58.

XX New inhibitory peptide, useful for preparing a composition for
 PT diagnosing, preventing or treating disorders associated with amyloid-like
 PT fibril deposits, e.g. Alzheimer's disease, or prion related
 PT encephalopathies.

XX Claim 1; Page 28; 52pp; English.

XX The invention relates to inhibitory peptide comprising a portion of at
 CC least three amino acid residues and a sequence predicted not to adopt a
 CC beta-sheet structure that associates with a hydrophobic beta-sheet
 CC cluster on a protein or peptide involved in the abnormal folding into a
 CC beta-sheet structure, to structurally block the abnormal folding of the
 CC protein or peptide. The inhibitory peptide is useful for preparing a
 CC composition for preventing, treating or detecting disorders or diseases
 CC associated with amyloid-like fibril deposits e.g. Alzheimer's disease and
 CC prion related encephalopathies. The invention is also useful in gene
 CC therapy. The present sequence is a peptide used in the invention

XX Sequence 9 AA;

Query Match 91.2%; Score 31; DB 7; Length 9;

Best Local Similarity 85.7%; Pred. No. 2e+06;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7

Db 2 KLVFFAE 8

RESULT 63

ADI36003

ID ADI36003 standard; peptide; 9 AA.

XX AC

XX ADI36003;

XX 22-APR-2004 (first entry)

XX Amyloid beta peptide SEQ ID NO:157.

XX amyloid beta peptide; vaccine; immunisation; neuroprotective;
 KW Alzheimer's disease.

XX Synthetic.

XX WO2004006861-A2.

XX 22-JAN-2004.

XX 16-JUL-2003; 2003WO-US022280.

XX 17-JUL-2002; 2002US-0396245P.

XX (MIND-) MINDSET BIOPHARMACEUTICALS INC.

XX Chain DG, Fitzer-Attas C;

XX WPI; 2004-122759/12.

CC determining the resulting score of all amino acids of the subsequence,
 CC based on the binding value of each amino acids obtained in step (1); and
 CC (c) comparing the resulting score to a preselected value. Also described:
 CC (1) a vaccine comprising the isolated amyloid beta peptide and a carrier
 CC or diluent; (2) determining T-cell epitopes within amyloid beta peptide;
 CC (3) predicting the reaction of an individual to a vaccine; (4) matching a
 CC vaccine comprising a beta amyloid or homologue peptide to an individual,
 CC for immunisation of an individual based on the HLA haplotype of the
 CC individual; (5) a kit for matching a vaccine comprising amyloid beta
 CC peptide to an individual based on the HLA haplotype of the individual;
 CC and (6) preventing the formation or progression of amyloid plaques. The
 CC amyloid beta peptide has neuroprotective activity, and can be used in
 CC vaccines. The amyloid beta peptide is useful for preparing a composition
 CC for preventing the formation or progression of amyloid plaques for
 CC preventing or treating Alzheimer's disease. The present sequence
 CC represents an amyloid beta (Abeta) peptide, which is used in an example
 CC from the present invention.

XX Sequence 9 AA;

Query Match 91.2%; Score 31; DB 8; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
 DB 1 KLVFFAE 7
 |||||:

RESULT 66
 ADI35903
 ID ADI35903 standard; peptide; 9 AA.

XX AC ADI35903;

XX DT 22-APR-2004 (first entry)

XX DE Amyloid beta homologue LV/EE HLA-A2.01 epitope SEQ ID NO:57.

XX KW amyloid beta peptide; vaccine; immunisation; neuroprotective;
 XX KW Alzheimer's disease; epitope.

XX OS Synthetic.

XX PN WO2004006861-A2.

XX PD 22-JAN-2004.

XX PF 16-JUL-2003; 2003WO-US022280.

XX PR 17-JUL-2002; 2002US-0396245P.

XX PA (MIND-) MINDSET BIOPHARMACEUTICALS INC.

XX PI Chain DG, Fitzer-Attas C;

XX DR WPI; 2004-122759/12.

XX PT New amyloid beta peptide, useful for preparing a composition for
 PT preventing the formation or progression of amyloid plaques for preventing
 PT or treating Alzheimer's disease.

XX PS Example 3; SEQ ID NO 57; 69pp; English.

XX CC The present invention describes an isolated amyloid beta peptide or its
 CC homologue which is selected by a method comprising: (a) determining the
 CC binding value of each amino acid of a subsequence of amyloid beta peptide
 CC upon binding to a HLA class I and/or class II molecule of interest; (b)
 CC determining the resulting score of all amino acids of the subsequence,
 CC based on the binding value of each amino acids obtained in step (1); and
 CC (c) comparing the resulting score to a preselected value. Also described:
 CC (1) a vaccine comprising the isolated amyloid beta peptide and a carrier
 CC or diluent; (2) determining T-cell epitopes within amyloid beta peptide;

CC (3) predicting the reaction of an individual to a vaccine; (4) matching a
 CC vaccine comprising a beta amyloid or homologue peptide to an individual,
 CC for immunisation of an individual based on the HLA haplotype of the
 CC individual; (5) a kit for matching a vaccine comprising amyloid beta
 CC peptide to an individual based on the HLA haplotype of the individual;
 CC and (6) preventing the formation or progression of amyloid plaques. The
 CC amyloid beta peptide has neuroprotective activity, and can be used in
 CC vaccines. The amyloid beta peptide is useful for preparing a composition
 CC for preventing the formation or progression of amyloid plaques for
 CC preventing or treating Alzheimer's disease. The present sequence
 CC represents an amyloid beta (Abeta) homologue LV/EE HLA-A2.01 epitope
 CC peptide, which is used in an example from the present invention.

XX Sequence 9 AA;

Query Match 91.2%; Score 31; DB 8; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
 DB 1 KLVFFAE 7
 |||||:

RESULT 67
 AEA51414
 ID AEA51414 standard; peptide; 9 AA.

XX AC AEA51414;

XX DT 08-SEP-2005 (first entry)

XX DE A 16-23-C peptide immunogen, SEQ ID NO: 45.

XX KW immunoconjugate; immunostimulant; neuroprotective; neurotropic; virucide;
 XX KW cytostatic; amyloidosis; Alzheimer's disease; Down's syndrome;
 XX KW viral infection; cancer.

XX OS Unidentified.

XX PN WO2005058941-A2.

XX PD 30-JUN-2005.

XX PF 17-DEC-2004; 2004WO-US044093.

XX PR 17-DEC-2003; 2003US-0530481P.

XX PA (ELAN-) ELAN PHARM INC.

XX PA (AMHP) WYETH.

XX PI Arumugham RG, Prasad AK;

XX DR WPI; 2005-467099/47.

XX PT Conjugating peptide immunogen by reacting derivatized protein/polypeptide
 PT carrier with a reactive group of an amino acid of the peptide immunogen
 PT so that the peptide immunogen is conjugated to derivatized
 PT protein/polypeptide carrier.

XX PS Example 10; SEQ ID NO 45; 150pp; English.

XX CC The present invention relates to methods of producing an immunogenic
 CC conjugate of a peptide immunogen comprising Abeta peptide or fragments of
 CC Abeta or analogs with a protein/polypeptide carrier. Given is a method of
 CC conjugating a peptide immunogen, Abeta peptide, via a reactive group of a
 CC residue to a protein/polypeptide carrier. The method comprises reacting a
 CC derivatized protein/polypeptide carrier with a reactive group of an amino
 CC acid of the Abeta peptide. In conjugating a peptide immunogen, the
 CC carrier is selected from many substances such as human serum albumin,
 CC keyhole limpet hemocyanin (KLH), immunoglobulin molecules, thyroglobulin,
 CC and growth factors or hormones and preferably contains a T-cell epitope,
 CC or is a bacterial toxoid. The growth factor or hormone is selected from

CC IL-1, IL-2, gamma-interferon, IL-10, GM-CSF, MIP-1alpha, MIP-1beta, or
 CC RANTES. Described is a method of inducing an immune response in a
 CC mammalian subject by administering an amount of the immunogenic
 CC composition to the subject. The conjugate is useful in the manufacture of an
 CC a medicament for use in the treatment, prophylaxis, or amelioration of an
 CC amyloidogenic disease. The disease is Alzheimer's disease or Down's
 CC syndrome. It is also useful for treating viral infection or cancers. The
 CC present sequence is the A 16-23-C peptide immunogen, SEQ ID NO: 45.
 XX Sequence 9 AA;

Query Match 91.2%; Score 31; DB 9; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 DB 1 KLVFFPAE 7
 |||||:

RESULT 68

AEA51417
 ID AEA51417 standard; peptide; 9 AA.

XX AC AEA51417;

XX DT 08-SEP-2005 (first entry)

XX DE C-A 16-23 peptide immunogen, SEQ ID NO: 48.

XX KW immunoconjugate; immunostimulant; neuroprotective; nootropic; virucide;
 KW cytostatic; amyloidosis; Alzheimers disease; Down's syndrome;
 KW viral infection; cancer.

XX OS Unidentified.

XX PN WO2005058941-A2.

XX PD 30-JUN-2005.

XX PF 17-DEC-2004; 2004WO-US044093.

XX PR 17-DEC-2003; 2003US-0530481P.

XX PA (ELAN-) ELAN PHARM INC.
 XX PA (AMHP) WYETH.

XX PI Arumugham RG, Prasad AK;

XX DR WPI; 2005-467099/47.

XX PT Conjugating peptide immunogen by reacting derivatized protein/polypeptide
 PT carrier with a reactive group of an amino acid of the peptide immunogen
 PT so that the peptide immunogen is conjugated to derivatized
 PT protein/polypeptide carrier.

XX PS Example 10; SEQ ID NO 48; 150pp; English.

XX CC The present invention relates to methods of producing an immunogenic
 CC conjugate of a peptide immunogen comprising Abeta peptide or fragments of
 CC Abeta or analogs with a protein/polypeptide carrier. Given is a method of
 CC conjugating a peptide immunogen, Abeta peptide, via a reactive group of a
 CC residue to a protein/polypeptide carrier. The method comprises reacting a
 CC derivatized protein/polypeptide carrier with a reactive group of an amino
 CC acid of the Abeta peptide. In conjugating a peptide immunogen, the
 CC carrier is selected from many substances such as human serum albumin,
 CC keyhole limpet hemocyanin (KLH), immunoglobulin molecules, thyroglobulin,
 CC and growth factors or hormones and preferably contains a T-cell epitope,
 CC or is a bacterial toxoid. The growth factor or hormone is selected from
 CC IL-1, IL-2, gamma-interferon, IL-10, GM-CSF, MIP-1alpha, MIP-1beta, or
 CC RANTES. Described is a method of inducing an immune response in a
 CC mammalian subject by administering an amount of the immunogenic
 CC composition to the subject. The conjugate is useful in the manufacture of

CC a medicament for use in the treatment, prophylaxis, or amelioration of an
 CC amyloidogenic disease. The disease is Alzheimer's disease or Down's
 CC syndrome. It is also useful for treating viral infection or cancers. The
 CC present sequence is the C-A 16-23 peptide immunogen, SEQ ID NO: 48.

XX Sequence 9 AA;

Query Match 91.2%; Score 31; DB 9; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 DB 2 KLVFFPAE 8
 |||||:

RESULT 69

AEA62825
 ID AEA62825 standard; peptide; 9 AA.

XX AC AEA62825;

XX DT 08-SEP-2005 (first entry)

XX DE Immunoconjugate Abeta peptide, SEQ ID NO 45.

XX KW immunoconjugate; immunotherapy; immunotoxin; tumor-associated antigen;
 KW antigen; antibacterial; virucide; fungicide; antiparasitic;
 KW neuroprotective; nootropic; cytostatic; Immunotherapy; immunostimulant;
 KW Alzheimer's disease; cancer.

XX OS Homo sapiens.

XX PN WO2005058940-A2.

XX PD 30-JUN-2005.

XX PF 17-DEC-2004; 2004WO-US042701.

XX PR 17-DEC-2003; 2003US-0530480P.

XX PA (AMHP) WYETH.

XX PI Arumugham RG, Prasad AK;

XX DR WPI; 2005-488538/49.

XX PT Conjugating peptide immunogen, by derivatizing functional groups of
 PT protein or polypeptide carrier, reacting reactive group of amino acid
 PT residue of peptide immunogen with carrier having functional groups, to
 PT produce conjugate.

XX PS Example 10; SEQ ID NO 45; 155pp; English.

XX CC The present invention relates to producing an immunogenic conjugate of a
 CC peptide immunogen with a protein or polypeptide carrier. Specifically,
 CC conjugating (M1) the peptide immunogen through a reactive group of an
 CC amino acid residue to a protein/polypeptide carrier (PC) having
 CC functional groups, by derivatizing functional groups of PC, reacting
 CC derivatized PC with a peptide immunogen to produce the conjugate,
 CC reacting the conjugate with a capping reagent to inactive free, reactive
 CC unreacted functional groups, so that the conjugate elicits immune
 CC responses against peptide immunogen. In (M1), the carrier is chosen from
 CC for example, human serum albumin, keyhole limpet hemocyanin (KLH), and
 CC immunoglobulin molecules, hepatitis B surface antigen (HBsAg), and
 CC cholera toxin. The carrier contains a T-cell epitope. The carrier is a
 CC bacterial or viral protein such as influenza hemagglutinin, and malaria
 CC circumsporozoite (CS) protein. Preferably, the carrier is C.pneumoniae ORF
 CC T858. The peptide immunogen can also be an antigen from a malignant
 CC tumor. Antibacterial; Virucide; Fungicide; Antiparasitic; Neuroprotective
 CC ; Nootropic; Cytostatic. Immunotherapy. The method is useful for inducing
 CC an immune response against pathogens, in a mammalian subject, and
 CC Alzheimer's disease and cancer. The present sequence is a Abeta16-23-C

CC peptide.

XX Sequence 9 AA;

SQ

Query Match 91.2%; Score 31; DB 9; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||:
 Db 1 KLVFFPAE 7

RESULT 70

AEA62828

ID AEA62828 standard; peptide; 9 AA.

XX

AC AEA62828;

XX

DT 08-SEP-2005 (first entry)

XX

DE Immunoconjugate Abeta peptide, SEQ ID NO 48.

XX

KW Immunoconjugate; immunotherapy; immunotoxin; tumor-associated antigen;
 KW antigen; antibacterial; virucide; fungicide; antiparasitic;
 KW neuroprotective; nootropic; cytostatic; immunotherapy; immunostimulant;
 KW Alzheimer's disease; cancer.

XX

OS Homo sapiens.

XX

PN WO2005058940-A2.

XX

PD 30-JUN-2005.

XX

PF 17-DEC-2004; 2004WO-US042701.

XX

PR 17-DEC-2003; 2003US-0530480P.

XX

PA (AMHP) WYETH.

XX

PI Arumugham RG, Prasad AK;

XX

DR WPI; 2005-488538/49.

XX

PT Conjugating peptide immunogen, by derivatizing functional groups of
 PT protein or polypeptide carrier, reacting reactive group of amino acid
 PT residue of peptide immunogen with carrier having functional groups, to
 PT produce conjugate.

XX

PS Example 10; SEQ ID NO 48; 155pp; English.

XX

CC The present invention relates to producing an immunogenic conjugate of a
 CC peptide immunogen with a protein or polypeptide carrier. Specifically,
 CC conjugating (M1) the peptide immunogen through a reactive group of an
 CC amino acid residue to a protein/polypeptide carrier (PC) having
 CC functional groups, by derivatizing functional groups of PC, reacting
 CC derivatized PC with a peptide immunogen to produce the conjugate,
 CC reacting the conjugate with a capping reagent to produce free, reactive
 CC unreacted functional groups, so that the conjugate elicits immune
 CC responses against peptide immunogen. In (M1), the carrier is chosen from
 CC for example, human serum albumin, keyhole limpet hemocyanin (KLH), and
 CC immunoglobulin molecules, hepatitis B surface antigen (HBsAg), and
 CC cholera toxin. The carrier contains a T-cell epitope. The carrier is a
 CC bacterial or viral protein such as influenza hemagglutinin, and malaria
 CC circumsporozoite (CS) protein. Preferably, the carrier is C.pneumoniae ORF
 CC T858. The peptide immunogen can also be an antigen from a malignant
 CC tumor. Antibacterial; virucide; fungicide; Antiparasitic; Neuroprotective
 CC ; Nootropic; Cytostatic. Immunotherapy. The method is useful for inducing
 CC an immune response against pathogens, in a mammalian subject, and
 CC Alzheimer's disease and cancer. The present sequence is a C-Abeta16-23
 CC peptide.

XX

SQ Sequence 9 AA;

Query Match 91.2%; Score 31; DB 9; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||:
 Db 2 KLVFFPAE 8

RESULT 71

AAV79938

ID AAY79938 standard; peptide; 10 AA.

XX

AC AAY79938;

XX

DT 11-MAY-2000 (first entry)

XX

DE Beta-amyloid recognition peptide SEQ ID NO:3.

XX

KW Beta-amyloid; inhibitor; recognition element; hybrid; aggregation;
 KW Alzheimer's disease; neuroprotective; nootropic.

XX

OS Homo sapiens.

XX

PN US6022859-A.

XX

PD 08-FEB-2000.

XX

PF 14-NOV-1997; 97US-00970833.

XX

PR 15-NOV-1996; 96US-0030840P.

XX

PA (WISC) WISCONSIN ALUMNI RES FOUND.

XX

PI Murphy RM, Kiessling LL;

XX

DR WPI; 2000-160387/14.

XX

PT Beta-amyloid inhibitor useful for treating Alzheimer's disease.

XX

PS Example; Col 7; 15pp; English.

XX

CC The present invention describes a beta-amyloid inhibitor peptide. Beta-
 CC amyloid inhibitors have neuroprotective and nootropic properties. The
 CC inhibitor peptides are useful for the treatment of Alzheimer's disease.
 CC The present sequence represents a beta-amyloid recognition peptide used
 CC in the exemplification of present invention

XX

SQ Sequence 10 AA;

Query Match 91.2%; Score 31; DB 3; Length 10;
 Best Local Similarity 85.7%; Pred. No. 3.1;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||:
 Db 1 KLVFFPAE 7

RESULT 72

AAB46226

ID AAB46226 standard; peptide; 10 AA.

XX

AC AAB46226;

XX

DT 04-APR-2001 (first entry)

XX

DE Human APP derived immunogenic peptide #22.

XX

KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KW PC receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.

XX

XX OS Homo sapiens.
 XX PN WO200072880-A2.
 XX PD 07-DEC-2000.
 XX PF 26-MAY-2000; 2000WO-US014810.
 XX PR 28-MAY-1999; 99US-00322289.
 XX PA (NEUR-) NEURALAB LTD.
 XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 XX DR WPI; 2001-032104/04.
 XX PT Preventing or treating a disease associated with amyloid deposits,
 XX PT especially Alzheimer's disease, comprises administering amyloid specific
 XX PT antibody.
 XX PS Disclosure; Fig 19; 143pp; English.
 XX CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease
 XX SQ Sequence 10 AA;
 Query Match 91.2%; Score 31; DB 4; Length 10;
 Best Local Similarity 85.7%; Pred. No. 3.1;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFPAQ 7
 |||||:
 Db 3 KLVFFPAE 9
 RESULT 73
 AAB46225
 ID AAB46225 standard; peptide; 10 AA.
 AC AAB46225;
 XX DT 04-APR-2001 (first entry)
 XX DE Human APP derived immunogenic peptide #21.
 XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 XX OS Homo sapiens.
 XX PN WO200072880-A2.
 XX PD 07-DEC-2000.
 XX PF 26-MAY-2000; 2000WO-US014810.
 XX PR 28-MAY-1999; 99US-00322289.
 XX PA (NEUR-) NEURALAB LTD.

XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 XX DR WPI; 2001-032104/04.
 XX PT Preventing or treating a disease associated with amyloid deposits,
 XX PT especially Alzheimer's disease, comprises administering amyloid specific
 XX PT antibody.
 XX PS Disclosure; Fig 19; 143pp; English.
 XX CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease
 XX SQ Sequence 10 AA;
 Query Match 91.2%; Score 31; DB 4; Length 10;
 Best Local Similarity 85.7%; Pred. No. 3.1;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFPAQ 7
 |||||:
 Db 4 KLVFFPAE 10
 RESULT 74
 AAB46228
 ID AAB46228 standard; peptide; 10 AA.
 AC AAB46228;
 XX DT 04-APR-2001 (first entry)
 XX DE Human APP derived immunogenic peptide #24.
 XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 XX OS Homo sapiens.
 XX PN WO200072880-A2.
 XX PD 07-DEC-2000.
 XX PF 26-MAY-2000; 2000WO-US014810.
 XX PR 28-MAY-1999; 99US-00322289.
 XX PA (NEUR-) NEURALAB LTD.
 XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 XX DR WPI; 2001-032104/04.
 XX PT Preventing or treating a disease associated with amyloid deposits,
 XX PT especially Alzheimer's disease, comprises administering amyloid specific
 XX PT antibody.
 XX PS Disclosure; Fig 19; 143pp; English.
 XX CC This invention describes a novel method of preventing or treating a

CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease

XX SQ Sequence 10 AA;

Query Match 91.2%; Score 31; DB 4; Length 10;
 Best Local Similarity 85.7%; Pred. No. 3.1;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFFAQ 7
 |||||:
 Db 1 KLVFFFAE 7

RESULT 75

AAB46227
 ID AAB46227 standard; peptide; 10 AA.

XX AC AAB46227;

XX DT 04-APR-2001 (first entry)

XX DE Human APP derived immunogenic peptide #23.

XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.

XX OS Homo sapiens.

XX PN WO200072880-A2.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US014810.

XX PR 28-MAY-1999; 99US-00322289.

XX PX (NEUR-) NEURALAB LTD.

XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX PT WPI; 2001-032104/04.

XX PS Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid specific
 PT antibody.

XX PS Disclosure; Fig 19; 143pp; English.

XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease

XX SQ Sequence 10 AA;

Query Match 91.2%; Score 31; DB 4; Length 10;
 Best Local Similarity 85.7%; Pred. No. 3.1;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFFAQ 7
 |||||:
 Db 2 KLVFFFAE 8

Search completed: December 29, 2005, 17:33:42
 Job time : 96.4032 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78.1936 Seconds
(without alignments)
54.137 Million cell updates/sec

Title: US-10-009-122-17
Perfect score: 29
Sequence: 1 KVVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	186	1	P98853 oryza sativ
2	29	100.0	186	2	P93414 oryza sativ
3	29	100.0	231	2	Q8C6Y8 mus musculus
4	29	100.0	372	2	Q6D7U3 erwinia car
5	29	100.0	373	2	Q7M9N5 wolinnella s
6	29	100.0	387	2	Q8K110 bacillus ce
7	29	100.0	387	2	Q4MT39 bacillus ce
8	29	100.0	387	2	Q63DD4 bacillus ce
9	29	100.0	387	2	Q6HKU6 bacillus th
10	29	100.0	387	2	Q73AP3 bacillus ce
11	29	100.0	387	2	Q81SK9 bacillus an
12	29	100.0	410	2	Q8C513 mus musculus
13	29	100.0	442	2	Q9PHV5 campylobact
14	29	100.0	703	2	Q4HYE1 homo sapien
15	29	100.0	721	2	Q6AG25 leifsonia x
16	29	100.0	925	2	Q95786 homo sapien
17	29	100.0	925	2	Q5VYT1 homo sapien
18	29	100.0	926	2	Q8Q899 mus musculus
19	29	100.0	940	2	Q9G1V6 sus scrofa
20	29	100.0	1144	1	NOS2 MOUSE
21	29	100.0	1144	2	Q5SXT3 mus musculus
22	29	100.0	1145	2	Q8R410 mus musculus
23	29	100.0	1145	2	Q6P6A0 mouse
24	28	96.6	164	2	Q73N39 treponema d
25	28	96.6	203	2	Q6AKE9 desulfoale
26	28	96.6	380	2	Q67225 aquifex aeo
27	28	96.6	387	2	Q81FH5 bacillus ce
28	28	96.6	399	2	Q5WPU9 lutzomyia l
29	28	96.6	450	2	Q4TRF8 erythroba
30	28	96.6	464	2	Q4S4T5 tetrag
31	28	96.6	606	2	Q91VU5 mus musculus

Q4WBU2	asparagillus
Q5K7E5	cryptococcus
Q6RUU2	mus musculus
Q831B2	tropheryma
Q55HW1	cryptococcus
Q62G91	mus musculus
Q5F3M1	gallus gall
Q4Q5Q4	leishmania
Q41BQ8	sodalis glo
Q9RQ09	bacteroides
Q61C67	caenorhabdi
Q4HSJ7	campylobact
Q9V7J0	drosophila
Q612B4	picophilus
Q59243	pyrococcus
Q95S93	drosophila
Q9V719	drosophila
Q68K27	chlamydomon
Q7QE0	anopheles g
Q5V6R0	drosophila
Q5BI64	drosophila
Q7KTZ4	drosophila
Q8A67	bacteroides
Q9UC33	homo sapien
Q56JJ6	grampus gri
Q56JJ7	tursiops tr
Q7M088	cavia porce
Q8WZ99	homo sapien
Q8WZ99	nitrosomona
Q2919	u alzheimer
Q28280	c alzheimer
Q28748	o alzheimer
Q28757	o alzheimer
Q28053	b alzheimer
Q5WJ18	bacillus cl
Q35463	cricketulus
P30748	escherichia
Q9APP7	uncultured
Q57RF2	salmonella
Q57RF2	salmonella
Q57RF2	salmonella
Q7N6P4	photobacteri
Q8D897	vibrio vuln
Q9K78	vibrio chol
Q83S38	shigella fl
Q7MM72	vibrio vuln
Q8X807	escherichia
Q5PG40	salmonella
Q82886	salmonella
Q8ZQ00	salmonella
Q8ZQ00	salmonella
Q6YVX4	oryza sativ
Q8JH58	chrysa eadiv
Q8JH58	chrysa eadiv
Q7UP1	rhodospirell
Q5LGT9	bacteroides
Q64XP1	bacteroides
Q8EMC6	oceanobacil
Q9ET29	arabidopsis
Q5PB66	anaplasma m
Q380V9	sulfolobus
Q7N3A0	photobacteri
Q9PM1	campylobact
Q4HDT2	campylobact
Q5HSI7	campylobact
Q8BPV5	mus musculus
Q6AMY5	desulfoale
Q8VY56	arabidopsis
Q9SV79	arabidopsis
Q73M22	treponema d
Q9FGJ8	arabidopsis
Q4SV83	tetradon n
Q29414	archaeoglob

105	26	89.7	294	2	Q97XW2_SULSO	Q97XW2 sulfolobus	178	26	89.7	751	2	Q6RH28_CANFA	Q6rh28 canis famil
106	26	89.7	294	2	Q62HR5_BURMA	Q62hr5 burkholderi	179	26	89.7	751	2	Q56JK5_CANFA	Q56jk5 canis famil
107	26	89.7	300	2	Q9XU61_CABEL	Q9xu61 caenorhabdi	180	26	89.7	751	2	Q4R4R8_MACFA	Q4r4r8 macaca fasc
108	26	89.7	314	2	Q7S8K9_NEUCR	Q7s8k9 neurospora	181	26	89.7	751	2	Q4RGJ7_CHICK	Q4rgj7 gallus gall
109	26	89.7	330	2	Q9PG18_XYLFA	Q9pg18 xylolla fas	182	26	89.7	754	2	Q4RY33_TETNG	Q4ry33 tetraodon n
110	26	89.7	339	1	MURG_THEME	Q9wy74 thermotoga	183	26	89.7	759	2	Q4S0J4_TETNG	Q4soj4 tetraodon n
111	26	89.7	349	2	Q9XU59_CABEL	Q9xu59 caenorhabdi	184	26	89.7	770	1	A4_CAVFO	Q60495 c amyloid b
112	26	89.7	352	2	Q9XGY6_SIMCH	Q9xgy6 simmondsia	185	26	89.7	770	1	A4_HUMAN	P05067 h amyloid b
113	26	89.7	352	2	Q87EP8_XYLFT	Q87ep8 xylolla fas	186	26	89.7	770	1	A4_MACFA	P53601 m amyloid b
114	26	89.7	357	2	Q8U460_PYRFU	Q8u460 pyrococcus	187	26	89.7	770	1	A4_MOUSE	P12023 m amyloid b
115	26	89.7	357	2	Q8UUI8_BRARE	Q8uui8 brachydanio	188	26	89.7	770	1	A4_PANTR	Q51580 p amyloid b
116	26	89.7	366	2	Q8PPL1_XANNC	Q8ppl1 xanthomonas	189	26	89.7	770	1	A4_PIG	P79307 p amyloid b
117	26	89.7	370	2	Q65SJI_MANSM	Q65sj1 manheimia	190	26	89.7	770	1	A4_RAT	P08592 r amyloid b
118	26	89.7	374	2	Q7MAT1_WOLSU	Q7mat1 wolliella s	191	26	89.7	770	2	Q6RH30_CANFA	Q6rh30 canis famil
119	26	89.7	384	2	Q8BPC7_MOUSE	Q8bpc7 mus musculus	192	26	89.7	770	2	Q56JK6_CANFA	Q56jk6 canis famil
120	26	89.7	391	2	Q4NSU7_THRPA	Q4nsu7 theileria p	193	26	89.7	770	2	Q53ZT3_MOUSE	Q53zt3 mus musculu
121	26	89.7	395	2	Q95WD9_9DIPT	Q95wd9 phlebotomus	194	26	89.7	770	2	Q547B7_RAT	Q547b7 rattus norv
122	26	89.7	403	2	Q5L117_GEOKA	Q5l117 geobacillus	195	26	89.7	780	1	A4_TETFL	Q73583 tetraodon f
123	26	89.7	404	2	Q4UY85_XANCP	Q4uy85 xanthomonas	196	26	89.7	817	2	Q6QP9_VIBVU	Q6qp9 vibrio vuln
124	26	89.7	404	2	Q8P597_XANCP	Q8p597 xanthomonas	197	26	89.7	817	2	Q87FQ8_VIBPU	Q87fq8 vibrio para
125	26	89.7	428	2	Q9MIQ8_ARATH	Q9miq8 arabidopsis	198	26	89.7	817	2	Q8D4P2_VIBVU	Q8d4p2 vibrio vuln
126	26	89.7	443	2	Q4RHQ1_CAMCO	Q4rhq1 campylobact	199	26	89.7	817	2	Q9KNF1_VIBCH	Q9knf1 vibrio chol
127	26	89.7	461	2	Q89J29_9POTV	Q89j29 zucchini ye	200	26	89.7	840	2	Q7MG92_VIBVU	Q7mg92 vibrio vuln
128	26	89.7	467	2	Q4L319_STAHO	Q4l319 staphylococ	201	26	89.7	939	2	Q6CET0_YARLI	Q6cet0 yarrowia li
129	26	89.7	469	2	Q4Y318_PLACH	Q4y318 plasmodium	202	26	89.7	955	2	Q8ORZ2_9POTV	Q8orz2 calla lily
130	26	89.7	470	2	Q7T910_9POTV	Q7t910 zucchini ye	203	26	89.7	962	2	Q4NTK2_9DELT	Q4ntk2 anaeromyxob
131	26	89.7	472	2	Q6UUS0_BRARE	Q6uus0 brachydanio	204	26	89.7	1016	2	Q05912_9POTV	Q05912 zucchini ye
132	26	89.7	477	1	VPUM_RHOCA	P26176 rhodobacter	205	26	89.7	1056	2	Q6FKH6_CANGA	Q6fkh6 candida gla
133	26	89.7	488	2	Q52NV6_9POTV	Q52nv6 zucchini ye	206	26	89.7	1083	2	Q8I311_PLAF7	Q8i311 plasmodium
134	26	89.7	490	2	Q7T911_9POTV	Q7t911 zucchini ye	207	26	89.7	1497	2	Q95YH6_DROME	Q95yh6 drosophila
135	26	89.7	490	2	Q7T912_9POTV	Q7t912 zucchini ye	208	26	89.7	1571	2	Q95YH7_DROME	Q95yh7 drosophila
136	26	89.7	493	2	Q5K4D4_9POTV	Q5k4d4 soybean mos	209	26	89.7	1571	2	Q8MSQ4_DROME	Q8msq4 drosophila
137	26	89.7	493	2	Q5K4D5_9POTV	Q5k4d5 soybean mos	210	26	89.7	1612	2	Q9VE37_DROME	Q9ve37 drosophila
138	26	89.7	496	2	Q5K4D0_9POTV	Q5k4d0 daeheen mos	211	26	89.7	1916	2	Q8QKUA_9POTV	Q8qkua zucchini ye
139	26	89.7	508	2	Q5GV85_XANOR	Q5gv85 xanthomonas	212	26	89.7	3080	1	POLG_ZTMVC	P18479 z genome po
140	26	89.7	520	2	Q9K207_CHLPN	Q9k207 chlamydia p	213	26	89.7	3080	2	Q6WN47_9POTV	Q6wn47 zucchini ye
141	26	89.7	534	2	Q93296_CHICK	Q93296 gallus gall	214	26	89.7	3080	2	Q6WN48_9POTV	Q6wn48 zucchini ye
142	26	89.7	554	2	Q7P7T7_FUSNV	Q7p7t7 fusobacteri	215	26	89.7	3080	2	Q6WN49_9POTV	Q6wn49 zucchini ye
143	26	89.7	559	2	Q9PVL1_CHICK	Q9pvl1 gallus gall	216	26	89.7	3080	2	Q6Y2U7_9POTV	Q6y2u7 zucchini ye
144	26	89.7	594	2	Q9JSK0_CHLPN	Q9jsk0 chlamydia p	217	26	89.7	3080	2	Q7T908_9POTV	Q7t908 zucchini ye
145	26	89.7	603	2	Q9XIQ9_THEME	Q9xiq9 thermotoga	218	26	89.7	3080	2	Q7T914_9POTV	Q7t914 zucchini ye
146	26	89.7	609	2	Q6CFJ3_YARLI	Q6cfj3 yarrowia li	219	26	89.7	3083	1	POLG_ZTMVS	Q36979 z genome po
147	26	89.7	612	2	Q919E7_BRARE	Q919e7 brachydanio	220	26	89.7	3105	2	Q7OXR2_9POTV	Q7oxr2 soybean mos
148	26	89.7	613	2	Q8HML1_9TELE	Q8hml1 hiodon alos	221	25	86.2	40	2	Q91FF3_IRV6	Q91ff3 chilo iride
149	26	89.7	614	2	Q94YP6_9TELE	Q94yp6 osteoglossu	222	25	86.2	66	2	Q728F0_DESVH	Q728f0 desulfovibr
150	26	89.7	615	2	Q50Z85_ENTHI	Q50z85 entamoeba h	223	25	86.2	74	1	Y131_MYCGE	P47377 mycoplasma
151	26	89.7	617	2	Q9Z9B2_CHLPN	Q9z9b2 chlamydia p	224	25	86.2	81	2	Q6D3D0_ERWCT	Q6d3d0 erwinia car
152	26	89.7	617	2	Q8RDN8_FUSNP	Q8rdn8 fusobacteri	225	25	86.2	89	2	Q83VF2_LACLC	Q83vf2 lactococcus
153	26	89.7	634	2	Q7SD58_NEUCR	Q7sd58 neurospora	226	25	86.2	104	2	Q5LXX2_STRT1	Q5lxx2 streptococc
154	26	89.7	638	2	Q5B3V4_EMENI	Q5b3v4 aspergillus	227	25	86.2	104	2	Q5M2H4_STRT2	Q5m2h4 streptococc
155	26	89.7	670	2	Q8KGX2_RHILO	Q8kgx2 rhizobium l	228	25	86.2	105	2	Q64CV5_9ARCH	Q64cv5 uncultured
156	26	89.7	678	2	Q7Z2T1_BRARE	Q7z2t1 brachydanio	229	25	86.2	107	2	Q59MN1_CANAL	Q59mn1 candida alb
157	26	89.7	682	2	Q64DY0_9ARCH	Q64dy0 uncultured	230	25	86.2	107	2	Q8E222_STRAS	Q8e222 streptococc
158	26	89.7	693	2	Q98SG0_XENLA	Q98sg0 xenopus lae	231	25	86.2	107	2	Q8E7H9_STRAS	Q8e7h9 streptococc
159	26	89.7	695	2	Q64BX4_9ARCH	Q64bx4 uncultured	232	25	86.2	109	2	Q9X292_THEME	Q9x292 thermotoga
160	26	89.7	695	2	Q5R477_PONFY	Q5r477 pongo pygma	233	25	86.2	122	2	Q4Y0Z7_PLACH	Q4y0z7 plasmodium
161	26	89.7	695	2	Q6RH29_CANFA	Q6rh29 canis famil	234	25	86.2	124	2	Q61N30_CAFBR	Q61n30 caenorhabdi
162	26	89.7	695	2	Q56JK3_CANFA	Q56jk3 canis famil	235	25	86.2	125	2	Q6U9U2_9CAUD	Q6u9u2 bacterioph
163	26	89.7	695	2	Q6GR78_MOUSE	Q6gr78 mus musculu	236	25	86.2	125	2	Q56F01_9CAUD	Q56f01 aeromonas p
164	26	89.7	695	2	Q9DGJ8_CHICK	Q9dgj8 gallus gall	237	25	86.2	128	2	Q6LGS9_PHOPR	Q6lgs9 photobacter
165	26	89.7	695	2	Q98SF9_XENLA	Q98sf9 xenopus lae	238	25	86.2	136	2	Q18208_CAEEL	Q18208 caenorhabdi
166	26	89.7	695	2	Q7ZXQ0_XENLA	Q7zxq0 xenopus lae	239	25	86.2	141	2	Q8U3A1_PYRFU	Q8u3a1 pyrococcus
167	26	89.7	714	2	Q56JK4_CANFA	Q56jk4 canis famil	240	25	86.2	143	2	Q91Y69_MESAU	Q91y69 mesocricetu
168	26	89.7	733	2	Q6PQ05_RAT	Q6pq05 rattus norv	241	25	86.2	145	2	Q5USA9_9PEZI	Q5usa9 monacraspor
169	26	89.7	737	1	A4_FUGRU	Q93279 fugu rubrip	242	25	86.2	146	2	Q9V0B4_PYFAB	Q9v0b4 pyrococcus
170	26	89.7	738	2	Q6NUZ1_BRARE	Q6nuz1 brachydanio	243	25	86.2	148	2	Q17202_CAEEL	Q17202 caenorhabdi
171	26	89.7	738	2	Q90W28_BRARE	Q90w28 brachydanio	244	25	86.2	156	2	Q8DN20_STRR6	Q8dn20 streptococc
172	26	89.7	747	2	Q91963_9PIPI	Q91963 xenopus ap	245	25	86.2	156	2	Q97N92_STRPN	Q97n92 streptococc
173	26	89.7	749	2	Q56JK2_STECO	Q56jk2 stenella co	246	25	86.2	157	2	Q8XNL2_CLOPE	Q8xnl2 clostridium
174	26	89.7	749	2	Q6NRR1_XENLA	Q6nrr1 xenopus lae	247	25	86.2	159	2	Q58626_PYRHO	Q58626 pyrococcus
175	26	89.7	750	2	Q6DJB6_XENTR	Q6djbb6 xenopus tro	248	25	86.2	161	2	Q32197_9LILI	Q32197 eichornia
176	26	89.7	751	1	A4_SAISC	Q95241 r amyloid b	249	25	86.2	162	2	Q9N284_BOVIN	Q9n284 bos taurus
177	26	89.7	751	2	Q6GSC0_HUMAN	Q6gsc0 homo sapien	250	25	86.2	163	2	Q32164_9LILI	Q32164 eichornia

251 25 86.2 163 2 Q32179 9LILI Q32179 eichhornia
 252 25 86.2 163 2 Q32190 9LILI Q32190 eichhornia
 253 25 86.2 163 2 Q32201 9LILI Q32201 eichhornia
 254 25 86.2 163 2 Q32202 9LILI Q32202 eichhornia
 255 25 86.2 163 2 Q32210 9LILI Q32210 eichhornia
 256 25 86.2 163 2 Q32390 9LILI Q32390 heteranther
 257 25 86.2 163 2 Q32419 9LILI Q32419 heteranther
 258 25 86.2 163 2 Q32424 9LILI Q32424 heteranther
 259 25 86.2 163 2 Q32430 9LILI Q32430 heteranther
 260 25 86.2 163 2 Q32441 9LILI Q32441 heteranther
 261 25 86.2 163 2 Q32556 9LILI Q32556 monochoria
 262 25 86.2 163 2 Q32579 9LILI Q32579 monochoria
 263 25 86.2 163 2 Q32648 9LILI Q32648 monochoria
 264 25 86.2 163 2 Q32802 PONCO Q32802 pontederia
 265 25 86.2 163 2 Q32892 9LILI Q32892 pontederia
 266 25 86.2 163 2 Q32915 9LILI Q32915 pontederia
 267 25 86.2 164 2 Q81Y15 BACAN Q81Y15 bacillus an
 268 25 86.2 165 2 Q37011 PONCO Q37011 pontederia
 269 25 86.2 172 2 Q33PK3 ORISA Q33PK3 oriza sativ
 270 25 86.2 180 2 Q5NLQ4 ZYMMO Q5NLQ4 zymomonas m
 271 25 86.2 188 2 Q8W2G3 ORISA Q8W2G3 oriza sativ
 272 25 86.2 188 2 Q7VR27 CANBF Q7VR27 candidatus
 273 25 86.2 188 2 Q67835 AQUAE Q67835 aquifex aeo
 274 25 86.2 190 2 Q92WB8 RHIME Q92WB8 rhizobium m
 275 25 86.2 194 2 Q97G46 CLOAB Q97G46 clostridium
 276 25 86.2 196 2 Q6HVS9 BACAN Q6HVS9 bacillus an
 277 25 86.2 196 2 Q4U6V3 9VIRU Q4U6V3 potato viru
 278 25 86.2 197 2 Q7VR77 CANBF Q7VR77 candidatus
 279 25 86.2 198 2 Q46025 CORDI Q46025 corynebacte
 280 25 86.2 198 2 Q847W0 VIBPA Q847W0 vibrio para
 281 25 86.2 198 2 Q6NGT3 CORDI Q6NGT3 corynebacte
 282 25 86.2 198 2 Q87168 VIBPA Q87168 vibrio para
 283 25 86.2 199 2 Q7MFJ3 VIBVY Q7MFJ3 vibrio vuln
 284 25 86.2 200 1 COAE LISIN Q92BF2 listeria in
 285 25 86.2 200 2 Q73L44 TREDE Q73L44 treponema d
 286 25 86.2 202 2 Q7P578 FUSNV Q7P578 fusobacteri
 287 25 86.2 202 2 Q8RE19 FUSNV Q8RE19 fusobacteri
 288 25 86.2 208 2 Q5QBU5 9ACTO Q5QBU5 nonomuraea
 289 25 86.2 210 2 Q8T312 DROME Q8T312 dreophilila
 290 25 86.2 217 2 Q84019 PSECL Q84019 pseudomonas
 291 25 86.2 218 2 Q5CYB3 CRYPV Q5CYB3 cryptospori
 292 25 86.2 218 2 Q5CIV9 CRYHO Q5CIV9 cryptospori
 293 25 86.2 220 2 Q5Z2T4 PEMVM Q5Z2T4 peanut mott
 294 25 86.2 228 2 Q51V22 MAGGR Q51V22 magnaporthe
 295 25 86.2 229 2 Q70Z41 9VIRU Q70Z41 potato viru
 296 25 86.2 229 2 Q7TD31 9VIRU Q7TD31 potato viru
 297 25 86.2 229 2 Q7TD37 9VIRU Q7TD37 potato viru
 298 25 86.2 230 2 Q7RDM9 PLAYO Q7RDM9 plasmodium
 299 25 86.2 231 2 Q637W5 BACCZ Q637W5 bacillus ce
 300 25 86.2 232 2 Q84601 CHLTR Q84601 chlamydia t

ALIGNMENTS

RESULT 1
 GL19 ORISA
 ID GL19 ORISA STANDARD; PRT; 186 AA.
 AC P29835;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE 19 kDa globulin precursor (Alpha-globulin).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 ON NCBI_TaxID=4530;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
 RC STRAIN=cv. Japonica / Nipponbare; TISSUE=Endosperm;
 RX MEDLINE=92119226; PubMed=1731968;
 RA Shorrosh B.S., Wen L., Zen K.C., Huang J.K., Pan J.S., Hermodson M.A.,

Tanaka K., Muthukrishnan S., Reeck G.R.;
 "A novel cereal storage protein: molecular genetics of the 19 kDa
 Globulin of rice."
 Plant Mol. Biol. 18:151-154 (1992).
 [2]
 NUCLEOTIDE SEQUENCE OF 5-186.
 RC STRAIN=cv. Japonica / Lemont; TISSUE=Endosperm;
 RC MEDLINE=93277591; PubMed=8503935;
 RX Krishnan H.B., Pueppke S.G.;
 "Nucleotide sequence of an abundant rice seed globulin: homology with
 the high molecular weight glutelins of wheat, rye and tritcale."
 Biochem. Biophys. Res. Commun. 193:460-466(1993).
 CC -1- FUNCTION: Seed storage protein.
 CC -1- SIMILARITY: Belongs to the 2S seed storage albumins family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 CC EMBL; X63990; CAA45400.1; -; mRNA.
 DR EMBL; L12252; AAA72362.1; ALT_INIT; mRNA.
 DR PIR; S20024; WMEZ19.
 DR HSP; P24565; IPNB.
 DR Gramene; P29835; -.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001419; Glutenin.
 DR PANTHER; PTHR14054; Glutenin; 1.
 DR Pfam; PF00234; Tryp alpha amyl; 1.
 DR PRINTS; PR00210; GLUTENIN.
 DR SMART; SM00499; AAI; 1.
 DR Direct protein sequencing; Seed storage protein; Signal;
 KW Storage protein.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 186 19 kDa globulin.
 SQ SEQUENCE 186 AA; 21050 MW; 9E09BA74CB086810 CRC64;
 Query Match 100.0%; Score 29; DB 1; Length 186;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KWVFFA 6
 Db |||||
 4 KWVFFA 9
 RESULT 2
 P93414 ORISA
 ID P93414 ORISA PRELIMINARY; PRT; 186 AA.
 AC P93414;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE 26 kDa globulin (Alpha-globulin).
 GN Name=P010D04.16; Synonyms=QJ1057_B02.5;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 ON NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Endosperm;
 RX MEDLINE=96235139; PubMed=8666249; DOI=10.1016/0378-1119(95)00887-X;
 RA Nakase M., Hotta H., Adachi T., Aoki N., Nakamura R., Masumura T.,
 RA Tanaka K., Matsuda T.;
 "Cloning of the rice seed alpha-globulin-encoding gene: sequence
 similarity of the 5'-flanking region to those of the genes encoding
 wheat high molecular-weight glutenin and barley D hordein."
 Gene 170:223-226(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN
RN NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RT "Oryza sativa BAC QJ1057.B02 genomic sequence.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; D50643; BAA03308.1; -; Genomic DNA.
DR ENBL; AC130605; AAT44292.1; -; Genomic DNA.
DR ENBL; AC113332; AAT93857.1; -; Genomic DNA.
DR PIR; JC4784; JC4784.
DR HSP; P24565; 1PNB.
DR Gramene; P33414; -.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutinin.
DR Pfam; PF00234; Tryp alpha amyl; 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 186 AA; 21055 MW; AE2B8F1107C8BC94 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 4 KVVFFA 9
|||||
|||||

RESULT 3
ID Q8C6Y8_MOUSE PRELIMINARY; PRT; 231 AA.
AC Q8C6Y8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched
DE library, clone:D830015B12 product:hypothetical DEAD/DEAH box helicase
DE containing protein, full insert sequence. (Fragment).
GN Names=Ddx58;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gotjohori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
RA Guscincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai C., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AK052871; BAC35183.1; -; mRNA.
DR MGI; MGI:2442858; Ddx58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR Pfam; PF00270; DEAD; 1.
DR SMART; SM00487; DEXDc; 1.
DR HeliCase; Hypothetical protein.
FT NON_TER 231 231
SQ SEQUENCE 231 AA; 25524 MW; 1D191607390D7FBB CRC64;

Query Match

100.0%; Score 29; DB 2; Length 231;

```

Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy 1 KVVFFA 6
Db 145 KVVFFA 150

RESULT 4
Q6D7U3 ERWCT
ID Q6D7U3 ERWCT PRELIMINARY; PRT; 372 AA.
AC Q6D7U3
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hydrogenase isoenzymes formation protein.
GN Name=hypD; OrderedLocusNames=KCA1232;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebatia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holleva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RA "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
DR EMBL; BX950851; CAG74142.1; -; Genomic_DNA.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR PIRSF; PIRSF005622; Hydrn_mat_hypD; 1.
DR TIGRFAMs; TIGR00075; hypD; 1.
KW Complete proteome.
SQ SEQUENCE 372 AA; 41130 MW; A001A18AC015E620 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 139 KVVFFA 144

RESULT 5
Q7M9N5 WOLSU
ID Q7M9N5 WOLSU PRELIMINARY; PRT; 373 AA.
AC Q7M9N5
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE HYDROGENASE PROTEIN.
GN Name=HYPD; OrderedLocusNames=WS0793;
OS Wolinella succinogenes.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Wolinella.
OX NCBI_TaxID=844;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DSMZ 1740;
RX MEDLINE=22682897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
RA Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
RA Meyer F., Lederer H., Schuster S.C.;
RT "Complete genome sequence and analysis of Wolinella succinogenes.";

```

```

Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
DR EMBL; BX571659; CA09906.1; -; Genomic_DNA.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR PIRSF; PIRSF005622; Hydrn_mat_hypD; 1.
DR TIGRFAMs; TIGR00075; hypD; 1.
KW Complete proteome.
SQ SEQUENCE 373 AA; 41793 MW; 3B7815EDB25790A6 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 373;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 138 KVVFFA 143

RESULT 6
Q9KI10 BACCE
ID Q9KI10 BACCE PRELIMINARY; PRT; 387 AA.
AC Q9KI10;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE GerN.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1396;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC10876;
RX MEDLINE=20576148; PubMed=11133940; DOI=10.1128/JB.183.2.476-482.2001;
RA Thackray P.D., Behravan J., Southworth T.W., Moir A.;
RT "GerN, an antipporter homologue important in germination of Bacillus
RT cereus endospores.";
RL J. Bacteriol. 183:476-482(2001).
DR EMBL; AF246294; AAF91326.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antipporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; Keff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41093 MW; 40DE45B71B715D01 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 184 KVVFFA 189

RESULT 7
Q4MT39 BACCE
ID Q4MT39 BACCE PRELIMINARY; PRT; 387 AA.
AC Q4MT39;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Na+/H+ antipporter.
GN ORFNames=BCE_G9241_1647;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;

```

```

OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Ralston J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR ENBL; AAE01000008; EMBL15336.1; -; Genomic DNA.
SQ SEQUENCE 387 AA; 41122 MW; 15CC136E79912C38 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 184 KVVFFA 189

RESULT 8
Q63DD4_BACCZ
ID Q63DD4_BACCZ PRELIMINARY; PRT; 387 AA.
AC Q63DD4;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN;
OS Bacillus cereus (strain ZK).
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; CP000001; AAU18770.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
SQ SEQUENCE 387 AA; 41090 MW; DBA5991F6DD63F33 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 184 KVVFFA 189

RESULT 9
Q63DD4_BACCZ
ID Q63DD4_BACCZ PRELIMINARY; PRT; 387 AA.
AC Q63DD4;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN;
OS Bacillus cereus (strain ZK).
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; CP000001; AAU18770.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
SQ SEQUENCE 387 AA; 41090 MW; DBA5991F6DD63F33 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 184 KVVFFA 189

RESULT 9

```

```

Q6HKU6_BACHK
ID Q6HKU6_BACHK PRELIMINARY; PRT; 387 AA.
AC Q6HKU6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN; OrderedLocusNames=BT9727_1493;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=97-27;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; AE017355; AAT63168.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
SQ SEQUENCE 387 AA; 41076 MW; DFECD90985F951 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 184 KVVFFA 189

RESULT 10
Q73AP3_BACCI
ID Q73AP3_BACCI PRELIMINARY; PRT; 387 AA.
AC Q73AP3;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Germination protein gerN.
GN OrderedLocusNames=BCB1729;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14960714; DOI=10.1093/nar/gkh358;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pX01.";
RL Nucleic Acids Res. 32:977-988(2004).
DR ENBL; AE017269; AAS40658.1; -; Genomic DNA.
DR TIGR; BCB1729; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.

```



```
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41104 MW; DC7CD48C609FEB3A3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 184 KVVFFA 189

RESULT 11
O81SK9_BACAN PRELIMINARY; PRT; 387 AA.
AC O81SK9; Q610J3; Q6KUP8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Germination protein Gen.
OS OrderedLocusNames=BA1639, BAS1521, GBAA1639;
OC Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Risetone J., Wu M.,
RA Kolony J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ames / isolate 0581;
RX Ravel J., Raeko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Sterne;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne.";
RL EMBL; AB017029; AAT25572.1; -; Genomic DNA.
DR EMBL; AB017334; AAT30749.1; -; Genomic DNA.
DR EMBL; AE017225; AAT53839.1; -; Genomic DNA.
DR TIGR; BA1639; -.
DR TIGR; GBAA1639; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0008324; F: cation transporter activity; IEA.
DR GO; GO:0015299; F: solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P: cation transport; IEA.
DR GO; GO:0006885; P: regulation of pH; IEA.

DR GO; GO:0006810; P: transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 40932 MW; D59F6A08A283BCA3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 184 KVVFFA 189

RESULT 12
O8C5I3_MOUSE PRELIMINARY; PRT; 410 AA.
AC O8C5I3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
DE enriched library, clone:6430573D20 product:hypothetical DEAD/DEAH box
DE helicase containing protein, full insert sequence.
GN Names=Ddx58;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085650; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai J., Offelli D., Bojunga N., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
```

```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishimi T., Hatada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AK078287; BAC37205.1; -; mRNA.
DR Ensembl; ENSMUSG0000040296; Mus musculus.
DR MGI; MGI:242858; Ddx58.
DR GO; GO:0005224; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR Pfam; PF00270; DEAD; 1.
DR SMART; SM00487; DEXDC; 1.
DR Helicase; Hypothetical protein; Nuclear protein.
SQ SEQUENCE 410 AA; 46841 MW; ECC9E3D2D2BC5FE0 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 293 KVVFFA 298
|||||

RESULT 13
Q9PHV5_CAMJ6 PRELIMINARY; PRT; 442 AA.
AC Q9PHV5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Putative integral membrane protein.
GN OrderedLocusNames=Cj0560;
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]

```

```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
RA Parkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtrold S.,
RA Jagels K., Karyshnev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajadream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL; ALI39075; CAB75196.1; -; Genomic_DNA.
DR FIC; H81402; H81402.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; P:anion transporter activity; IEA.
DR GO; GO:0015238; P:drug transporter activity; IEA.
DR GO; GO:0008855; P:multidrug transport; IEA.
DR InterPro; IPR002114; HPR_SerP_S.
DR InterPro; IPR002528; MatE; 1.
DR Pfam; PF01554; MatE; 1.
DR TIGRFAMs; TIGR00797; matE; 1.
DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
SQ SEQUENCE 442 AA; 49452 MW; 38EA04E7AB1A8F3E CRC64;

Query Match 100.0%; Score 29; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 313 KVVFFA 318
|||||

RESULT 14
QSHYEL_HUMAN PRELIMINARY; PRT; 703 AA.
AC QSHYEL;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein DKFP686N19181 (fragment).
GN Name=DKFP686N19181;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin endothel;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX647917; CAI46068.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICc; 1.
KW Hypothetical protein.
FT NON_TER 703
SQ SEQUENCE 703 AA; 80308 MW; 3CF7500F4F955586 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 703;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 KVFFFA 6
Db 247 KVFFFA 252

RESULT 15
Q6AG25 LEIXX
ID Q6AG25 LEIXX PRELIMINARY; PRT; 721 AA.
AC Q6AG25;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE ATP-dependent RNA helicase.
GN OrderedLocusNames=Lxx07490;
OS Leifsonia xyl (subsp. xyl).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcales; Microbacteriaceae; Leifsonia.
OX NCBI_TaxID=59736;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CTCB07;
RX PubMed=15305603;
RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R., C.Y.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
RA Almeida N.F. Jr., Carrer H., Coutinho L.L., El-Dorri H.A.,
RA Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,
RA Lemos M.V.P., Oliveira R.C., Machado M.A., Marino C.L., Menck C.F.,
RA Nunes L.R., Pereira S.C., Pereira G.G., Siqueira W., de Souza A.A.,
RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;
RA "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
RT xyl subsp. xyl.";
RL Mol. Plant Microbe Interact. 17:827-836(2004).
DR EMBL; AB016822; AAT8670.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
KW Complete proteome; DNA-binding; Helicase; Hydrolase.
SQ SEQUENCE 721 AA; 7860 MW; 73F5D2A8435BADE3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 721;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFFFA 6
Db 564 KVFFFA 569

RESULT 16
Q95786 HUMAN
ID Q95786_HUMAN PRELIMINARY; PRT; 925 AA.
AC Q95786;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RNA helicase.
GN Name=DDX58; Synonyms=RIG-I;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

Sun Y.W.;
"RIG-I, a human homolog gene of RNA helicase, is induced by retinoic
acid during the differentiation of acute promyelocytic leukemia
cell.";
Thesis (1997), Shanghai Institute of Hematology, Rui-Jin Hospital,
Shanghai Second Medical University.
[2]
NUCLEOTIDE SEQUENCE.
Yi-Wu S.;
Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
EMBL; AF038963; AAD19826.1; -; mRNA.
Ensembl; ENSG00000107201; Homo sapiens.
HGNC; HGNC:19102; DDX58.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004386; F:helicase activity; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
GO; GO:0000166; F:nucleotide binding; IEA.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR011545; DEAD/DEAH_N.
InterPro; IPR001650; Helicase_C.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; Helicase_C; 1.
SMART; SM00382; AAA; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
KW Helicase.
SQ SEQUENCE 925 AA; 106613 MW; 5922B4F3DD0F00D4 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 925;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFFFA 6
Db 292 KVFFFA 297

RESULT 17
Q5VYTI HUMAN
ID Q5VYTI_HUMAN PRELIMINARY; PRT; 925 AA.
AC Q5VYTI;
DT 01-FEB-2005 (Tremblrel. 29, Created)
DT 01-FEB-2005 (Tremblrel. 29, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE OTTHUMP00000021185.
GN Name=RP11-334P12.2; ORFNames=RP11-334P12.2-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Doggett S.;
Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
[2]
NUCLEOTIDE SEQUENCE.
Sehra H.;
Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
-1- SUBCELLULAR LOCATION: Nuclear (By similarity).
EMBL; AL353671; CAH71251.1; -; Genomic_DNA.
EMBL; AL161783; CAH72600.1; -; Genomic_DNA.
EMBL; AL161783; CAH71251.1; JOINED; Genomic_DNA.
EMBL; AL353671; CAH72600.1; JOINED; Genomic_DNA.
Ensembl; ENSG00000107201; Homo sapiens.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004386; F:helicase activity; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR011545; DEAD/DEAH_N.
InterPro; IPR001650; Helicase_C.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; Helicase_C; 1.

```

```

DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Helicase; Hydrolase; Nuclear protein.
SQ SEQUENCE 925 AA; 106600 MW; BF0D501C395BAE25 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 925;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |||||
Db 292 KVVFFA 297

RESULT 18
Q60899 MOUSE
ID Q60899_MOUSE PRELIMINARY; PRT; 926 AA.
AC Q60899
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DEAD/H box polypeptide RIG-I.
GN Names=Ddx58;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wei J., Gu J.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY553221; AAS59532.1; -; mRNA.
DR MGI; MGI:2442858; Ddx58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:Helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR006935; ResIII.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF04851; ResIII; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
SQ SEQUENCE 926 AA; 105877 MW; 632462010107698E CRC64;

Query Match 100.0%; Score 29; DB 2; Length 926;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |||||
Db 293 KVVFFA 298

RESULT 19
Q9GLV6_PIG
ID Q9GLV6_PIG PRELIMINARY; PRT; 940 AA.
AC Q9GLV6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNA helicase.
GN Names=RHIV-1;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zhang X., Wang C., Schook L.B., Hawken R.J., Rutherford M.S.;

```

```

RT "An RNA helicase, RHIV -1, induced by porcine reproductive and
RT respiratory syndrome virus (PRRSV) is mapped on porcine chromosome
RT 10q13."
RL Microb. Pathog. 28:267-278(2000).
CC -1- SURCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF181119; AAG09428.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:Helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Helicase; Hydrolase; Nuclear protein; Repeat.
SQ SEQUENCE 940 AA; 107584 MW; 118CA910B0AF7821 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 940;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |||||
Db 290 KVVFFA 295

RESULT 20
NOS2_MOUSE
ID NOS2_MOUSE STANDARD; PRT; 1144 AA.
AC P29477; O70515; O70516;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
DE (Inducible NOS) (iNOS) (Macrophage NOS) (MAC-NOS).
GN Name=Nos2; Synonyms=Inos1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Xie Q.-W., Cho H.J., Calaycay J., Mumford R.A., Swiderek K.M.,
RA Lee T.D., Ding A., Troso T., Nathan C.;
RT "Cloning and characterization of inducible nitric oxide synthase from
RT mouse macrophages."
RL Science 256:225-228(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX Lowenstein C.J., Glatz C.S., Bredt D.S., Snyder S.H.;
RA "Cloned and expressed macrophage nitric oxide synthase contrasts with
RT the brain enzyme."
RL Proc. Natl. Acad. Sci. U.S.A. 89:6711-6715(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX Lyons C.R., Orloff G.J., Cunningham J.M.;
RA "Molecular cloning and functional expression of an inducible nitric
RT oxide synthase from a murine macrophage cell line."
RL J. Biol. Chem. 267:6370-6374(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX Kone B.C., Schwoebel J., Turner P., Mohaupt M.G., Cangro C.B.;
RA "Role of NF-kappa B in the regulation of inducible nitric oxide
RT synthase in an MTL cell line."
RL Am. J. Physiol. 269:F718-F729(1995).
RN [5]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS ARG-211; LEU-967 AND PHE-968.

```

RC STRAIN-B10.S/J, BALB/cBYJ, DBA/2J, NOD/LtJ, and SJL/J; TISSUE-Spleen;
 RX MEDLINE=99370037; PubMed=10438970;
 RA Blankenhorn E.P.;
 RA "Sequence polymorphisms in the chemokines Sclal (TCA-3), Sclal2
 RT (monocyte chemoattractant protein (MCP)-1), and Sclal2 (MCP-5) are
 RT candidates for eae7, a locus controlling susceptibility to monophasic
 RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
 RL J. Immunol. 163:2262-2266(1999).
 [6]
 RN EFFECT OF ASPIRIN.
 RC TISSUE=Macrophage;
 RX MEDLINE=95372392; PubMed=7544010;
 RA Amin A.R., Vyas P., Attur M., Leszczynska-Piziak J., Patel I.R.,
 RA Weissmann G., Abramson S.B.;
 RA "The mode of action of aspirin-like drugs: effect on inducible nitric
 RT oxide synthase.";
 RT Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).
 [7]
 RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 116-496.
 RX MEDLINE=97477482; PubMed=9334294; DOI=10.1126/science.278.5337.425;
 RA Crane B.R., Arvai A.S., Gachhui R., Wu C., Ghosh D.K., Getzoff E.D.,
 RA Stuehr D.J., Tainer J.A.;
 RA "The structure of nitric oxide synthase oxygenase domain and inhibitor
 RT complexes.";
 RL Science 278:425-431(1997).
 [8]
 RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.
 RX MEDLINE=98182450; PubMed=9516116; DOI=10.1126/science.279.5359.2121;
 RA Crane B.R., Arvai A.S., Ghosh D.K., Wu C., Getzoff E.D., Stuehr D.J.,
 RA Tainer J.A.;
 RA "Structure of nitric oxide synthase oxygenase dimer with pterin and
 RT substrate.";
 RL Science 279:2121-2126(1998).
 [9]
 RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
 RX MEDLINE=20031637; PubMed=10562539; DOI=10.1093/emboj/18.22.6260;
 RA Ghosh D.K., Crane B.R., Ghosh S., Wolan D., Gachhui R., Crooks C.,
 RA Presta A., Tainer J.A., Getzoff E.D., Stuehr D.J.;
 RA "Inducible nitric oxide synthase: role of the N-terminal beta-hairpin
 RT hook and pterin-binding segment in dimerization and
 RT tetrahydrobiopterin interaction.";
 RL EMBO J. 18:6260-6270(1999).
 [10]
 RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499.
 RX MEDLINE=20031638; PubMed=10562539; DOI=10.1093/emboj/18.22.6271;
 RA Crane B.R., Rosenfeld R.J., Arvai A.S., Ghosh D.K., Ghosh S.,
 RA Tainer J.A., Stuehr D.J., Getzoff E.D.;
 RA "N-terminal domain swapping and metal ion binding in nitric oxide
 RT synthase dimerization.";
 RL EMBO J. 18:6271-6281(1999).
 [11]
 RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
 RX MEDLINE=20233702; PubMed=10769116; DOI=10.1021/bi992409a;
 RA Crane B.R., Arvai A.S., Ghosh S., Getzoff E.D., Stuehr D.J.,
 RA Tainer J.A.;
 RA "Structures of the N(omega)-hydroxy-L-arginine complex of inducible
 RT nitric oxide synthase oxygenase dimer with active and inactive
 RT pterins.";
 RL Biochemistry 39:4608-4621(2000).
 [12]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF TRP-457 MUTANTS.
 RX MEDLINE=21526413; PubMed=11669619; DOI=10.1021/bi011183k;
 RA Aoyagi M., Arvai A.S., Ghosh S., Stuehr D.J., Tainer J.A.,
 RA Getzoff E.D.;
 RA "Structures of tetrahydrobiopterin binding-site mutants of inducible
 RT nitric oxide synthase oxygenase dimer and implicated roles of
 RT Trp457.";
 RL Biochemistry 40:12826-12832(2001).
 [13]
 RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
 RX MEDLINE=22325496; PubMed=12437346; DOI=10.1021/bi026313j;
 RA Rosenfeld R.J., Garcin E.D., Panda K., Andersson G., Aberg A.,

RA Wallace A.V., Morris G.M., Olson A.J., Stuehr D.J., Tainer J.A.,
 RA Getzoff E.D.;
 RA "Conformational changes in nitric oxide synthase induced by
 RT chlorozoxone and nitroindazoles: crystallographic and computational
 RT analyses of inhibitor potency.";
 RL Biochemistry 41:13915-13925(2002).
 [14]
 RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 77-495.
 RX MEDLINE=22351717; PubMed=12464241; DOI=10.1016/S0003-9861(02)00555-6;
 RA Fedorov R., Ghosh D.K., Schlichting I.;
 RA "Crystal structures of cyanide complexes of P450cam and the oxygenase
 RT domain of inducible nitric oxide synthase - structural models of the
 RT short-lived oxygen complexes.";
 RL Arch. Biochem. Biophys. 409:25-31(2003).
 CC -I- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule
 CC with diverse functions throughout the body. In macrophages, NO
 CC mediates tumoricidal and bactericidal actions.
 CC -I- CATALYTIC ACTIVITY: L-arginine + n NADPH + m O(2) = citrulline +
 CC nitric oxide + n NADP(+).
 CC -I- COFACTOR: Heme.
 CC -I- COFACTOR: FAD. Binds 1 mole of FAD.
 CC -I- COFACTOR: FMN. Binds 1 mole of FMN.
 CC -I- COFACTOR: Tetrahydrobiopterin (BH4). May stabilize the dimeric
 CC form of the enzyme.
 CC -I- ENZYME REGULATION: Not stimulated by calcium/calmodulin. Aspirin
 CC inhibits expression and function of this enzyme and effects may be
 CC exerted at the level of translational/posttranslational
 CC modification and directly on the catalytic activity.
 CC -I- SUBUNIT: Homodimer. Binds SLC9A3R1 (By similarity).
 CC -I- TISSUE SPECIFICITY: Macrophages.
 CC -I- INDUCTION: By treatment with endotoxins or cytokines.
 CC -I- SIMILARITY: Belongs to the NOS family.
 CC -I- SIMILARITY: Contains 1 flavodoxin-like domain.

 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

 DR EMBL; M87039; AAA39315.1; -; mRNA.
 DR EMBL; M92649; -; NOT ANNOTATED CDS; mRNA.
 DR EMBL; M84373; AAA39834.1; -; mRNA.
 DR EMBL; U43428; AAC52356.1; -; mRNA.
 DR EMBL; AF065919; AAC17914.1; -; mRNA.
 DR EMBL; AF065920; AAC17915.1; -; mRNA.
 DR EMBL; AF065921; AAC17916.2; -; mRNA.
 DR EMBL; AF065922; AAC17917.2; -; mRNA.
 DR EMBL; AF065923; AAC17918.2; -; mRNA.
 DR PIR; A43271; A43271.
 DR PDB; 1DD7; X-ray; A=114-498.
 DR PDB; 1DF1; X-ray; A/B=77-499.
 DR PDB; 1DWV; X-ray; A/B=77-496.
 DR PDB; 1DWH; X-ray; A/B=77-496.
 DR PDB; 1DXX; X-ray; A/B=77-496.
 DR PDB; 1JWK; X-ray; A/B=66-498.
 DR PDB; 1JMK; X-ray; A/B=66-498.
 DR PDB; 1MB8; X-ray; A/B=65-498.
 DR PDB; 1MBE; X-ray; A/B=65-498.
 DR PDB; 1MBH; X-ray; A/B=65-498.
 DR PDB; 1MB1; X-ray; A/B=65-498.
 DR PDB; 1M9T; X-ray; A/B=77-495.
 DR PDB; 1N2N; X-ray; A/B=77-495.
 DR PDB; 1NOC; X-ray; A=115-498.
 DR PDB; 1NOD; X-ray; A/B=77-499.
 DR PDB; 1NOS; X-ray; A=115-498.
 DR PDB; 1QOM; X-ray; A/B=65-498.
 DR PDB; 1QW4; X-ray; A/B=77-495.
 DR PDB; 1QW5; X-ray; A/B=77-495.
 DR PDB; 1R35; X-ray; A/B=66-498.
 DR PDB; 1VAF; X-ray; A/B=77-495.
 DR PDB; 2BHJ; X-ray; A=77-498.
 DR PDB; 2NOD; X-ray; A/B=77-499.

```

DR PDB; 2NOS; X-ray; @=115-498.
DR PDB; 3NOD; X-ray; A/B=77-499.
DR IntAct; P29477; -.
DR Ensembl; ENSMUSG00000020826; Mus musculus.
DR MGI; MGI:97361; Nos2.
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0005516; F:calmodulin binding; TAS.
DR GO; GO:0020037; F:heme binding; NAS.
DR GO; GO:0020037; F:heme binding; NAS.

Query Match 100.0%; Score 29; DB 1; Length 1144;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFFFA 6
Db 514 KVFFFA 519

RESULT 21
Q5SXT3 MOUSE
ID Q5SXT3_MOUSE PRELIMINARY; PRT; 1144 AA.
AC Q5SXT3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Nitric oxide synthase 2, inducible, macrophage (Inducible nitric oxide
synthase).
GN Names=Nos2; ORFNames=RP23-341J22.2-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE.
RA Hopkins B.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CD-1;
RA Coxe F., Levacher B., Rique H., Leopold O., Boutin J.A.,
RA Gallizzi J.-P.;
RT "Genomic structure of the murine inducible nitric oxide synthase (i-
nos) gene.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL592185; CAI25275.1; -; Genomic_DNA.
DR EMBL; AF427516; AAL24076.1; -; Genomic_DNA.
SQ SEQUENCE 1144 AA; 130574 MW; 0735BE676113457F CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1144;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFFFA 6
Db 514 KVFFFA 519

RESULT 22
Q8R410 MOUSE
ID Q8R410_MOUSE PRELIMINARY; PRT; 1145 AA.
AC Q8R410;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inducible nitric oxide synthase.
GN Names=Nos2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

```

```

OX NCBI_TaxID=10090;
RN [1]
RC STRAIN=ICR;
RA Hagiwara K., Endo Y., Xin H., Takahashi M., Huqun, Nukiwa T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY090567; AAM11887.1; -; mRNA.
DR HSSP; P29477; 1DWV.
DR MGI; MGI:97361; Nos2.
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.
DR GO; GO:0042803; F:protein homodimerization activity; IDA.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0001542; P:ovulation (sensu Mammalia); IMP.
DR GO; GO:0045585; P:positive regulation of cytotoxic T-cell dif. .; ISS.
DR GO; GO:0001666; P:response to hypoxia; IDA.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR008254; Flav_nitox_synth.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO_synthase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO_synthase; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS0902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN 1.
SQ SEQUENCE 1145 AA; 130685 MW; DAD5AAF53680B005 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1145;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFFFA 6
Db 515 KVFFFA 520

RESULT 23
Q6P6A0 MOUSE
ID Q6P6A0_MOUSE PRELIMINARY; PRT; 1145 AA.
AC Q6P6A0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Nos2 protein.
GN Name=Nos2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner C.M., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

```

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RC Strausberg R.;
 RA Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC062378; AA062378.1; -; mRNA.
 DR HSSP; P29477; 1JWK.
 DR MGI; MGI:97361; Nos2.
 DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
 DR GO; GO:0048471; C:perinuclear region; IDA.
 DR GO; GO:0004517; F:nitric-oxide synthase activity; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0042803; F:protein homodimerization activity; IDA.
 DR GO; GO:0042742; P:defense response to bacteria; IMP.
 DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
 DR GO; GO:0001666; P:response to hypoxia; IDA.
 DR GO; GO:0006801; P:superoxide metabolism; IMP.
 DR InterPro; IPR003097; FAD binding.
 DR InterPro; IPR001094; Flavodoxin like.
 DR InterPro; IPR008254; Flavodoxin synth.
 DR InterPro; IPR001709; FPN_Cyt_redtse.
 DR InterPro; IPR012144; NOS.
 DR InterPro; IPR004030; NO synthase.
 DR InterPro; IPR001433; Oxid FAD/NAD(P).
 DR Pfam; PF00667; FAD binding_1; 1.
 DR Pfam; PF00258; Flavodoxin_1; 1.
 DR Pfam; PF00175; NAD binding_1; 1.
 DR Pfam; PF02898; NO synthase; 1.
 DR PIRSF; PIRSF000333; NOS; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 DR PROSITE; PS0902; FLAVODOXIN LIKE; 1.
 DR PROSITE; PS60001; NOS; UNKNOWN 1.
 SQ SEQUENCE 1145 AA; 130671 MW; C26E09F56923295 CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 1145;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVVFPA 6
 Db 515 KVVFPA 520
 |||||
 RESULT 24
 ID Q73N39 TREDE PRELIMINARY; PRT; 164 AA.
 AC Q73N39;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Membrane protein, putative.
 GN OrderedLocusNames=TDE1317;
 OS Treponema denticola.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=158;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 35405 / DSM 14222;
 RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
 RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
 RA Dodson R.J., Davidson T.M., DeBoy R.T., Fouts D.B., Haft D.H.,
 RA Salengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
 RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
 RA Gebregeorgis E., Geer K., Teegaye G., Malek J.A., Ayodeji B.,
 RA Shatsman S., McNeill T.Z., Smajs D., Howell J.K., Pal S., Amin A.,
 RA Vashisth P., Norris S.J., Fraser C.M., Paulsen I.T.;
 RA Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
 RT "Comparison of the genome of the oral pathogen Treponema denticola
 RT with other spirochete genomes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).
 DR EMBL; AE017250; AAS11834.1; -; Genomic_DNA.
 DR TIGR; TDE1317; -.
 KW Complete proteome.
 SQ SEQUENCE 164 AA; 18968 MW; 27E92778DDA9117C CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 164;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVVFPA 6
 Db 50 KVVFPA 55
 |||||
 RESULT 25
 Q6AKE9 DESPS PRELIMINARY; PRT; 203 AA.
 ID Q6AKE9 DESPS PRELIMINARY;
 AC Q6AKE9;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Related to McbG protein.
 GN OrderedLocusNames=DP2447;
 OS Desulfotalea psychrophila.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
 OC Desulfobulbaceae; Desulfotalea.
 OX NCBI_TaxID=84980;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=LSV54 / DSM 12343;
 RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
 RA Rabus R., Ruepp A., Frickey T., Rattei T., Partmann B., Stark M.,
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
 RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
 RA Klenk H.-P.;
 RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
 RT from permanently cold Arctic sediments.";
 RL Environ. Microbiol. 6:887-902 (2004).
 DR EMBL; CR522870; CAG37176.1; -; Genomic_DNA.
 DR InterPro; IPR001646; S-peptide_repeat.
 DR Pfam; PF00805; Pentapeptide; 3.
 KW Complete proteome.
 SQ SEQUENCE 203 AA; 23270 MW; 2EA1CD022861292D CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 203;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVVFPA 6
 Db 52 KVVFPA 57
 |||||
 RESULT 26
 O67225 AQUAE PRELIMINARY; PRT; 380 AA.
 ID O67225 AQUAE PRELIMINARY;
 AC O67225;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```

DE Hydrogenase expression/formation protein HypD.
GN Name=hypD; OrderedLocusNames=AQ_1157;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus.";
RL Nature 392:353-358(1998).
DR EMBL; AB000726; AAC07185.1; -; Genomic_DNA.
DR PIR; F70399; F70399.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR PIRSF; PIRSF005622; Hydrgn_mat_hypd; 1.
DR TIGRFAMs; TIGR00075; hypd; 1.
KW Complete proteome.
SQ SEQUENCE 380 AA; 42791 MW; 49C0E52BA655A5F5 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 380;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 141 KVIFFA 146

RESULT 27
Q81FH5_BACCR PRELIMINARY; PRT; 387 AA.
ID Q81FH5;
AC Q81FH5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Na+/H+ antiporter Napa (Inosine-dependent germination).
GN OrderedLocusNames=BC1612;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017003; NAP08591.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41037 MW; 907C03E6BA150B4A CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

us-10-009-122-17.rup

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 184 KIVFFA 189

RESULT 28
Q5WPU9_LUTLO PRELIMINARY; PRT; 399 AA.
ID Q5WPU9;
AC Q5WPU9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 43.2 kDa salivary protein.
GN ORFNames=LJTM11.Clu9;
OS Lutzomyia longipalpis (Sand fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea;
OC Psychodidae; Lutzomyia; Lutzomyia.
OX NCBI_TaxID=7200;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Salivary gland;
RX PubMed=15371479; DOI=10.1242/jeb.01185;
RA Valenzuela J.G., Garfield M., Rowton E.D., Pham V.M.;
RT "Identification of the most abundant secreted proteins from the
salivary glands of the sand fly Lutzomyia longipalpis, vector of
Leishmania chagasi.";
RL J. Exp. Biol. 207:3717-3729(2004).
DR EMBL; AY445935; AAS05318.1; -; mRNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
SQ SEQUENCE 399 AA; 45277 MW; F4E19F115794AAE8 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 399;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 305 KVIFFA 310

RESULT 29
Q4TRF8_9SPHN PRELIMINARY; PRT; 450 AA.
ID Q4TRF8;
AC Q4TRF8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Membrane protein.
GN ORFNames=ELI0568;
OS Erythrobacter litoralis HTCC2594.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=314225;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTCC2594;
RA Giavannoni S.J., Cho J.-C., Ferrera S., Johnson J., Kravitz S.,
Halpern A., Remington K., Beeson K., Tran B., Rogers Y.-H.,
Friedman R., Venter J.C.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AAG0100001; EAL76762.1; -; Genomic DNA.
SQ SEQUENCE 450 AA; 50280 MW; 077F448E75ADF977 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 450;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```



```

Qy 1 KVVFPA 6
Db 116 KIVFFA 121

RESULT 30
Q4S4T5_TETNG PRELIMINARY; PRT; 464 AA.
ID Q4S4T5_TETNG PRELIMINARY; PRT; 464 AA.
AC Q4S4T5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 2 SCAF14738, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00024047001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet P., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RN Nature 431:946-957(2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAG01014738; CAG04347.1; -; Genomic_DNA.
FT NON TER 464 464
SQ SEQUENCE 464 AA; 53213 MW; 0F9FF81DB193CE5C CRC64;

Query Match 96.6%; Score 28; DB 2; Length 464;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 304 KIVFFA 309

RESULT 31
Q91VU5_MOUSE PRELIMINARY; PRT; 606 AA.
ID Q91VU5_MOUSE PRELIMINARY; PRT; 606 AA.
AC Q91VU5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Wdccc2 protein.
GN Name=A1661311; Synonyms=Wdccc2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

```

RN NUCLEOTIDE SEQUENCE.
RP STRAIN=129; TISSUE=Mammary tumor. Brcal-/Fl;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttrick A.Y., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=129; TISSUE=Mammary tumor. Brcal-/Fl;
RG NTH MGC Project;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009019; AAH09019.1; -; mRNA.
DR Ensembl; ENSMUSG0000024169; Mus musculus.
DR MGI; MGI:2146906; A1661311.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like helical.
SQ SEQUENCE 606 AA; 70992 MW; 4BB6057E07ADA16C CRC64;

Query Match 96.6%; Score 28; DB 2; Length 606;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 376 KIVFFA 381

RESULT 32
Q4WB22_ASFPF PRELIMINARY; PRT; 623 AA.
ID Q4WB22_ASFPF PRELIMINARY; PRT; 623 AA.
AC Q4WB22;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Afu806810;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Af293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman N., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Iu C.,
RA Majors W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
RA Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,

```

```

RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Roming C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekaja F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Gilegan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAH0100013; EAL85442.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 623 AA; 72379 MW; 08795F0DEF6C18E2 CRC64;

Query Match          96.6%; Score 28; DB 2; Length 623;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   ||:||||
Db 96 KVIFFA 101

RESULT 33
Q5K7E5_CRYNE PRELIMINARY; PRT; 630 AA.
AC Q5K7E5;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DE Hypothetical protein.
GN ORFNames=CN00130;
OS Cryptococcus neoformans var. neoformans JEC21.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=214684;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JEC21;
RA Loftus B.J., Fung E., Roncaglia P., Vamathevan J., Utterback T.,
RA Van Aken S., Fraser C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=JEC21;
RX PubMed=15653466; DOI=10.1126/science.1103773;
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA D'Souza C.A., Fox D.S., Gribberg V., Fu J., Fukushima M., Haas B.J.,
RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
RA Kwon-Chung K.J., Lengler K.B., Maiti R., Marra M.A., Marra R.E.,
RA Mathewson C.A., Mitchell T.G., Perlea M., Riggs F.R., Salzberg S.L.,
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
RA Fraser C.M., Hyman R.W.;
RL "The genome of the basidiomycetous yeast and human pathogen
RT Cryptococcus neoformans.";
RL Science 307:1321-1324 (2005).
DR EMBL; AS017356; AA047004.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR007219; Fungal trans.
DR InterPro; IPR001138; Fungi_Trcsrp_N.
DR Pfam; PF04082; Fungal_trans; 1.

```

```

DR Pfam; PF00172; Zn_clus; 1.
DR PRINTS; PR00054; FUNGALZNCYS.
DR SMART; SM00066; GAL4; 1.
DR PROSITE; PS00463; ZN2_CV6_FUNGAL_1; 1.
DR PROSITE; PS50048; ZN2_CV6_FUNGAL_2; 1.
KW Complete proteome; DNA-binding; Hypothetical protein; Metal-binding;
KW Nuclear protein; Transcription; Transcription regulation; Zinc.
SQ SEQUENCE 630 AA; 68912 MW; 730A7C02A87D683B CRC64;

Query Match          96.6%; Score 28; DB 2; Length 630;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   ||:||||
Db 572 KVIFFA 577

RESULT 34
Q6RUU2_MOUSE PRELIMINARY; PRT; 663 AA.
AC Q6RUU2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Hypothetical protein (Fragment).
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY491413; AAS21643.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 663 AA; 77192 MW; CEB02E3EED356F1C CRC64;

Query Match          96.6%; Score 28; DB 2; Length 663;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   ||:||||
Db 433 KIVFFA 438

RESULT 35
Q83IB2_TROW8 PRELIMINARY; PRT; 690 AA.
AC Q83IB2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Putative helicase regulator.
GN OrderedLocNames=TW130;
OS Tropheryma whipplei (strain TW08/27) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococccineae; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=218496;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22495039; PubMed=12606174; DOI=10.1016/S0140-6736(03)12597-4;
RA Bentley S.D., Mairwald M., Murphy L.D., Pallen M.J., Yeats C.A.,
RA Dover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.E.,
RA von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
RA Barrell B.G., Parkhill J., Rutter D.A.;
RT "Sequencing and analysis of the genome of the Whipple's disease
RT bacterium Tropheryma whipplei.";
RL Lancet 361:637-644 (2003).
DR EMBL; BX251410; CAD66810.1; -; Genomic_DNA.

```

DR GO: 0005524; F:ATP binding; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR GO: 0004386; F:Helicase activity; IEA.
 DR InterPro: IPR011545; DEAD/DEAH_N.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR000330; SNF2_N.
 DR Pfam: PF00271; Helicase_C_1.
 DR Pfam: PF00176; SNF2_N; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC; 1.
 KW Complete proteome.
 SQ SEQUENCE 690 AA; 76266 MW; CD3633B94B669B32 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 690;
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 :|||
 Db 526 KIVFFA 531

RESULT 36

Q83GW3 TROWT
 ID Q83GW3 TROWT PRELIMINARY; PRT; 698 AA.
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE DNA helicase.
 GN OrderedLocustNames=TW118;
 OS Tropheryma whipplei (strain Twist) (Whipple's bacillus).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcineae; Cellulomonadaceae; Tropheryma.
 OX NCBI_TaxID=203267;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Twist;
 RX MEDLINE=22784088; PubMed=12902375;
 RA Raoult D., Ogata H., Audic S., Robert C., Suhre K., Drancourt M.,
 RA Claverie J.-M.;
 RT "Tropheryma whipplei Twist: a human pathogenic Actinobacteria with a
 RT reduced genome.";
 RL Genome Res. 13:1800-1809(2003).
 DR ENBL; AE016850; AAC4215.1; -; Genomic_DNA.
 DR GO: 0005524; F:ATP binding; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR GO: 0004386; F:Helicase activity; IEA.
 DR InterPro: IPR011545; DEAD/DEAH_N.
 DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF00271; Helicase_C_1.
 DR Pfam: PF00176; SNF2_N; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC; 1.
 KW Complete proteome; Helicase.
 SQ SEQUENCE 698 AA; 77193 MW; 6D104BF533CDDE72 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 698;
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 :|||
 Db 534 KIVFFA 539

RESULT 37

Q55HW1 CRYNE
 ID Q55HW1 CRYNE PRELIMINARY; PRT; 760 AA.
 AC Q55HW1
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 DE ORFNames=CNBN0110;
 GN Cryptococcus neoformans var. neoformans B-3501A.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=283643;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B-3501A;
 RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
 RA Wickes B.L., Fu J., Davis R.W.;
 RT "Cryptococcus neoformans serotype D sequencing.";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABY01000066; EAL17182.1; -; Genomic_DNA.
 DR GO: 0005634; C:nucleus; IEA.
 DR GO: 0003700; F:transcription factor activity; IEA.
 DR GO: 0008270; F:zinc ion binding; IEA.
 DR GO: 0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO: 0006350; P:transcription; IEA.
 DR DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;
 KW Transcription; Transcription regulation; Zinc.
 SQ SEQUENCE 760 AA; 84062 MW; 735C53C64AB54619 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 760;
 Best Local Similarity 83.3%; Pred. No. 6.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 :|||
 Db 702 KIVFFA 707

RESULT 38

Q6ZQ91 MOUSE
 ID Q6ZQ91 MOUSE PRELIMINARY; PRT; 1265 AA.
 AC Q6ZQ91;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MKIAA0590 protein (Fragment).
 GN Name=MKIAA0590;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX PubMed=14621295;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
 RA Saga Y., Nagase T., Ohara O., Koga H.;
 RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
 RT iii. the complete nucleotide sequences of 500 mouse KIAA-homologous
 RT cDNAs identified by screening of terminal sequences of cDNA clones
 RT randomly sampled from size-fractionated libraries.";
 RL DNA Res. 10:167-180(2003).
 DR EMBL; AK129167; HAC97977.1; -; mRNA.
 DR NON TER 1
 FT SQ SEQUENCE 1265 AA; 143403 MW; C9C157ABE80FF928 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1265;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 :|||
 Db 1081 KIVFFA 1086

```

RESULT 39
Q5F3M1 CHICK
ID Q5F3M1_CHICK PRELIMINARY; PRT; 1412 AA.
AC Q5F3M1_
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=RCJMB04.13m2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
RA Fiedler P., Rutter S., Blagodatski A., Kostovska D., Kotter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis."
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; AJ851629; CAH65263.1; -; mRNA.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein.
SQ SEQUENCE 1412 AA; 158448 MW; FA0050885B274747 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1412;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6
Db 1225 KIVFFA 1230

RESULT 40
Q4Q5Q4 LEIMA
ID Q4Q5Q4_LEIMA PRELIMINARY; PRT; 1655 AA.
AC Q4Q5Q4_
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LmjF32.0310;
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Foker N., Harris D., Oliver K., O'Neil S.,
RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CF005269; CAJ08491.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1655 AA; 181249 MW; 2B5317E9ED469A55 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1655;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6
Db 1397 KIVFFA 1402

```

```

RESULT 41
Q4LBQ8 SODGL
ID Q4LBQ8_SODGL PRELIMINARY; PRT; 88 AA.
AC Q4LBQ8_
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Chey protein.
GN Name=chey;
OS Sodalis glossinidius.
OC Plasmid pSG4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=63612;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PLASMID=pSG4;
RA Darby A.C., Lagnel J., Matthew C.Z., Bourtzis K., Maudlin I.,
RA Welburn S.C.;
RT "Extrachromosomal DNA of the symbiont Sodalis glossinidius."
RL J. Bacteriol. 187:5003-5007(2005).
DR EMBL; AJ868439; CAI59440.1; -; Genomic_DNA.
DR EMBL; AJ868438; CAI59427.1; -; Genomic_DNA.
KW Plasmid.
SQ SEQUENCE 88 AA; 10177 MW; F4168F2A56B8DOAC CRC64;

Query Match 93.1%; Score 27; DB 2; Length 88;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6
Db 42 KIIFFA 47

RESULT 42
Q9RQ09 BACTN
ID Q9RQ09_BACTN PRELIMINARY; PRT; 183 AA.
AC Q9RQ09_07C422;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE RNA polymerase sigma factor SigZ-like protein (RNA polymerase ECF-type
DE sigma factor).
GN Name=sigZ; OrderedLocusNames=BT1278;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482;
RX MEDLINE=99380605; PubMed=10449780; DOI=10.1073/pnas.96.17.9833;
RA Hooper L.V., Xu J., Falk P.G., Midtvedt T., Gordon J.I.;
RT "A molecular sensor that allows a gut commensal to control its
RT nutrient foundation in a competitive ecosystem."
RL Proc. Natl. Acad. Sci. U.S.A. 96:9833-9838(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482; ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482; ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076(2003).
DR EMBL; AF137263; AAF01488.1; -; Genomic_DNA.
DR EMBL; AE016931; AAO76385.1; -; Genomic_DNA.
DR GO; GO:0016987; F:sigma factor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006352; P:transcription initiation; IEA.
DR InterPro; IPR007627; Sigma70_r2.

```

DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF04542; Sigma70_r2; 1.
KW Complete proteome; DNA-binding; DNA-directed RNA polymerase;
KW Nucleotidyltransferase; Sigma factor; Transcription;
KW Transcription regulation; Transferase.
SQ SEQUENCE 183 AA; 22042 MW; 6824DABC99BEC643 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 183;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
|:|:|:|
Db 172 KIIFFA 177

RESULT 43

Q61C67_CABR PRELIMINARY; PRT; 315 AA.
AC Q61C67;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG13055 (Fragment).
GN Name=CBG13055;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
[1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; CAAC01000061; CAB67532.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN
DR PROSITE; PS0262; G-PROTEIN_RECP F1.2; 1.
KW G-protein coupled receptor; Hypothetical protein; Receptor;
KW Transducer; Transmembrane.
FT NON TER 1 315
FT NON TER 315 315
SQ SEQUENCE 315 AA; 35855 MW; 579B590D01874512 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 315;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
|:|:|:|
Db 117 KIIFFA 122

RESULT 44

Q4HSJ7_CAMUP PRELIMINARY; PRT; 362 AA.
AC Q4HSJ7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hydrogenase expression/formation protein HypD.
GN Name=hypD; ORFNames=CUP0294;
OS Campylobacter upsaliensis RM3195.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=306264;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=RM3195;
RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Raeko D.A.,
RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
RA Nelson K.E.;
RT "Major structural and novel potential virulence mechanisms from the
RT genomes of multiple Campylobacter species.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAEJ01000002; EAL53713.1; -; Genomic DNA.
SQ SEQUENCE 362 AA; 40365 MW; 15B0A8B12D60CAED CRC64;

Query Match 93.1%; Score 27; DB 2; Length 362;
Best Local Similarity 66.7%; Pred. No. 6.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
|:|:|:|
Db 132 KIIFFA 137

RESULT 45

Q9V7J0_DROME PRELIMINARY; PRT; 382 AA.
AC Q9V7J0; Q9GQ81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE C98421-PB, isoform B (Aspartyl beta-hydroxylase variant 2).
GN Name=Asph; ORFNames=C98421;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fessler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclab J.M., Pan S.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,

```

QY 1 KVFFFA 6
|::|||
Db 53 KIIFFA 58

RESULT 46
Q6L2B4_PICTO
ID Q6L2B4_PICTO PRELIMINARY; PRT; 410 AA.
AC Q6L2B4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Lipolyasaccharide N-acetylglucosaminyltransferase.
GN OrderedLocusNames=PTO0303;
OS Picrophilus torridus.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Picrophilaceae; Picrophilus.
OX NCBI_TaxID=82076;
RN [1]
NN NUCLEOTIDE SEQUENCE.
RP STRAIN=DSM 9790 / ATCC 700027;
RC PubMed=15184674; DOI=10.1073/pnas.0401356101;
RA Fueterz O., Anglov A., Liesgang H., Gottschalk G., Schleper C.,
RA Schneper B., Dock C., Antranikian G., Liebl W.;
RT "Genome sequence of Picrophilus torridus and its implications for life
RT around pH 0.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
DR EMBL; AR017261; AAT42888.1; -; Genomic_DNA.
DR GO; GO:0016757; P:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR001296; Glyco trans 1.
DR Pfam; PF00534; Glycos transf 1; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 410 AA; 48120 MW; C192F0152866E9B0 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 410;
Best Local Similarity 66.7%; Pred. No. 6.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFFFA 6
|::|||
Db 235 KIIFFA 240

RESULT 47
O59243_PYRHO
ID O59243_PYRHO PRELIMINARY; PRT; 447 AA.
AC O59243;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein PH1606.
GN OrderedLocusNames=PH1606;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
NN NUCLEOTIDE SEQUENCE.
RP STRAIN=OT3;
RC MEDLINE=98344137; PubMed=9679194;
RA Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kushi N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb P.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:555-76(1998).
DR EMBL; BA000001; BAA30718.1; -; Genomic_DNA.
DR FIR; F71039; F71039.
DR GO; GO:0016020; C:membrane; IEA.

```

```

DR GO: GO:0005355; F:glucose transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000803; GLUC TRANSPORT.
DR PRINTS; PR00172; GLUCRNSPORT.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 447 AA; 51173 MW; 509F45A302D3B059 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 447;
Best Local Similarity 66.7%; Pred. No. 7.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPPA 6
Db 207 KIIFPA 212

RESULT 48
ID Q95S93 DROME PRELIMINARY; PRT; 556 AA.
AC Q95S93;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE GMS02239P.
GN Name=Asph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY060905; AAL28453.1; -; mRNA.
DR FlyBase; FBGN0034075; Asph.
DR FlyBase; FBGN0034075; CG8421.
SQ SEQUENCE 556 AA; 63089 MW; 95D82EAC57D11F88 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 556;
Best Local Similarity 66.7%; Pred. No. 8.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPPA 6
Db 53 KIIFPA 58

RESULT 49
Q9V719 DROME PRELIMINARY; PRT; 556 AA.
AC Q9V719;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG8421-PD, isoform D (CG8421-pe, isoform e).
GN Name=Asph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,

```

```

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Dey A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster."
Science 287:2185-2195(2000).
[2]
RP NUCLEOTIDE SEQUENCE.
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RA "Finishing a whole-genome shotgun: release 3 of the Drosophila
RA melanogaster euchromatic genome sequence."
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RA "The transposable elements of the Drosophila melanogaster euchromatin:
RA a genomic perspective."
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
[4]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Battencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RA "Annotation of the Drosophila melanogaster euchromatic genome: a
RA systematic review."
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[5]
RP NUCLEOTIDE SEQUENCE.
RA Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,

```

```

RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RG NUCLEOTIDE SEQUENCE.
RP FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- INTERACTION:
CC O46085:EG:63B12.5; NDExp=1; IntAct=EBI-123244, EBI-151469;
DR EMBL; AB003808; AAF58064.2; -; Genomic_DNA.
DR IntAct; Q9V719; -;
DR Ensembl; CG8421; Drosophila melanogaster.
DR FlyBase; FBgn0034075; Asph.
DR FlyBase; FBgn0034075; CG8421.
SQ SEQUENCE 556 AA; 63144 MW; B420980CB6C357A CRC64;

Query Match 93.1%; Score 27; DB 2; Length 556;
Best Local Similarity 66.7%; Pred. No. 8.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 53 KLIFFA 58

RESULT 50
Q9GQ82 DROME PRELIMINARY; PRT; 785 AA.
ID Q9GQ82
AC Q9GQ82;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Aspartyl beta-hydroxylase variant 1 (CG8421-PA, isoform A).
GN Name=Asph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20564328; PubMed=10956665; DOI=10.1074/jbc.M006753200;
RL Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
RA O'Neil K.T., Focht R.J., Scully M.S., Hollis J.N., Hollis G.F.,
RA Friedman P.A.;
RT "Aspartyl beta-hydroxylase (Asph) and an evolutionarily conserved
RT isoform of Asph missing the catalytic domain share exons with
RT junctin."
RL J. Biol. Chem. 275:39543-39554 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherzer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodeon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

```

```

RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sridharan A.C., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Stadling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasegama D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskaas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RP FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF289493; AAG40806.1; -; mRNA.
RL EMBL; AE003808; AAM70947.1; -; Genomic_DNA.
DR Ensembl; CG8421; Drosophila melanogaster.
DR FlyBase; FBgn0034075; Asph.
DR FlyBase; FBgn0034075; CG8421.
DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004597; F:peptide-aspartate beta-dioxygenase activity; IEA.
DR GO; GO:0018193; P:peptidyl-amino acid modification; IEA.

```



```

DR InterPro; IPRO07803; Asp_Arg_Hydrox.
DR InterPro; IPRO06025; Pept_M_En_BS.
DR InterPro; IPRO01440; TPR.
DR InterPro; IPRO11990; TPR-like helical.
DR Pfam; PF05118; Asp_Arg_Hydrox; 1.
DR PROSITE; PS50293; TPR_REGION; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 785 AA; 89843 MW; 30A8DFC6836F7F1 CRC64;

Query Match          93.1%; Score 27; DB 2; Length 785;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 53 KIIFPA 58

RESULT 51
Q68K27 CHLRE
ID Q68K27 CHLRE PRELIMINARY; PRT; 1384 AA.
AC Q68K27;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Intraflagellar transport particle protein 140.
GN Name=IFT140;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
OC Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Walker B.L., Hou Y., Dentler W.L., Witman G.B., Pazour G.J.;
RT "Intraflagellar transport protein IFT140."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
EMBL; AY866103; AA795430.1; -, mRNA.
DR GO; GO:0019861; C:flagellum; IEA.
DR InterPro; IPRO02885; PPR.
DR InterPro; IPRO01680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 5.
DR TIGRFAMs; TIGR00756; PPR; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Flagellum.
SQ SEQUENCE 1384 AA; 154603 MW; 5D3E70C8440DABCD CRC64;

Query Match          93.1%; Score 27; DB 2; Length 1384;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 1154 KIIFPA 1159

RESULT 52
Q7QEF0 ANOGA
ID Q7QEF0 ANOGA PRELIMINARY; PRT; 1408 AA.
AC Q7QEF0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000001545 (Fragment).
GN ORFNames=ENSANG00000001308;
OS Anopheles gambiae str. FEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.

STRAIN=PEST;
RC The Anopheles gambiae Sequence Committee;
RG "Anopheles gambiae re-annotation.";
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008847; EAA06855.1; -, Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPRO11990; TPR-like_helical.
DR InterPro; IPRO01680; WD40.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
FT NON TER 1408 1408
SQ SEQUENCE 1408 AA; 157382 MW; FF63317DAB976DB2 CRC64;

Query Match          93.1%; Score 27; DB 2; Length 1408;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 1212 KIIFPA 1217

RESULT 53
Q9VPR0 DROME
ID Q9VPR0 DROME PRELIMINARY; PRT; 1443 AA.
AC Q9VPR0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG11838-PA, isoform A.
GN Names=Ose93; ORFNames=CG11838;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodeon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Foorler C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hradek N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

```

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupeki M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley *Drosophila* Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003589; AAF51483.1; -; Genomic_DNA.
DR FlyBase; FB00031262; Ose93.
DR GO; GO:0005488; F0binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR SMART; SM00320; WD40; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat.
SQ SEQUENCE 1443 AA; 163136 MW; A8C5997678040B88 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 1443;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
|::|||

Db 1204 KIIFFA 1209

RESULT 54
Q5BI64 DROME PRELIMINARY; PRT; 1458 AA.
ID Q5BI64;
AC Q5BI64;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE LP14662p.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; *Drosophila*.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkeley;
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; EF021360; AAX33508.1; -; mRNA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat.
SQ SEQUENCE 1458 AA; 163133 MW; 2D704C9970E541EC CRC64;

Query Match 93.1%; Score 27; DB 2; Length 1458;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
|::|||

Db 1219 KIIFFA 1224

RESULT 55
Q7KTZ4 DROME PRELIMINARY; PRT; 1503 AA.
ID Q7KTZ4;
AC Q7KTZ4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG11838-PB, Isoform B.
GN Name=Ose93; ORFNames=CG11838;
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; *Drosophila*.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfaffner B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*;"
RL Science 287:2185-2195(2000).
[2]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence;"
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomes perspective;"
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaninker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review;"
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[5]
RN NUCLEOTIDE SEQUENCE.
RG Berkeley *Drosophila* Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence;"
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[6]
RN NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003589; AAS6435.1; -; Genomic DNA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS00294; WD_REPEATS_REGION; 1.
KW Repeat.

SQ SEQUENCE 1503 AA; 167957 MW; A0DD3F532590486 CRC64;
Query Match 93.1%; Score 27; DB 2; Length 1503;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
DB 1264 KIIFFA 1269
RESULT 56
Q8A6R7_BACTN
ID Q8A6R7_BACTN PRELIMINARY; PRT; 1676 AA.
AC Q8A6R7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Conserved protein, with weak BamHI domain.
GN OrderedLocustNames-BT1809;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjurstedt M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis;"
RL Science 299:2074-2076(2003).
RL EMBL; AE016933; AA076916.1; -; Genomic DNA.
DR InterPro; IPR002048; EF-hand.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 1676 AA; 193673 MW; 28065878C0F6C961 CRC64;
Query Match 93.1%; Score 27; DB 2; Length 1676;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
DB 1656 KIIFFA 1661
RESULT 57
Q9UC33_HUMAN
ID Q9UC33_HUMAN PRELIMINARY; PRT; 33 AA.
AC Q9UC33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
NUCLEOTIDE SEQUENCE.
RP MEDLINE=1406936; PubMed=1406936; DOI=10.1038/359325a0;
RX Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids;"
RL Nature 359:325-327(1992).
RL HSP; Q16019; IBA4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.

DR PRINTS; PR00204; BETAAMYLOID.
SQ SEQUENCE 33 AA; 3674 MW; BIDEFE2F4167ABD0 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 33;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 58
Q56JJ6 GRAGR
ID Q56JJ6 GRAGR PRELIMINARY; PRT; 42 AA.
AC Q56JJ6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Grampus griseus (Risso's dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Grampus.
OX NCBI_TaxID=83653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926589; AAX81918.1; -; mRNA.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 59
Q56JJ7 TURTR
ID Q56JJ7 TURTR PRELIMINARY; PRT; 42 AA.
AC Q56JJ7;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Tursiops.
OX NCBI_TaxID=9739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926588; AAX81917.1; -; mRNA.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||

Db 16 KLVFFA 21

RESULT 60
Q7M088 CAVPO
ID Q7M088 CAVPO PRELIMINARY; PRT; 42 AA.
AC Q7M088;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid protein (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93290653; PubMed=7685598;
RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,
RA Kamiya H., Ohno M.;
RT "Receptor-mediated specific biological activity of a beta-amyloid
protein fragment for NK-1 substance p receptors.";
RL Biochem. Biophys. Res. Commun. 193:624-630(1993).
DR PIR; PNO512; PNO512.
DR HSSP; Q16019; 1IYT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 61
Q8WZ99 HUMAN
ID Q8WZ99 HUMAN PRELIMINARY; PRT; 52 AA.
AC Q8WZ99;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Amyloid protein (Fragment).
GN Name=APP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15201367; DOI=10.1136/jnnp.2003.010611;
RA Wakutani Y., Watanabe K., Adachi Y., Wada-Isoe K., Urakami K.,
RA Ninomiya H., Saigo T.C., Hashimoto T., Iwatsubo T., Nakashima K.;
RT "Novel amyloid precursor protein gene missense mutation (D678N) in
probable familial Alzheimer's disease.";
RL J. Neurol. Neurosurg. Psychiatr. 75:1039-1042(2004).
DR EMBL; AB066441; BAB71958.2; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1

```
PT  NON TER      52      52
SQ  SEQUENCE     52 AA;  5597 MW;  3F0E8E9EC18011AD CRC64;

Query Match      89.7%;  Score 26;  DB 2;  Length 52;
Best Local Similarity 83.3%;  Pred. No. 1.9e+02;
Matches 5;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy  1 KVVFPA 6
Db  16 KLVFPA 21

RESULT 62
Q82VG8_NITEU PRELIMINARY; PRT; 55 AA.
ID  Q82VG8;
DT  01-JUN-2003 (TrEMBLrel. 24, Created)
DT  01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Hypothetical protein.
GN  OrderedLocusNames=NE1120;
OS  Nitrosomonas europaea.
OC  Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC  Nitrosomonadaceae; Nitrosomonas.
OX  NCBI_TaxID=915;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=ATCC 19718 / IFO 14298;
RX  MEDLINE=22586410; PubMed=12700255;
RA  DOI=10.1128/JB.185.9.2759-2773.2003;
RA  Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA  Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA  Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT  "Complete genome sequence of the ammonia-oxidizing bacterium and
RT  obligate chemolithoautotroph Nitrosomonas europaea.";
RL  J. Bacteriol. 185:2759-2773(2003).
DR  EMBL; BX321859; CAB85031.1; -; Genomic_DNA.
DR  InterPro; IPR009760; DUF1328.
DR  Pfam; PF07043; DUF1328; 1.
DR  PIRSF; PIRSF036466; UCP036466; 1.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE 55 AA; 5845 MW; 4F68395F53BE30BC CRC64;

Query Match      89.7%;  Score 26;  DB 2;  Length 55;
Best Local Similarity 83.3%;  Pred. No. 2e+02;
Matches 5;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy  1 KVVFPA 6
Db  32 KLVFPA 37

RESULT 63
A4_UR5MA
ID  A4_UR5MA STANDARD; PRT; 57 AA.
AC  Q29149;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  10-MAY-2005 (Rel. 47, Last annotation update)
DE  Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE  beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE  Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE  C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE  fragment 57)] (Fragment).
GN  Name=APP;
OS  Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
OC  Ursus.
OX  NCBI_TaxID=29073;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Brain;

MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
"Conservation of the sequence of the Alzheimer's disease amyloid
RT  peptide in dog, polar bear and five other mammals by cross-species
RT  polymerase chain reaction analysis.";
RL  Brain Res. Mol. Brain Res. 10:299-305(1991).
CC  -!- FUNCTION: Functional neuronal receptor which couples to
CC  intracellular signaling pathway through the GTP-binding protein
CC  G(O) (By similarity).
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- SIMILARITY: Belongs to the APP family.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
EMBL; X56128; CAA39593.1; -; mRNA.
DR  PIR; B60045; B60045.
DR  HSSP; P08592; INMU.
DR  InterPro; IPR008155; A4_APP.
DR  InterPro; IPR001255; Beta-APP.
DR  PANTHER; PTHR10083:SP6; Beta-APP; 1.
DR  Pfam; PF03494; Beta-APP; 1.
DR  PRINTS; PR00204; BETAAMYLOID.
DR  PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR  PROSITE; PS00320; A4_INTRA; PARTIAL.
KW  Amyloid; Transmembrane.
FT  CHAIN <1..5 Soluble APP-beta (By similarity).
FT  CHAIN 6..57 CTF-alpha (By similarity).
FT  CHAIN 6..47 Beta-amyloid protein 42 (By similarity).
FT  CHAIN 6..45 Beta-amyloid protein 40 (By similarity).
FT  CHAIN 46..57 Gamma-CTF(59) (By similarity).
FT  CHAIN 48..57 Gamma-CTF(57) (By similarity).
FT  TOPO_DOM <1..33 Extracellular (Potential).
FT  TRANSMEM 34..57 Potential.
FT  NON_TER 1..1
FT  NON_TER 57
SQ  SEQUENCE 57 AA; 6172 MW; 84209D8E8BA82DFA CRC64;

Query Match      89.7%;  Score 26;  DB 1;  Length 57;
Best Local Similarity 83.3%;  Pred. No. 2e+02;
Matches 5;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy  1 KVVFPA 6
Db  21 KLVFPA 26

RESULT 64
A4_CANFA
ID  A4_CANFA STANDARD; PRT; 58 AA.
AC  Q28280;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  10-MAY-2005 (Rel. 47, Last annotation update)
DE  Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE  beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE  Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE  C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE  fragment 57)] (Fragment).
GN  Name=APP;
OS  Canis familiaris (Dog).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC  Canis.
OX  NCBI_TaxID=9615;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Kidney;
RX  MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
```

```

RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -|- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X56125; CAA39590.1; -, mRNA.
DR HSSP; P08592; INMU.
DR Ensembl; ENSCAFG0000008557; Canis familiaris.
DR InterPro; IPR008155; A4_APP.
DR PANTHER; PTHR10083:SP6; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PTH10083:SP6; Beta-APP; 1.
DR PROSITE; PS00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT CHAIN 7 >58 CTF-alpha (By similarity).
FT CHAIN 7 46 Beta-amyloid protein 42 (By similarity).
FT CHAIN 7 48 Beta-amyloid protein 40 (By similarity).
FT CHAIN 47 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 34 Extracellular (Potential).
FT TRANSMEM 35 58 Potential.
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D48A2E12DFA CRC64;

Query Match 89.7%; Score 26; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 22 KLVFFA 27

RESULT 65
A4_RABIT
ID A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).

```

```

RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -|- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X56129; CAA39594.1; -, mRNA.
DR HSSP; P08592; INMU.
DR InterPro; IPR008155; A4_APP.
DR PANTHER; PTHR10083:SP6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 89.7%; Score 26; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 21 KLVFFA 26

RESULT 66
A4_SHEEP
ID A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).

```

```

CC CC -1- FUNCTION: Functional neuronal receptor which couples to
CC CC intracellular signaling pathway through the GTP-binding protein
CC CC G(O) (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -1- SIMILARITY: Belongs to the APP family.
CC CC -----
CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use as long as its content is in no way modified and this statement is not
CC CC removed.
CC CC -----
CC CC EMBL; X56130; CAA39595.1; -; mRNA.
CC CC HSSP; P08592; INMJ.
CC CC InterPro; IPR008155; A4_APP.
CC CC InterPro; IPR001255; Beta-APP.
CC CC PANTHER; PTHR10083:SF6; Beta-APP; 1.
CC CC Pfam; PF03494; Beta-APP; 1.
CC CC PRINTS; PR00204; BETAAMYLOID.
CC CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC CC Amyloid; Transmembrane.
CC CC KW CHAIN <1 5 Soluble App-beta (By similarity).
CC CC FT CHAIN 6 >58 CTF-alpha (By similarity).
CC CC FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
CC CC FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
CC CC FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
CC CC FT CHAIN <1 33 Extracellular (Potential).
CC CC FT TOPO_DOM 34 57 Potential.
CC CC FT TRANSMEM 34 57 Cytoplasmic (Potential).
CC CC FT TOPO_DOM 58 >58
CC CC FT NON_TER 1 1
CC CC FT NON_TER 58 58
CC CC SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 89.7%; Score 26; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db |:|:|:|
21 KLVFFA 26

RESULT 67
A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) Gamma-secretase
DE C-terminal fragment 59]; Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
CC NCBI_TaxId=9913;
CC [1]
CC NUCLEOTIDE SEQUENCE.
CC TISSUE=Brain;
CC MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
CC RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
CC RT "Conservation of the sequence of the Alzheimer's disease amyloid
CC RT peptide in dog, polar bear and five other mammals by cross-species
CC RT polymerase chain reaction analysis.";
CC RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC CC -1- FUNCTION: Functional neuronal receptor which couples to
CC CC intracellular signaling pathway through the GTP-binding protein

```

```

CC CC G(O) (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -1- SIMILARITY: Belongs to the APP family.
CC CC -----
CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use as long as its content is in no way modified and this statement is not
CC CC removed.
CC CC -----
CC CC EMBL; X56124; CAA39589.1; -; mRNA.
CC CC EMBL; X56126; CAA39591.1; -; mRNA.
CC CC HSSP; P08592; INMJ.
CC CC InterPro; IPR008155; A4_APP.
CC CC InterPro; IPR001255; Beta-APP.
CC CC PANTHER; PTHR10083:SF6; Beta-APP; 1.
CC CC Pfam; PF03494; Beta-APP; 1.
CC CC PRINTS; PR00204; BETAAMYLOID.
CC CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC CC Amyloid; Transmembrane.
CC CC KW CHAIN <1 6 Soluble APP-beta (By similarity).
CC CC FT CHAIN 7 >59 CTF-alpha (By similarity).
CC CC FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
CC CC FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
CC CC FT CHAIN 47 >59 Gamma-CTF(59) (By similarity).
CC CC FT CHAIN 49 >59 Gamma-CTF(57) (By similarity).
CC CC FT TOPO_DOM <1 34 Extracellular (Potential).
CC CC FT TRANSMEM 35 58 Potential.
CC CC FT TOPO_DOM 59 >59 Cytoplasmic (Potential).
CC CC FT NON_TER 1 1
CC CC FT NON_TER 59 59
CC CC FT NON_TER 59 59
CC CC SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 89.7%; Score 26; DB 1; Length 59;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db |:|:|:|
22 KLVFFA 27

RESULT 68
Q5WJL8_BACSK PRELIMINARY; PRT; 79 AA.
AC Q5WJL8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Molybdopterin converting factor subunit 1 Moad.
GN Name=moad; OrderedLocNames=ABC0898;
OS Bacillus clausii (strain KSM-K16).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CC NCBI_TaxId=66692;
CC [1]
CC NUCLEOTIDE SEQUENCE.
CC RP STRAIN=KSM-K16;
CC RA Takaki Y., Kagayama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,
CC RA Kawai S., Ito S., Horikoshi K.;
CC RT "The complete genome sequence of the alkaliphilic Bacillus clausii
CC RT KSM-K16.";
CC RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC EMBL; AP006627; BAD63437.1; -; Genomic DNA.
CC GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
CC GO; GO:0006790; P:sulfur metabolism; IEA.
CC InterPro; IPR010034; Moad.
CC Pfam; PF02597; This; 1.
CC TIGRFAMs; TIGR01682; moad; 1.
CC Complete proteome.
CC KW SEQUENCE 79 AA; 8341 MW; 37F0600DEC90F10A CRC64;

```

```

Query Match      89.7%; Score 26; DB 2; Length 79;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   ||:||||
DB 3 KLVFFA 8

RESULT 69
O35463 CRIGR
ID O35463 CRIGR PRELIMINARY; PRT; 79 AA.
AC O35463
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alzheimer's amyloid beta protein (Fragment).
GN Name=beta APP;
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetinae; Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Samdamurti K., Pinnix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RE EMBL; AF030413; AAB86608.1; -; mRNA.
DR HSP; P08592; 1NWJ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 8538 MW; 37F26C3BFF3F597 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 79;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   ||:||||
DB 36 KLVFFA 41

RESULT 70
MOAD_ECOLI
ID MOAD_ECOLI STANDARD; PRT; 81 AA.
AC P30748; P77422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Molybdopterine converting factor subunit 1 (MPT synthase subunit 1)
DE (Molybdopterine synthase subunit 1) (Molybdenum cofactor biosynthesis
DE protein D) (Molybdopterine converting factor small subunit).
GN Name=moaD; Synonyms=chlA4, chlM; OrderedLocusNames=b0784;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K12 / MC4100;
RX MEDLINE=93368423; PubMed=8361352;
RA Rivers S.L., McNairn E., Blasco F., Giordano G., Boxer D.H.;
RT "Molecular genetic analysis of the moa operon of Escherichia coli K-12
RT required for molybdenum cofactor biosynthesis.";
RL Mol. Microbiol. 8:1071-1081(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12 / MG1655;

```

```

RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [4]
RP PROTEIN SEQUENCE OF 1-15, CHARACTERIZATION, AND MASS SPECTROMETRY.
RX MEDLINE=93293873; PubMed=8514782;
RA Pitterle D.M., Rajagopalan K.V.;
RT "The biosynthesis of molybdopterine in Escherichia coli. Purification
RT and characterization of the converting factor.";
RL J. Biol. Chem. 268:13499-13505(1993).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS).
RX MEDLINE=20577273; PubMed=11135669; DOI=10.1038/83034;
RA Rudolph M.J., Wuebbens M.M., Rajagopalan K.V., Schindelin H.;
RT "Crystal structure of molybdopterine synthase and its evolutionary
RT relationship to ubiquitin activation.";
RL Nat. Struct. Biol. 8:42-46(2001).
CC -!- FUNCTION: Converts molybdopterine precursor Z into molybdopterine.
CC This requires the incorporation of two sulfur atoms into precursor
CC Z to generate a dithiolene group. The sulfur atoms are provided by
CC the active form of the small subunit, whose activation involves
CC the acquisition of sulfur and the activity of moeB/chlN.
CC -!- PATHWAY: Molybdenum cofactor biosynthesis.
CC -!- SUBUNIT: Heterodimer of 2 moaD subunits and 2 moaE subunits.
CC -!- INTERACTION: moaE; NbExp=1; IntAct=EBI-554366, EBI-554376;
CC P30749; moaE; NbExp=1; IntAct=EBI-554366, EBI-543702;
CC -!- INDUCTION: By anaerobiosis, repressed by the molybdenum cofactor.
CC -!- MASS SPECTROMETRY: MW=8773.6; MW_ERR=0.2; METHOD=Electrospray;
CC RANGE=1-81; NOTE=Ref. 4.
CC -!- SIMILARITY: Belongs to the moaD family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X70420; AAC49864.1; -; Genomic DNA.
CC EMBL; U00096; AAC73871.1; -; Genomic DNA.
CC EMBL; D90716; BAA35442.1; -; Genomic DNA.
CC PIR; H64814; H64814.
CC PDB; 1PM0; X-ray; D=1-81.
CC PDB; 1FMA; X-ray; D=1-81.
CC PDB; 1JW9; X-ray; D=1-81.
CC PDB; 1JWA; X-ray; D=1-81.
CC PDB; 1JWB; X-ray; D=1-81.
CC PDB; 1NVI; X-ray; D=3-81.
CC IntAct; P30748; -.
CC EcoHase; EBI554; -.
CC EcoGene; EG11597; moaD.
CC InterPro; IPR010034; MoaD.
CC InterPro; IPR003749; This.
CC Pfam; PF02597; This; 1.
CC TIGRFAMs; TIGR01682; moaD; 1.
CC 3D-structure; Complete proteome; Direct protein sequencing;
KW

```


KW Molybdenum cofactor biosynthesis.
 FT CONFLICT 9 9 Q -> B (in Ref. 4).
 FT CONFLICT 45 45 A -> R (in Ref. 1).
 FT STRAND 2 6
 FT HELIX 8 14
 FT STRAND 18 21
 FT STRAND 27 27
 FT STRAND 36 36
 FT TURN 37 37
 FT HELIX 40 45
 FT TURN 46 46
 FT TURN 48 49
 FT STRAND 52 55
 FT TURN 56 57
 FT STRAND 58 59
 FT TURN 62 63
 FT STRAND 65 65
 FT TURN 68 69
 FT STRAND 71 75
 SQ SEQUENCE 81 AA; 8758 MW; 1E0A440520EE82F4 CRC64;
 Query Match 89.7%; Score 26; DB 1; Length 81;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 ||:||||
 Db 3 KVLFFA 8

RESULT 71
 Q9APP7_9BACT Q9APP7_9BACT PRELIMINARY; PRT; 81 AA.
 AC Q9APP7;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative molybdenum cofactor biosynthesis protein D.
 GN Name=moab;
 OS uncultured bacterium pCosHEL.
 OC Bacteria; environmental samples.
 NCBI_TaxID=143796;
 RX NUCLEOTIDE SEQUENCE.
 RP MEDLINE=20575196; PubMed=11133432; DOI=10.1128/AEM.67.1.89-99.2001;
 RA Entcheva P., Liebl W., Johann A., Hartsch T., Streit W.R.;
 RT "Direct cloning from enrichment cultures, a reliable strategy for
 isolation of complete operons and genes from microbial consortia.";
 RL Appl. Environ. Microbiol. 67:89-99(2001).
 DR EMBL; AF250774; AAG60573.1; -; Genomic_DNA.
 DR HSSP; P30748; 1JW9.
 DR SMR; Q9APP7; 1-81.
 DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
 DR GO; GO:0006790; P:sulfur metabolism; IEA.
 DR InterPro; IPR010034; Moad.
 DR InterPro; IPR003749; This.
 DR Pfam; PF02597; This; 1.
 DR TIGRFAMs; TIGR01682; moad; 1.
 SQ SEQUENCE 81 AA; 8739 MW; 21361C1FCA3AA24C CRC64;

Query Match 89.7%; Score 26; DB 2; Length 81;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 ||:||||
 Db 3 KVLFFA 8

RESULT 72
 Q57RF2_SALCH Q57RF2_SALCH PRELIMINARY; PRT; 81 AA.
 ID Q57RF2_SALCH PRELIMINARY;
 AC Q57RF2;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Molybdopterin biosynthesis protein.
 GN Name=moab; OrderedLocusNames=SC0803;
 OS Salmonella cholerae-suis (Salmonella enterica).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 NCBI_TaxID=591;
 RN [1]
 RX NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SC-B67;
 RX PubMed=15781495;
 RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
 Wang H.-S., Lee Y.-S.;
 RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
 highly invasive and resistant zoonotic pathogen.";
 RL Nucleic Acids Res. 33:1690-1698(2005).
 DR EMBL; AE017220; AAX64709.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 81 AA; 8772 MW; 5821119685621426 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 81;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 ||:||||
 Db 3 KVLFFA 8

RESULT 73
 Q65TT0_MANSM Q65TT0_MANSM PRELIMINARY; PRT; 81 AA.
 ID Q65TT0;
 AC Q65TT0;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Moad protein.
 GN Name=moab; OrderedLocusNames=MS1023;
 OS Mannheimia succiniciproducens (strain MBEL55E).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Mannheimia.
 NCBI_TaxID=221988;
 RX NUCLEOTIDE SEQUENCE.
 RP PubMed=15378067; DOI=10.1038/nbt1010;
 RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
 Kim C.H., Jeong H., Hur C.G., Kim J.J.;
 RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
 succiniciproducens.";
 RL Nat. Biotechnol. 22:1275-1281(2004).
 DR EMBL; AE016827; AAU37630.1; -; Genomic DNA.
 DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
 DR GO; GO:0006790; P:sulfur metabolism; IEA.
 DR InterPro; IPR010034; Moad.
 DR InterPro; IPR003749; This.
 DR Pfam; PF02597; This; 1.
 DR TIGRFAMs; TIGR01682; moad; 1.
 KW Complete proteome.
 SQ SEQUENCE 81 AA; 8617 MW; E529ED840985D661 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 81;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 ||:||||
 Db 3 KVLFFA 8

RESULT 74
 Q7N6P4_PHOLL

```
ID Q7N6P4_PHOLL PRELIMINARY; PRT; 81 AA.
AC Q7N6P4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Molybdopterin.
DE Molybdopterin.
GN Name-moad; OrderedLocusNames=plu1501;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]_TaxID=141679;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens."
RT Nat. Biotechnol. 21:1307-1313(2003).
DR EMBL; BX571864; CAFE13794.1; -; Genomic_DNA.
DR HSSP; P30748; 1JW9.
DR PhotoList; plu1501; -.
DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
DR GO; GO:0006790; P:sulfur metabolism; IEA.
DR InterPro; IPR010034; Moad.
DR InterPro; IPR003749; This.
DR Pfam; PF02597; This; 1.
DR TIGRFAMs; TIGR01682; moad; 1.
KW Complete proteome.
SQ SEQUENCE 81 AA; 8886 MW; 6646B5932531F136 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 81;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db ||:||||
3 KVLFFA 8

RESULT 75
Q8D897_VIBVU PRELIMINARY; PRT; 81 AA.
AC Q8D897;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Molybdenum cofactor biosynthesis protein D.
GN OrderedLocusNames=VW13085;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]_TaxID=672;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6."
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016807; AAO11408.1; -; Genomic_DNA.
DR HSSP; P30748; 1JW9.
DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
DR GO; GO:0006790; P:sulfur metabolism; IEA.
DR InterPro; IPR010034; Moad.
DR InterPro; IPR003749; This.
DR Pfam; PF02597; This; 1.
DR TIGRFAMs; TIGR01682; moad; 1.
KW Complete proteome.
```

```
SQ SEQUENCE 81 AA; 8731 MW; 4BE52C0ABDE06418 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 81;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db ||:||||
3 KVLFFA 8

Search completed: December 29, 2005, 17:47:29
Job time : 79.1936 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:57 ; Search time 15.129 Seconds
(without alignments)
44.518 Million cell updates/sec

Title: US-10-009-122-2
Perfect score: 34
Sequence: 1 KKLVFFA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	91.2	447	2 F71039	hypothetical prote
2	30	88.2	33	2 S23094	beta-amyloid prote
3	30	88.2	42	2 P00512	beta-amyloid prote
4	30	88.2	57	2 A00045	Alzheimer's diseas
5	30	88.2	57	2 F60045	Alzheimer's diseas
6	30	88.2	57	2 D60045	Alzheimer's diseas
7	30	88.2	57	2 G60045	Alzheimer's diseas
8	30	88.2	57	2 G60045	Alzheimer's diseas
9	30	88.2	57	2 B60045	Alzheimer's diseas
10	30	88.2	82	2 P04338	Alzheimer's diseas
11	30	88.2	346	2 D81288	probable fucose sy
12	30	88.2	359	2 C94983	hypothetical prote
13	30	88.2	380	2 F70399	hydrogenase expres
14	30	88.2	479	2 F96285	F9L1.11 protein -
15	30	88.2	586	1 RNEGB1	DNA-directed RNA p
16	30	88.2	655	2 G36524	protein T1N15.9 [i
17	30	88.2	695	1 A47995	Alzheimer's diseas
18	30	88.2	695	1 A27485	Alzheimer's diseas
19	30	88.2	695	2 S00550	Alzheimer's diseas
20	30	88.2	747	2 JH0773	Alzheimer's diseas
21	30	88.2	770	1 ORHUA4	Alzheimer's diseas
22	29	85.3	96	2 A05035	translation initia
23	29	85.3	109	2 B72213	conserved hypothet
24	29	85.3	152	2 T06645	hypothetical prote
25	29	85.3	176	1 I64161	cytochrome c bioge
26	29	85.3	231	2 H85138	hypothetical prote
27	29	85.3	316	2 AH1155	membrane proteins
28	29	85.3	316	2 AC1514	membrane protein h
29	29	85.3	352	2 T48903	wax synthase [limp

30	29	85.3	421	2 D81374	probable oxidoredu
31	29	85.3	428	2 T48008	hypothetical prote
32	29	85.3	484	2 E64432	spore coat polysac
33	29	85.3	593	2 T21510	hypothetical prote
34	29	85.3	610	2 T23836	hypothetical prote
35	29	85.3	763	2 C86733	penicillin-binding
36	29	85.3	774	2 F96639	protein Tif9.8 [im
37	29	85.3	1016	2 S30236	genome polypeptid
38	28	82.4	123	2 H90367	hypothetical prote
39	28	82.4	214	2 T47892	hypothetical prote
40	28	82.4	218	2 H72361	conserved hypothet
41	28	82.4	236	2 S18783	exotoxin type A pr
42	28	82.4	236	2 S18786	hypothetical prote
43	28	82.4	245	2 B69841	streptococcal pro
44	28	82.4	250	1 A26152	exotoxin type A pr
45	28	82.4	251	1 S29659	hypothetical prote
46	28	82.4	254	2 T28170	hypothetical prote
47	28	82.4	276	2 B82243	hypothetical prote
48	28	82.4	293	2 D69355	glycerol kinase (g
49	28	82.4	294	2 H90318	NADH2 dehydrogenas
50	28	82.4	315	2 A70313	hypothetical prote
51	28	82.4	321	2 H71729	sugar binding tran
52	28	82.4	333	2 A95039	transcription regu
53	28	82.4	355	2 B97909	hydrogenase expres
54	28	82.4	383	2 AF1893	hypothetical prote
55	28	82.4	528	2 T50330	hypothetical prote
56	28	82.4	605	2 T33750	genome polypeptid
57	28	82.4	1016	2 JQ0498	P-type ATPase - Te
58	28	82.4	1133	2 T03302	hypothetical prote
59	27	79.4	41	2 T07329	hypothetical prote
60	27	79.4	91	2 H97796	probable membrane
61	27	79.4	110	2 A10493	hypothetical prote
62	27	79.4	147	2 T24057	flagellar biosynth
63	27	79.4	208	2 D70134	transcription init
64	27	79.4	211	2 JC4540	hypothetical prote
65	27	79.4	215	2 S74602	hypothetical prote
66	27	79.4	231	2 C64703	hypothetical prote
67	27	79.4	263	2 G97198	HAD superfamily hy
68	27	79.4	266	2 F97176	HAD superfamily hy
69	27	79.4	300	2 T26245	hypothetical prote
70	27	79.4	313	2 T25850	hypothetical prote
71	27	79.4	313	2 T23207	hypothetical prote
72	27	79.4	315	2 T28942	hypothetical prote
73	27	79.4	326	2 S76400	hypothetical prote
74	27	79.4	329	2 D88109	protein T24B12.6 [
75	27	79.4	331	2 S51490	chaperone (cpn60)
76	27	79.4	334	2 T20562	hypothetical prote
77	27	79.4	349	2 T26247	hypothetical prote
78	27	79.4	352	2 S51893	hypothetical prote
79	27	79.4	363	2 F70195	UDF-N-acetylglucos
80	27	79.4	377	2 AB0715	probable membrane
81	27	79.4	379	2 T39743	hydrogenase homolo
82	27	79.4	412	2 S23208	mRNA maturase b12
83	27	79.4	420	2 B97276	glycosyltransferas
84	27	79.4	423	2 E90569	conserved hypothet
85	27	79.4	446	2 D95061	sensor histidine k
86	27	79.4	487	2 AB2269	hypothetical prote
87	27	79.4	556	2 D96791	hypothetical prote
88	27	79.4	572	2 H96685	probable AMP-bindi
89	27	79.4	601	2 H69274	probable long-chain
90	27	79.4	613	2 F69424	conserved hypothet
91	27	79.4	629	2 AE2497	hypothetical prote
92	27	79.4	689	2 S74764	hypothetical prote
93	27	79.4	754	2 T06249	protoporphyrin IX
94	27	79.4	758	2 T02925	protoporphyrin IX
95	27	79.4	778	2 B86218	protein T27G7.20 [
96	27	79.4	855	2 S46050	probable purine nu
97	27	79.4	1174	2 H84982	exodeoxyribonuclea
98	27	79.4	1175	2 D85089	cytochrome c bioge
99	27	79.4	1285	2 B72420	hypothetical prote
100	27	79.4	3066	1 JQ1661	genome polypeptid
101	27	79.4	3066	1 JQ1662	genome polypeptid
102	27	79.4	4466	1 S17231	dynein beta heavy

103	27	79.4	4466	1	S17653	dynein beta heavy	176	25	73.5	112	2	T31925	hypothetical prote
104	26	76.5	49	2	T07200	hypothetical prote	177	25	73.5	115	2	AE0523	conserved hypothet
105	26	76.5	56	2	F95227	hypothetical prote	178	25	73.5	121	2	S23781	insertion sequence
106	26	76.5	56	2	B98092	hypothetical prote	179	25	73.5	121	2	S74021	hypothetical prote
107	26	76.5	85	2	AG3408	molycoprotein (mpt	180	25	73.5	123	2	G86745	hypothetical prote
108	26	76.5	132	2	I40566	hypothetical prote	181	25	73.5	123	2	B10004	hypothetical prote
109	26	76.5	140	2	B95049	hypothetical prote	182	25	73.5	131	2	T32405	hypothetical prote
110	26	76.5	140	2	H97919	(3R)-hydroxymyrist	183	25	73.5	140	2	G84116	hydroxymyristoyl-(
111	26	76.5	144	2	A86722	hypothetical prote	184	25	73.5	142	2	C64717	hypothetical prote
112	26	76.5	186	1	WMR219	19K globulin precu	185	25	73.5	155	2	H95015	hypothetical prote
113	26	76.5	186	2	JC4784	alpha-globulin pre	186	25	73.5	156	2	B84735	yacc protein - Esc
114	26	76.5	194	2	G84145	hypothetical prote	187	25	73.5	156	2	F85495	hypothetical prote
115	26	76.5	220	2	A97739	hypothetical prote	188	25	73.5	156	2	F06644	hypothetical prote
116	26	76.5	220	2	D71677	hypothetical prote	189	25	73.5	157	2	D82209	probable antioxi
117	26	76.5	232	2	AH0299	probable membrane	190	25	73.5	160	2	T34322	hypothetical prote
118	26	76.5	240	2	H89692	protein C04A11.1 [191	25	73.5	161	2	C97454	hypothetical prote
119	26	76.5	249	2	A89592	protein T01B10.5 [192	25	73.5	161	2	AE2672	peroxiredoxin limp
120	26	76.5	257	2	AD3171	conserved hypothet	193	25	73.5	161	2	H97319	flavodoxin [import
121	26	76.5	274	2	C71685	hypothetical prote	194	25	73.5	170	2	G81375	hypothetical prote
122	26	76.5	281	2	G97749	hypothetical prote	195	25	73.5	182	2	T35807	hypothetical prote
123	26	76.5	288	2	A11245	phosphotransbutyry	196	25	73.5	189	2	G69262	conserved hypothet
124	26	76.5	288	2	AE1608	phosphotransbutyry	197	25	73.5	189	2	C71943	hypothetical prote
125	26	76.5	290	2	B90366	partial transposas	198	25	73.5	196	2	T32388	hypothetical prote
126	26	76.5	296	2	S53960	CTK3 protein - yea	199	25	73.5	197	2	A12184	hypothetical prote
127	26	76.5	300	2	F69997	hypothetical prote	200	25	73.5	203	2	T30317	chemotaxis protein
128	26	76.5	324	2	C90323	partial transposas	201	25	73.5	207	2	D70151	conserved hypothet
129	26	76.5	327	2	T27352	hypothetical prote	202	25	73.5	218	2	F86844	hypothetical prote
130	26	76.5	340	1	MMBE5	cell fusion protei	203	25	73.5	218	2	H75155	hypothetical prote
131	26	76.5	352	2	H97272	histidinol-phospha	204	25	73.5	219	2	A75004	hypothetical prote
132	26	76.5	356	2	D84280	hypothetical prote	205	25	73.5	220	2	S37100	ATAP2 protein - Ar
133	26	76.5	363	2	H81410	hydrogenase isoenz	206	25	73.5	223	2	T37974	probable peroxisom
134	26	76.5	364	2	B71139	hypothetical prote	207	25	73.5	229	2	S37101	ATAP1 protein - Ar
135	26	76.5	382	2	G83808	hypothetical prote	208	25	73.5	230	2	T32975	hypothetical prote
136	26	76.5	409	2	F83493	probable MFS trans	209	25	73.5	233	2	T10198	hypothetical prote
137	26	76.5	414	1	T46280	isocitrate dehydro	210	25	73.5	236	2	S18789	exotoxin A precurs
138	26	76.5	416	2	T32458	hypothetical prote	211	25	73.5	236	2	T16164	hypothetical prote
139	26	76.5	432	2	T27180	hypothetical prote	212	25	73.5	238	2	T40568	hypothetical prote
140	26	76.5	437	2	H64251	replication initia	213	25	73.5	252	2	B83801	ABC transporter (p
141	26	76.5	442	2	H81402	probable integral	214	25	73.5	258	2	A81355	probable processin
142	26	76.5	454	2	T29024	hypothetical prote	215	25	73.5	261	2	G86793	hypothetical prote
143	26	76.5	455	2	T34366	hypothetical prote	216	25	73.5	264	2	B71448	hypothetical prote
144	26	76.5	473	2	C84979	hypothetical prote	217	25	73.5	267	2	D64351	nitrate transport
145	26	76.5	476	2	G70175	aminoacyl-histidin	218	25	73.5	270	2	A99403	hypothetical prote
146	26	76.5	479	2	AD3564	4-hydroxybenzoate	219	25	73.5	274	2	H83707	bacitracin resista
147	26	76.5	494	2	AF1899	hypothetical prote	220	25	73.5	276	2	I40453	licheninase (EC 3.
148	26	76.5	496	2	A99952	conserved hypothet	221	25	73.5	277	2	E75187	sugar abc transpor
149	26	76.5	574	2	AC1414	ABC transporter re	222	25	73.5	277	2	D82392	conserved hypothet
150	26	76.5	574	2	AB1790	ABC transporter re	223	25	73.5	278	2	A83840	undecaprenol kinas
151	26	76.5	590	2	G90127	hypothetical prote	224	25	73.5	280	2	A12704	conserved hypothet
152	26	76.5	620	2	H69382	ABC transporter, A	225	25	73.5	281	2	H97124	hypothetical prote
153	26	76.5	630	2	T07966	probable ethylene	226	25	73.5	283	2	H70104	chemotaxis protein
154	26	76.5	641	2	H69651	lichenan operon tr	227	25	73.5	285	2	A82458	hypothetical prote
155	26	76.5	645	2	S29849	gene p74 protein -	228	25	73.5	285	2	A97487	probable iron-sulf
156	26	76.5	707	1	A34458	gelatinase B (EC 3	229	25	73.5	289	2	C71501	probable outer mem
157	26	76.5	707	1	A53796	gelatinase B (EC 3	230	25	73.5	289	2	E86148	TiNS.12 protein -
158	26	76.5	735	2	F84726	probable Na+/H+ an	231	25	73.5	291	2	A81659	transcription fact
159	26	76.5	740	2	S61568	probable membrane	232	25	73.5	291	2	A81659	conserved hypothet
160	26	76.5	751	1	WMXRGB	probable core prot	233	25	73.5	294	2	A27692	sarcotoxin IIA pre
161	26	76.5	760	2	E83610	conserved hypothet	234	25	73.5	294	2	B36351	sarcotoxin II-2 -
162	26	76.5	778	2	C70412	outer membrane pro	235	25	73.5	299	1	A69962	phosphatase butyryl
163	26	76.5	807	2	C85025	hypothetical prote	236	25	73.5	300	2	B81312	probable periplasm
164	26	76.5	817	2	A96640	protein TIP9.2 [im	237	25	73.5	300	2	AC1342	ABC transporter (A
165	26	76.5	826	2	JC5153	mitogen-activated	238	25	73.5	300	2	A11712	ABC transporter (A
166	26	76.5	1045	2	B30239	hydroxymethylgluta	239	25	73.5	303	2	T52345	OsmAC6 protein [im
167	26	76.5	1144	1	A43271	nitric-oxide synth	240	25	73.5	303	2	T23583	hypothetical prote
168	26	76.5	1552	2	T05408	hypothetical prote	241	25	73.5	305	2	T33578	hypothetical prote
169	26	76.5	2311	1	TVCHSR	kinase-related pro	242	25	73.5	306	2	T20012	hypothetical prote
170	26	76.5	2539	2	I42523	hypothetical prote	243	25	73.5	317	2	G88956	protein ZK697.3 [i
171	26	73.5	88	2	T41269	A-ORF-D protein -	244	25	73.5	304	2	T08933	hypothetical prote
172	25	73.5	92	2	T41269	hypothetical prote	245	25	73.5	321	2	G72347	hypothetical prote
173	25	73.5	95	2	T11229	probable succinate	246	25	73.5	329	2	T52344	OsmAC5 protein [im
174	25	73.5	100	2	D64642	conserved hypothet	247	25	73.5	331	2	T26871	hypothetical prote
175	25	73.5	101	2	AC0099	probable lipoprote	248	25	73.5	334	2	B72301	endoglucanase - Th

249 25 73.5 334 2 I64220 membrane protein h
250 25 73.5 334 2 C84984 hypothetical prote
251 25 73.5 337 2 S08459 hypothetical prote
252 25 73.5 341 2 A64383 hypothetical prote
253 25 73.5 343 1 C70418 probable alcohol d
254 25 73.5 346 2 B86715 transcription regu
255 25 73.5 346 2 G96643 hypothetical prote
256 25 73.5 347 2 T20618 hypothetical prote
257 25 73.5 348 2 B64552 conserved hypothet
258 25 73.5 364 2 C72402 cell division prot
259 25 73.5 366 2 T32598 hypothetical prote
260 25 73.5 367 2 G95158 glycosyl transfera
261 25 73.5 374 2 S53829 ribosomal protein
262 25 73.5 384 2 A51636 N-acetylornithine
263 25 73.5 384 2 H64161 hypothetical prote
264 25 73.5 385 2 G98024 conserved hypothet
265 25 73.5 388 2 B89777 capsular polysacch
266 25 73.5 402 2 B86038 probable LPS biosy
267 25 73.5 402 2 D91191 lipid A-core surfa
268 25 73.5 404 2 A54871 Gal beta-1, 3GalNA
269 25 73.5 405 2 A70146 tyrosine-trNA liga
270 25 73.5 406 2 AC2267 hypothetical prote
271 25 73.5 408 2 B72238 hypothetical prote
272 25 73.5 408 2 C96984 probable Mn transp
273 25 73.5 422 2 A98318 exopolysaccharide
274 25 73.5 422 2 AD2965 exopolysaccharide
275 25 73.5 423 2 S48817 hypothetical prote
276 25 73.5 431 2 A82470 hypothetical prote
277 25 73.5 433 2 T17654 hypothetical prote
278 25 73.5 435 2 AD1340 maltodextrin ABC-t
279 25 73.5 435 2 AB1711 maltodextrin ABC-t
280 25 73.5 440 1 OMBY ornithine carbamoy
281 25 73.5 443 2 T45574 anthranilate N-hyd
282 25 73.5 444 2 F96838 hypothetical prote
283 25 73.5 446 2 A81721 cytochrome D ubiqu
284 25 73.5 453 2 T75206 maltose-binding pe
285 25 73.5 471 2 T21102 hypothetical prote
286 25 73.5 472 1 S55379 cytochrome P450 CY
287 25 73.5 472 2 A60330 protein A precursor
288 25 73.5 474 2 T34193 G protein-coupled
289 25 73.5 475 2 B90545 atp synthase beta
290 25 73.5 481 2 I56246 lipopolysaccharide
291 25 73.5 481 2 B86285 hypothetical prote
292 25 73.5 495 2 T31944 hypothetical prote
293 25 73.5 497 2 T32090 hypothetical prote
294 25 73.5 500 2 H91283 hypothetical prote
295 25 73.5 500 2 B86125 hypothetical prote
296 25 73.5 500 2 S56489 hypothetical 54.3K
297 25 73.5 507 2 C82901 conserved hypothet
298 25 73.5 510 2 E71695 hypothetical prote
299 25 73.5 513 2 A80021 conserved hypothet
300 25 73.5 513 2 E71683 NADH2 dehydrogenas

ALIGNMENTS

RESULT 1
F71039
hypothetical protein PH1606 - Pyrococcus horikoshii
C/Species: Pyrococcus horikoshii
C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Oct-2004
C/Accession: F71039
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A/Reference number: A71000; MUID:98344137; PMID:9679194
A/Accession: F71039
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-447 <KAW>
A/Cross-references: UNIPROT:059243; UNIPARC:UPI00000630DB; GB:AP000006; NID:g3236133; PI

A;Experimental source: strain OT3
A/Note: this accession replaces an interim accession for a sequence replaced by GenBank
C/Genetics:
A/Gene: PH1606
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1142
Query Match 91.2%; Score 31; DB 2; Length 447;
Best Local Similarity 71.4%; Pred. No. 25; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0;
Qy 1 KKLVFPA 7
Db 206 KKLIFPA 212
||:||||
||:||||
RESULT 2
S23094
beta-amyloid protein precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C/Accession: S23094
R;Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A/Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A/Reference number: S23094; MUID:92316198; PMID:1618299
A/Accession: S23094
A/Molecule type: protein
A/Residues: 1-33 <KOJ>
A/Cross-references: UNIPARC:UPI00001777PB
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
Query Match 88.2%; Score 30; DB 2; Length 33;
Best Local Similarity 85.7%; Pred. No. 4.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKLVFPA 7
Db 20 QKLVFPA 26
:|||||
:|||||
RESULT 3
PN0512
beta-amyloid protein - guinea pig (fragment)
C/Species: Cavia porcellus (Guinea pig)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: PN0512
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno,
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A/Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragm
A/Reference number: PN0512; MUID:93290653; PMID:7685598
A/Accession: PN0512
A/Molecule type: protein
A/Residues: 1-42 <SHI>
A/Cross-references: UNIPROT:Q7M088; UNIPARC:UPI00000315E8
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C/Keywords: alternative splicing; amyloid
Query Match 88.2%; Score 30; DB 2; Length 42;
Best Local Similarity 85.7%; Pred. No. 5.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKLVFPA 7
Db 15 QKLVFPA 21
:|||||
:|||||
RESULT 4
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C/Species: Canis lupus familiaris (dog)
C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C/Accession: A60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

```

Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56125
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      88.2%; Score 30; DB 2; Length 57;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 20 QKLVPFA 26

RESULT 5
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:G1895; PIDN:CAA39592.1; PID:
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      88.2%; Score 30; DB 2; Length 57;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 20 QKLVPFA 26

RESULT 6
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56124
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      88.2%; Score 30; DB 2; Length 57;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 20 QKLVPFA 26

RESULT 7
E60045

```

```

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56130
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      88.2%; Score 30; DB 2; Length 57;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 20 QKLVPFA 26

RESULT 8
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56126
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      88.2%; Score 30; DB 2; Length 57;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 20 QKLVPFA 26

RESULT 9
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPROT:Q29149; UNIPARC:UPI0000125049; EMBL:X56128; NID:G2165; PIDN:
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      88.2%; Score 30; DB 2; Length 57;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||

```

Db 20 QKLVFFA 26

RESULT 10

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995

C;Accession: PQ0438; C60045

R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor

A;Reference number: PQ0438; MUID:93075180; PMID:1445331

A;Accession: PQ0438

A;Molecule type: DNA

A;Residues: 1-82 <DAV>

A;Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657

R;Johnstone, E.M.; Chaney, M.O.; Norris, P.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: C60045

A;Molecule type: mRNA

A;Residues: 12-68 <JOH>

A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56129

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 88.2%; Score 30; DB 2; Length 82;

Best Local Similarity 85.7%; Pred. No. 9.3; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 1;

Qy 1 KKLVFPA 7

Db 31 QKLVFFA 37

RESULT 11

D81288

probable fucose synthetase Cj1428c [imported] - Campylobacter jejuni (strain NCTC 11168)

C;Species: Campylobacter jejuni

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: D81288

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell

Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A;Reference number: A81250; MUID:20150912; PMID:10688204

A;Accession: D81288

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-346 <PAR>

A;Cross-references: UNIPROT:Q9PMW9; UNIPARC:UPI000000C1F0E; GB:AL1139078; GB:AL1111168; NID

C;Genetics:

A;Gene: fcl; Cj1428c

Query Match 88.2%; Score 30; DB 2; Length 346;

Best Local Similarity 100.0%; Pred. No. 34; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0;

Qy 1 KKLVPF 6

Db 100 KKLVPF 105

RESULT 12

C84983

hypothetical protein mlta [imported] - Buchnera sp. (strain APS)

C;Species: Buchnera sp.

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004

C;Accession: C84983

R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.

A;Reference number: A84930; MUID:20445173; PMID:10993077

A;Accession: C84983

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-359 <STO>

A;Cross-references: UNIPARC:UPI000005E5B6; GB:AP000398; GSPDB:GN00144

A;Experimental source: strain APS

C;Genetics:

A;Gene: mlta; BU458

C;Superfamily: membrane-bound lytic murein transglycosylase A homolog

Query Match 88.2%; Score 30; DB 2; Length 359;

Best Local Similarity 71.4%; Pred. No. 35; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 2;

Qy 1 KKLVFPA 7

Db 196 KKLIFFS 202

RESULT 13

F70399

hydrogenase expression/formation protein HypD - Aquifex aeolicus

C;Species: Aquifex aeolicus

C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C;Accession: F70399

R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O

Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Accession: F70399

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-380 <AQF>

A;Cross-references: UNIPROT:O67225; UNIPARC:UPI0000056543; GB:AE000726; NID:G2983612; P

A;Experimental source: strain VF5

C;Genetics:

A;Gene: hypD

C;Superfamily: [NiFe]-hydrogenase maturation factor, HypD type

Query Match 88.2%; Score 30; DB 2; Length 380;

Best Local Similarity 71.4%; Pred. No. 37; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 2;

Qy 1 KKLVFPA 7

Db 140 KKVIFPA 146

RESULT 14

F86285

F9Ll.11 protein - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: F86285

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizlar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: F86285

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-479 <STO>

A;Cross-references: UNIPROT:Q9XI52; UNIPARC:UPI000009A5C; GB:AE005172; NID:G5103814; PID:G96524
 C;Genetics:
 A;Map position: 1

Query Match 88.2%; Score 30; DB 2; Length 479;
 Best Local Similarity 71.4%; Pred. No. 45;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 |:|:|
 Db 36 KKLIPFA 42

RESULT 15
 RNEGB1
 DNA-directed RNA polymerase (EC 2.7.7.6) beta'-1 chain - Euglena gracilis chloroplast
 C;Species: chloroplast Euglena gracilis
 C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 09-Jul-2004
 C;Accession: S19258; S09211; S34555; S34922
 R;Hallick, R.B.
 submitted to the EMBL Data Library, November 1989
 A;Reference number: S19258
 A;Accession: S19258
 A;Molecule type: DNA
 A;Residues: 1-586 <HAL>
 A;Cross-references: UNIPROT:P23580; UNIPARC:UPI000013471B; EMBL:X17191; NID:g11501; PIDN:R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.; Monfort, A.; Orsat, B.; Spielmann, R.; Yezli-Plascencia, G.M.; Radebaugh, C.A.; Hallick, R.B.
 Nucleic Acids Res. 18, 1869-1878, 1990
 A;Title: The Euglena gracilis chloroplast rpoB gene. Novel gene organization and transcription
 A;Reference number: S09210; MUID:90245579; PMID:2110656
 A;Accession: S09211
 A;Molecule type: DNA
 A;Residues: 1-23 <YEP>
 A;Cross-references: UNIPARC:UPI00001726CE; EMBL:X17191
 R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.; Monfort, A.; Orsat, B.; Spielmann, submitted to the EMBL Data Library, January 1993
 A;Description: The complete sequence of the Euglena gracilis chloroplast genome (tentative)
 A;Reference number: S34494
 A;Accession: S34555
 A;Molecule type: DNA
 A;Residues: 1-586 <HAL>
 A;Cross-references: UNIPARC:UPI000013471B; EMBL:X70810; NID:g415327; PIDN:CAA50137.1; PIDN:R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.; Spielmann Nucleic Acids Res. 21, 3537-3544, 1993
 A;Title: Complete sequence of Euglena gracilis chloroplast DNA.
 A;Reference number: S34862; MUID:93347989; PMID:8346031
 A;Accession: S34922
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-586 <HAL>
 A;Cross-references: UNIPARC:UPI000013471B; EMBL:X70810; NID:g415327; PIDN:CAA50137.1; PIDN:R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.; Spielmann A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
 C;Genetics:
 A;Gene: rpoC1
 A;Genome: chloroplast
 A;Introns: 35/3; 104/2; 126/1; 176/2; 185/3; 267/1; 309/3; 361/1; 406/3; 515/3; 569/3
 C;Superfamily: chloroplast DNA-directed RNA polymerase beta'-1 chain
 C;Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 88.2%; Score 30; DB 1; Length 586;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 6
 |:|:|
 Db 564 KKLVPFA 569

RESULT 16
 G96524
 protein TIN15.9 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
 C;Accession: G96524
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: AB6141; MUID:21016719; PMID:11130712
 A;Accession: G96524
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-655 <STO>
 A;Cross-references: UNIPROT:Q9LP77; UNIPARC:UPI00000A1D67; GB:AE005173; NID:g8778688; PIDN:G96524
 C;Genetics:
 A;Gene: TIN15.9
 A;Map position: 1
 C;Superfamily: Receptor-like protein kinase

Query Match 88.2%; Score 30; DB 2; Length 655;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 6
 |:|:|
 Db 352 KKLVPFA 357

RESULT 17
 A49795
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
 C;Species: Macaca fascicularis (crab-eating macaque)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A49795
 R;Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.
 Am. J. Pathol. 138, 1423-1435, 1991
 A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a
 A;Reference number: A49795; MUID:91273117; PMID:1905108
 A;Accession: A49795
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-695 <POD>
 A;Cross-references: UNIPARC:UPI000002A2F2; GB:M58727; NID:g342062; PIDN:AAA36829.1; PIDN:R;Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C;Keywords: alternative splicing

Query Match 88.2%; Score 30; DB 1; Length 695;
 Best Local Similarity 85.7%; Pred. No. 63;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 |:|:|
 Db 611 KKLVPFA 617

RESULT 18
 A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N;Alternate names: proteinase nexin II
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text_change 09-Jul-2004
 C;Accession: A27485; S19727; I49485
 R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987
 A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor
 A;Reference number: A27485; MUID:88106489; PMID:3322280
 A;Accession: A27485
 A;Molecule type: mRNA
 A;Residues: 1-695 <YAM>

A;Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:g191569; PIDN:
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A;Reference number: S19727; MUID:92096458; PMID:1756177
A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210,'G','212-220','S','222-396','A','398-402','T','404-448','A','450-695 <STR>
A;Cross-references: UNIPARC:UPI000002A2P9; EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's
A;Reference number: 149485; MUID:92203998; PMID:1555768
A;Accession: 149485
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: UNIPARC:UPI00000003B7; GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:
C;Genetics:
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 88.2%; Score 30; DB 2; Length 695;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
:|||||
Db 611 QKLVPFA 617

RESULT 19
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A;Reference number: S00550; MUID:88312583; PMID:2900758
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <SH1>
A;Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2FB; EMBL:X07648; NID:g55616; PIDN:
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: Protein
A;Residues: 18-37,'X','39-40','X','42-44 <SH>
A;Cross-references: UNIPARC:UPI00001777FD
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempa, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Cross-references: UNIPARC:UPI00001777FE
A;Experimental source: brain

C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is a
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TM>

Query Match 88.2%; Score 30; DB 2; Length 695;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
:|||||
Db 611 QKLVPFA 617

RESULT 20
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: UNIPARC:UPI00000FC880; GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 88.2%; Score 30; DB 2; Length 747;
Best Local Similarity 85.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
:|||||
Db 663 QKLVPFA 669

RESULT 21
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhib
N;Contents: amyloid beta protein long, plaque form; amyloid beta protein short, vascula
protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A4
4668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Be
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288,'V','365-770 <LEM1>
A;Cross-references: UNIPARC:UPI000002A2P2; EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
A;Title: alternative splice form APP(695)
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14,'VW','17-288,'V','365-770 <LEM2>
A;Cross-references: UNIPARC:UPI000016A6FC; EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PJ:
A;Note: alternative splice form APP(695)
R;La Fauti, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prot
A;Reference number: A32277; MUID:89165870; PMID:2538123

A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LAF>
 A:Cross-references: UNIPARC:UPI000016A57D; GB:M24546; GB:M24547; NID:g341202; PIDN:AAAC13
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, P.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A>Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity
 A:Reference number: A33260; MUID:8932030; PMID:2675937
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <JOH>
 A:Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:gl78863; PIDN:AAAS1768.1; PID:
 R:Pirelli, F.; Levy, E.; van Duinen, S.G.; Bote, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A>Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
 A:Reference number: A35486; MUID:90321244; PMID:2196878
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE1>
 A:Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:gl78608; PIDN:AAAS59501.1; PID:
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990
 A>Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: I39451; MUID:90236318; PMID:2110105
 A:Accession: I39451
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: UNIPARC:UPI00002DB1C; GB:M33112; NID:gl78613; PIDN:AAAS59502.1; PID:
 A:Accession: I39451
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A:Molecule type: DNA
 A:Residues: 1-530, 'OWLMPVLPAPWEAKVGR' <YOS2>
 A:Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:gl78608; PIDN:AAAS59501.1; PID:
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168; PMID:1908403
 A:Contents: annotation; erratum
 A>Note: revised physical map for reference I39451
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
 Science 248, 1124-1126, 1990
 A>Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
 A:Reference number: I39453; MUID:90260663; PMID:2111584
 A:Accession: I39453
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:gl78618; PIDN:AAAS1727.1; PID:
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A>Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
 A:Reference number: I59562; MUID:92022553; PMID:1925564
 A:Accession: I59562
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'F', 718-737 <MUR>
 A:Cross-references: UNIPARC:UPI000011F7EA; GB:S57665; NID:g236720; PIDN:AAAB19991.1; PID:
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wijisman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A>Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
 A:Reference number: A44017; MUID:93035397; PMID:1415269
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692, 'G', 694-718 <KAM1>
 A:Cross-references: UNIPARC:UPI000011F7EB; GB:S45135; NID:g257377; PIDN:AAAB23645.1; PID:
 A:Experimental source: familial Alzheimer disease family SB
 A>Note: sequence extracted from NCBI backbone (NCBIP:115374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <KAM2>

A:Cross-references: UNIPARC:UPI000016B394; GB:S45136; NID:g257379; PIDN:AAAB23646.1; PID:
 A:Experimental source: familial Alzheimer disease family LIT
 A>Note: this sequence has a silent mutation
 R:Kang, J.; Lenoire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
 Nature 325, 733-736, 1987
 A>Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
 A:Reference number: A03134; MUID:87144572; PMID:2881207
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAN>
 A:Cross-references: UNIPARC:UPI000002A2F2; GB:Y00264; NID:g28525; PIDN:CAAB6374.1; PID:
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A>Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
 A:Reference number: A29030; MUID:87231971; PMID:3035574
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A:Cross-references: UNIPARC:UPI000016A545; GB:M16765; NID:gl78539; PIDN:AAAS1722.1; PID:
 A>Note: the authors translated the codon GAG for residue 647 as Asp
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A>Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
 A:Reference number: A47584; MUID:87120328; PMID:3810169
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', 758-770 <GOL>
 A:Cross-references: UNIPARC:UPI00001420E5; GB:M15533; NID:gl78706; PIDN:AAAS35540.1; PID:
 R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
 Science 235, 880-884, 1987
 A>Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
 A:Reference number: A47585; MUID:87120329; PMID:2949367
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TAN1>
 A:Cross-references: UNIPARC:UPI000016A46F; GB:M15532; NID:gl77957; PIDN:AAAS1564.1; PID:
 R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
 EMBO J. 7, 949-957, 1988
 A>Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
 A:Reference number: S02638; MUID:88296437; PMID:2900137
 A:Accession: S02638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DVR>
 A:Cross-references: UNIPARC:UPI0000035AB0
 R:Tanzi, R.E.; McChatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
 Nature 331, 528-530, 1988
 A>Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
 A:Reference number: S00707; MUID:88122640; PMID:2893290
 A:Accession: S00707
 A:Molecule type: mRNA
 A:Residues: 286-344, 'I', 365-366 <TAN2>
 A:Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PFI
 A:Experimental source: promyelocytic leukemia cell line HL60
 A>Note: alternative splice form APP(751)
 R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; D-
 Nature 331, 525-527, 1988
 A>Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
 A:Reference number: S00925; MUID:88122639; PMID:2893289
 A:Accession: S00925
 A:Molecule type: mRNA
 A:Residues: 1-344, 'I', 365-770 <PO2>
 A:Cross-references: UNIPARC:UPI000002A2F6; GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAAB3
 A>Note: alternative splice form APP(751)
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A>Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibit
 A:Reference number: A38949; MUID:88122641; PMID:2893291
 A:Accession: A38949
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>

A;Cross-references: UNIPARC:UPI000014553B; GB:X06981; NID:G28816; PIDN:CAA30041.1; PID:9
 A;Experimental source: glioblastoma cell line
 A;Note: alternative splice form APP(770)
 R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashtori
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
 A;Reference number: A30320
 A;Accession: A30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 284-288, 'V', 365-770 <VIT1>
 A;Cross-references: UNIPARC:UPI0000174094
 A;Accession: B30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 122-288, 'V', 365-770 <VIT2>
 A;Cross-references: UNIPARC:UPI0000174094
 A;Accession: C30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 606-770 <VIT3>
 A;Cross-references: UNIPARC:UPI0000174094
 R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
 A;Reference number: A31087; MUID:88124954; PMID:2893379
 A;Accession: A31087
 A;Molecule type: mRNA

Query Match 88.2%; Score 30; DB 1; Length 770;
 Best Local Similarity 85.7%; Pred. No. 69;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVEFA 7
 :|||||
 Db 686 QKLVEFA 692

RESULT 22
 A05035
 translation initiation factor IF-1 homolog - common tobacco chloroplast (fragment)
 N;Alternate names: hypothetical protein 96
 C;Species: chloroplast Nicotiana tabacum (common tobacco)
 C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
 C;Accession: A05035
 R;Sugiura, M.
 submitted to the EMBL Data Library, August 1986
 A;Reference number: A00149
 A;Accession: A05035
 A;Molecule type: DNA
 A;Residues: 1-96 <SUG>
 A;Cross-references: UNIPROT:P12136; UNIPARC:UPI000012D24A; EMBL:Z00044; NID:g11807; PID:
 A;Experimental source: cv. Bright Yellow 4
 R;Shinozaki, K.; Ohme, M.; Tanaka, M.; Makasugi, T.; Hayashida, N.; Matsubayashi, T.; Za
 Deno, H.; Kamogashira, T.; Yamada, K.; Kusuda, J.; Takaiwa, F.; Kato, A.; Tohdoh, N.; Sh
 EMBO J. 5, 2043-2049, 1986
 A;Title: The complete nucleotide sequence of the tobacco chloroplast genome: its gene or
 A;Reference number: A38013
 A;Contents: annotation; gene organization, sites, features
 C;Genetics:
 A;Genome: chloroplast
 C;Superfamily: translation initiation factor IF-1
 C;Keywords: chloroplast; protein biosynthesis

Query Match 85.3%; Score 29; DB 2; Length 96;
 Best Local Similarity 83.3%; Pred. No. 18;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVEFF 6
 :|||||
 Db 83 KKLVEFF 88

RESULT 23
 B72213
 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
 C;Species: Thermotoga maritima
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: B72213
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
 C.M.
 Nature 399, 323-329, 1999
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
 A;Reference number: A72200; MUID:99287316; PMID:10360571
 A;Accession: B72213
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-109 <ARN>
 A;Cross-references: UNIPROT:Q9X292; UNIPARC:UPI00000C120B; GB:AE001815; GB:AE000512; NI
 A;Experimental source: strain MSB8
 C;Genetics:
 A;Gene: TW1771
 C;Superfamily: Bacillus subtilis conserved hypothetical protein yghY

Query Match 85.3%; Score 29; DB 2; Length 109;
 Best Local Similarity 71.4%; Pred. No. 20;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVEFA 7
 :|||||
 Db 18 KKLVEFA 24

RESULT 24
 T06645
 hypothetical protein T20K18.220 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T06645
 R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkee, W.; Stiekema, W.; Bancroft, I.; Me
 submitted to the Protein Sequence Database, April 1999
 A;Reference number: Z15790
 A;Accession: T06645
 A;Molecule type: DNA
 A;Residues: 1-152 <BEV>
 A;Cross-references: UNIPROT:Q9ST29; UNIPARC:UPI00000A0722; EMBL:AL049640; GSPDB:GN00062
 A;Experimental source: cultivar Columbia; BAC clone T20K18
 C;Genetics:
 A;Gene: ATSP:T20K18.220
 A;Map position: 4
 A;Introns: 87/3; 109/3
 C;Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match 85.3%; Score 29; DB 2; Length 152;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKLVEFA 7
 :|||||
 Db 9 KKLVEFA 14

RESULT 25
 I64161
 cytochrome c biogenesis protein CycX homolog H10935 [similarity] - Haemophilus influenza
 C;Species: Haemophilus influenzae
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: I64161
 R;Feischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
 ; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
 Science 269, 496-512, 1995
 A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
 A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: I64161
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-176 <TIGR>
A;Cross-references: UNIPROT:P44943; UNIPARC:UPI0000130501; GB:U32775; GB:L42023; NID:g15
A;Note: best homolog was a hypothetical protein from *Escherichia coli*
C;Superfamily: cytochrome c biogenesis protein CyeC
C;Keywords: redox-active disulfide
F;75-78/Disulfide bonds: redox-active #status predicted

Query Match 85.3%; Score 29; DB 1; Length 176;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFF 6
| | | | |
Db 3 KKLIF 8

RESULT 26
H85138
hypothetical protein A74g12900 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85138
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: H85138
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-231 <STO>
A;Cross-references: UNIPROT:Q9SV79; UNIPARC:UPI00000A7E0E; GB:NC_001368; NID:g7267992; E
C;Genetics:
A;Gene: A74g12900
A;Map position: 4
C;Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match 85.3%; Score 29; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFFA 7
| | | | |
Db 12 KLVFFA 17

RESULT 27
AH1155
membrane proteins homolog lmo0648 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C;Accession: AH1155
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1155
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-316 <GLA>
A;Cross-references: UNIPROT:Q9Y985; UNIPARC:UPI0000055175; GB:NC_003210; PIDN:CAC98726.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo0648
C;Superfamily: divalent cation transporter, CorA type

Query Match 85.3%; Score 29; DB 2; Length 316;

Best Local Similarity 85.7%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
| | | | |
Db 182 KSLVFFA 188

RESULT 28
AC1514
membrane protein homolog lin0651 [imported] - *Listeria innocua* (strain Clip11262)
C;Species: *Listeria innocua*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C;Accession: AC1514
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1514
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-316 <GLA>
A;Cross-references: UNIPROT:Q92E10; UNIPARC:UPI00000CC2E0; GB:ALS92022; PIDN:CAC95883.1,
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0651
C;Superfamily: divalent cation transporter, CorA type

Query Match 85.3%; Score 29; DB 2; Length 316;
Best Local Similarity 85.7%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
| | | | |
Db 182 KSLVFFA 188

RESULT 29
T48903
wax synthase [imported] - *Simmondsia chinensis*
C;Species: *Simmondsia chinensis*
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T48903
R;Iardizabal, K.D.; Metz, J.G.; Sakamoto, T.; Hutton, W.C.; Pollard, M.R.; Lassner, M.W
Plant Physiol. 122, 645-655, 2000
A;Title: Purification of a *Jojoba* embryo wax synthase, cloning of its cDNA and production
A;Reference number: Z25002
A;Accession: T48903
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-352 <LAR>
A;Cross-references: UNIPROT:Q9XGY6; UNIPARC:UPI00000A1C81; EMBL:AF149919; PIDN:AAD38041

Query Match 85.3%; Score 29; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFFA 7
| | | | |
Db 135 KLVFFA 140

RESULT 30
DB1374
probable oxidoreductase ferredoxin-type electron transport protein Cj0991c [imported] -
C;Species: *Campylobacter jejuni*
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: DB1374
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
 Nature 403, 665-668, 2000
 A>Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp
 A;Reference number: A81250; MUID:20150912; PMID:10688204
 A;Accession: D81374
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:Q9PNU9; UNIPARC:UPI00000C1DC0; GB:AL111168; NID
 A;Experimental source: serotype O2, strain NCTC 11168
 C;Genetics:
 A;Gene: Cj0991c
 C;Superfamily: glycolate oxidase, iron-sulfur subunit

Query Match 85.3%; Score 29; DB 2; Length 421;
 Best Local Similarity 83.3%; Pred. No. 68;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVPF 6
 |||:|
 Db 98 KKLIFP 103

RESULT 31
 T48008
 hypothetical protein T17J13.120 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
 C;Accession: T48008
 R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer,
 submitted to the Protein Sequence Database, February 2000
 A;Reference number: Z24482
 A;Accession: T48008
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-428 <RIB>
 A;Cross-references: UNIPROT:Q9MIQ8; UNIPARC:UPI00000489B7; EMBL:AL138651
 A;Experimental source: cultivar Columbia; BAC clone T17J13
 C;Genetics:
 A;Map position: 3
 A;Introns: 137/3
 A;Note: T17J13.120
 C;Superfamily: N-hydroxycinnamoyl/benzoyl transferase

Query Match 85.3%; Score 29; DB 2; Length 428;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KLVFFA 7
 |||:|
 Db 271 KLVFFA 276

RESULT 32
 E6432
 spore coat polysaccharide biosynthesis protein G homolog - *Methanococcus jannaschii*
 C;Species: *Methanococcus jannaschii*
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C;Accession: E6432
 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 A;Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
 A;Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*
 A;Reference number: A64300; MUID:96337999; PMID:8688087
 A;Accession: E6432
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-484 <BUL>
 A;Cross-references: UNIPROT:Q58462; UNIPARC:UPI0000139F8D; GB:U67549; GB:L77117; NID:928
 C;Genetics:
 A;Map position: REV1004535-1003081

Query Match 85.3%; Score 29; DB 2; Length 484;
 Best Local Similarity 83.3%; Pred. No. 77;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPF 6
 |||:|
 Db 98 KKLIFP 103

RESULT 33

T21510

hypothetical protein F28P8.4 - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T21510

R;McMurray, A.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19432

A;Accession: T21510

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-593 <WIL>

A;Cross-references: UNIPROT:O17849; UNIPARC:UPI0000080E55; EMBL:Z81071; PIDN:CAB03015.1

A;Experimental source: clone F28P8

C;Genetics:

A;Gene: CESP:F28P8.4

A;Map position: 5

A;Introns: 33/2; 61/2; 202/3; 265/3; 294/2

Query Match

85.3%; Score 29; DB 2; Length 593;

Best Local Similarity 83.3%; Pred. No. 93;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPF 6

|||:|

Db 264 KKLIFP 269

RESULT 34

T23836

hypothetical protein M88.6a - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T23836

R;Sulston, J.

submitted to the EMBL Data Library, June 1994

A;Reference number: Z19806

A;Accession: T23836

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-610 <WIL>

A;Cross-references: UNIPROT:Q21604; UNIPARC:UPI000007610B; EMBL:Z34802; PIDN:CAA84337.1

A;Experimental source: clone M88

C;Genetics:

A;Gene: CESP:M88.6a

A;Map position: 3

A;Introns: 40/3; 60/2; 101/3; 216/2; 290/1; 427/3; 471/1; 560/3

Query Match

85.3%; Score 29; DB 2; Length 610;

Best Local Similarity 83.3%; Pred. No. 95;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPF 6

|||:|

Db 370 KKLIFP 375

RESULT 35

C86733

penicillin-binding protein [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL140;C;Species: *Lactococcus lactis* subsp. *lactis*

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

```

C;Accession: C86733
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-763 <STO>
A;Cross-references: UNIPROT:Q9CH71; UNIPARC:UPI00000C6923; GB:AE005176; PID:g12723796; E
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: pbpX

Query Match      85.3%; Score 29; DB 2; Length 763;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFF 6
   |||:|
Db 6 KKLIFP 11

RESULT 36
F96639
hypothetical protein T1F9.8 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
C;Accession: F96639
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F96639
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-774 <STO>
A;Cross-references: UNIPROT:O64777; UNIPARC:UPI00000A26B1; GB:AE005173; NID:g3056587; PI
C;Genetics:
A;Gene: T1F9.8
A;Map position: 1
A;Superfamily: S-locus receptor-like kinase SRK; protein kinase homology; S-locus-specif

Query Match      85.3%; Score 29; DB 2; Length 774;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFF 7
   |||:|
Db 4 KRIVPFA 10

RESULT 37
S30236
genome polyprotein - zucchini yellow mosaic virus (strain Singapore) (fragment)
N;Contains: coat protein; nuclear inclusion protein a; RNA-directed RNA polymerase (EC 2
C;Species: zucchini yellow mosaic virus, ZYMV
A;Variety: strain Singapore
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Accession: S30236
R;Wu, M.; Yeong, C.Y.; Lee, S.C.; Wong, S.M.
Nucleic Acids Res. 21, 1317, 1993
A;Title: Nucleotide sequence of the 3' half of zucchini yellow mosaic virus (Singapore i
A;Reference number: S30236; MUID:93219099; PMID:8464715
A;Accession: S30236
A;Status: nucleic acid sequence not shown; translation not shown

```

```

A;Molecule type: mRNA
A;Residues: 1-1016 <WUM>
A;Cross-references: UNIPROT:Q05912; UNIPARC:UPI00000ECC69; EMBL:X68509; NID:g288233; PTI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1992
C;Superfamily: tobacco etch virus genome polyprotein
C;Keywords: coat protein; genome-linked protein; nucleotidyltransferase; phosphoprotein,
F;9-61/Product: VPg protein #status predicted <VPG>
F;62-494/Product: nuclear inclusion protein a #status predicted <NIA>
F;495-1010/Product: RNA-directed RNA polymerase #status predicted <POL>
F;1011-1016/Product: coat protein (fragment) #status predicted <COP>
F;125/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted
Query Match      85.3%; Score 29; DB 2; Length 1016;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFFA 7
   |||||
Db 837 KLVFFA 842

RESULT 38
H90367
hypothetical protein SSO2013 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H90367
R;She, Q.; Singh, R.K.; Confalonieri, P.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-NGoc, H.P.; Redder, F.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: H90367
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-123 <KUR>
A;Cross-references: UNIPROT:Q97WV1; UNIPARC:UPI0000064642; GB:AE006641; NID:g13815291; F
C;Genetics:
A;Gene: SSO2013

Query Match      82.4%; Score 28; DB 2; Length 123;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   |||||
Db 114 KKLVIFA 120

RESULT 39
T47892
hypothetical protein T4C21.220 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47892
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24479
A;Accession: T47892
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-214 <CHO>
A;Cross-references: UNIPROT:Q9LYZ2; UNIPARC:UPI000009DAB0; EMBL:AL162295
A;Experimental source: cultivar Columbia; BAC clone T4C21
C;Genetics:
A;Map position: 3
A;Introns: 46/2; 65/2; 106/2; 128/3; 159/3; 197/3
A;Note: T4C21.220

Query Match      82.4%; Score 28; DB 2; Length 214;
Best Local Similarity 71.4%; Pred. No. 63;

```

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
:||||:
Db 18 KKLVPFA 24

RESULT 40
H72361
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C/Species: Thermotoga maritima
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: H72361
R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A/Reference number: A72200; MUID:99287316; PMID:10360571
A/Accession: H72361
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-218 <ARN>
A/Cross-references: UNIPROT:Q9WZ39; UNIPARC:UPI000000C13EB; GB:AE001731; GB:AE000512; NID
A/Experimental source: strain MSB8
C/Genetics:
A/Gene: TM0569

Query Match 82.4%; Score 28; DB 2; Length 218;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPF 6
:||||:
Db 20 KKLVPF 25

RESULT 41
S18783
exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 isol
N/Alternate names: scarlet fever toxin
C/Species: Streptococcus pyogenes phage
A/Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MG
C/Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C/Accession: S18783; S18793; S18794; S18801; S18798
R/Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A/Title: Characterization and clonal distribution of four alleles of the speA gene encod
A/Reference number: S18782; MUID:92044323; PMID:1940804
A/Accession: S18783
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-236 <NE>
A/Cross-references: UNIPARC:UPI000000BOA72; EMBL:X61568; NID:947289; PIDN:CAA43766.1; PID
A/Experimental source: strain MGAS158 isolate Nebraska unassigned phage
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A/Accession: S18793
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-236 <NE>
A/Cross-references: UNIPARC:UPI000000BOA72; EMBL:X61569; NID:947313; PIDN:CAA43767.1; PID
A/Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A/Accession: S18794
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-236 <NE>
A/Cross-references: UNIPARC:UPI000000BOA72; EMBL:X61570; NID:947315; PIDN:CAA43768.1; PID
A/Experimental source: strain MGAS491 isolate United Kingdom unassigned phage
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A/Accession: S18801
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA

A/Residues: 1-236 <NE>
A/Cross-references: UNIPARC:UPI000000BOA72; EMBL:X61572; NID:947333; PIDN:CAA43770.1; PI
A/Experimental source: strain MGAS624 isolate Germany unassigned phage
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A/Accession: S18798
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-236 <NE>
A/Cross-references: UNIPARC:UPI000000BOA72; EMBL:X61571; NID:947323; PIDN:CAA43769.1; PI
A/Experimental source: strain MGAS495 isolate Germany unassigned phage
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C/Genetics:
A/Gene: speA3
C/Superfamily: enterotoxin B
C/Keywords: exotoxin
F/1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F/23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 82.4%; Score 28; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPF 6
:||||:
Db 1 KKLVPF 6

RESULT 42
S18786
exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 iso
N/Alternate names: scarlet fever toxin
C/Species: Streptococcus pyogenes phage
A/Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain
isolate United Kingdom; strain MGAS496 isolate Germany
C/Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C/Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799
R/Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A/Title: Characterization and clonal distribution of four alleles of the speA gene enc
A/Reference number: S18782; MUID:92044323; PMID:1940804
A/Accession: S18786
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-236 <NE>
A/Cross-references: UNIPARC:UPI000000BEA6A; EMBL:X61561; NID:947297; PIDN:CAA43759.1; PI
A/Experimental source: strain MGAS250 isolate California unassigned phage
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A/Accession: S18787
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-236 <NE>
A/Cross-references: UNIPARC:UPI000000BEA6A; EMBL:X61562; NID:947299; PIDN:CAA43760.1; PI
A/Experimental source: strain MGAS251 isolate California unassigned phage
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A/Accession: S18788
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-236 <NE>
A/Cross-references: UNIPARC:UPI000000BEA6A; EMBL:X61563; NID:947301; PIDN:CAA43761.1; PI
A/Experimental source: strain MGAS256 isolate California unassigned phage
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A/Accession: S18790
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-236 <NE>
A/Cross-references: UNIPARC:UPI000000BEA6A; EMBL:X61564; NID:947305; PIDN:CAA43762.1; PI
A/Experimental source: strain MGAS285 isolate Colorado unassigned phage
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A/Accession: S18792
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-236 <NE>
A/Cross-references: UNIPARC:UPI000000BEA6A; EMBL:X61565; NID:947311; PIDN:CAA43763.1; PI

A;Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
A;Accession: S18795
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEH>
A;Cross-references: UNIPARC:UPI00000BEA6A; EMBL:X61566; NID:G47317; PIDN:CAA43764.1; PID
A;Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18799
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NES>
A;Cross-references: UNIPARC:UPI00000BEA6A; EMBL:X61567; NID:G47325; PIDN:CAA43765.1; PID
A;Experimental source: strain MGAS496 isolate Germany unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
A;Gene: speA2
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 82.4%; Score 28; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFF 6
||:||||
Db 1 KKMVFF 6

RESULT 43
B69841
Hypothetical protein yitQ - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: B69841
R;Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bexter
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galled
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Takakoshi, A.; Tanakoshi, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:198044033; PMID:9384377
A;Accession: B69841
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-245 <KUN>
A;Cross-references: UNIPROT:O06752; UNIPARC:UPI0000060186; GB:Z99109; GB:AL009126; NID:G
A;Experimental source: strain 168
C;Genetics:
A;Gene: yitQ
C;Superfamily: Bacillus subtilis hypothetical protein yitQ

Query Match 82.4%; Score 28; DB 2; Length 245;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFFA 7
|||||
Db 179 KKLVPFA 185

RESULT 44
A26152
streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
N;Alternate names: scarlet fever toxin; scarlet fever toxin
C;Species: Streptococcus sp.
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A26152
R;Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A;Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Sta
A;Reference number: A26152; MUID:86284313; PMID:3526093
A;Accession: A26152
A;Molecule type: DNA
A;Residues: 1-250 <JOH>
A;Cross-references: UNIPROT:P08095; UNIPARC:UPI0000017021E
C;Superfamily: enterotoxin B
C;Keywords: exotoxin

Query Match 82.4%; Score 28; DB 1; Length 250;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFF 6
||:||||
Db 9 KKMVFF 14

RESULT 45
S29659
exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12
N;Alternate names: erythrogenic toxin; scarlet fever toxin
C;Species: Streptococcus pyogenes phage T12
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800
R;Weeks, C.R.; Ferretti, J.J.
Infect. Immun. 52, 144-150, 1986
A;Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) g
A;Reference number: S29659; MUID:86166804; PMID:3514452
A;Accession: S29659
A;Molecule type: DNA
A;Residues: 1-251 <WES>
A;Cross-references: UNIPARC:UPI0000135DD7; GB:U40453; EMBL:M19350; NID:gl877426; PIDN:AA
R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene encod
A;Reference number: S18782; MUID:92044323; PMID:1940804
A;Accession: S18782
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-244 <NEL>
A;Cross-references: UNIPARC:UPI00000B1BCE; EMBL:X61560; NID:G47287; PIDN:CAA43758.1; PID
A;Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigned
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18784
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-244 <NEA>
A;Cross-references: UNIPARC:UPI00000B1BCE; EMBL:X61556; NID:G47291; PIDN:CAA43754.1; PID
A;Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigned
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18785
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-244 <NEZ>
A;Cross-references: UNIPARC:UPI00000B1BCE; EMBL:X61559; NID:G47293; PIDN:CAA43757.1; PID
A;Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18791
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-244 <NEY>
A;Cross-references: UNIPARC:UPI00000B1BCE; EMBL:X61555; NID:G47309; PIDN:CAA43753.1; PID
A;Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18796
A;Status: Nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-244 <NEO>
A;Cross-references: UNIPARC:UPI0000081BCE; EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PIDN:CAA43755.2
A;Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18797
A;Status: Nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-244 <NEH>
A;Cross-references: UNIPARC:UPI0000081BCE; EMBL:X61558; NID:g47321; PIDN:CAA43756.1; PIDN:CAA43756.2
A;Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18800
A;Status: Nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-228 <NES>
A;Cross-references: UNIPARC:UPI00001701AF; EMBL:X61554; NID:g47327; PIDN:CAA43752.1; PIDN:CAA43752.2
A;Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unassigned
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
A;Gene: speA; speA
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-251/Product: exotoxin type A #status predicted <MAT>

Query Match 82.4%; Score 28; DB 1; Length 251;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFF 6
||:||||
DB 9 KKLVPFF 14
||:||||

RESULT 46
T28170
hypothetical protein ORF9 - Melanoplus sanguinipes entomopoxvirus (strain Tuscon)
C;Species: Melanoplus sanguinipes entomopoxvirus
A;Variety: strain Tuscon
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T28170
R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: 220484; MUID:99102612; PMID:9847359
A;Accession: T28170
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-254 <AFO>
A;Cross-references: UNIPROT:Q9Y83; UNIPARC:UPI00000F390B; EMBL:AF063866; NID:g4049647;
A;Experimental source: strain Tuscon
C;Genetics:
A;Note: MSV009

Query Match 82.4%; Score 28; DB 2; Length 254;
Best Local Similarity 83.3%; Pred. No. 74;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFF 6
||:||||
DB 94 KKLVPFF 99
||:||||

RESULT 47
B82243
hypothetical protein VC1074 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82243

R;Heidelberg, J.P.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardonson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82243
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <HEI>
A;Cross-references: UNIPROT:Q9KT31; UNIPARC:UPI00000C2B83; GB:AE004189; GB:AE003852; N1
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC1074
A;Map position: 1

Query Match 82.4%; Score 28; DB 2; Length 276;
Best Local Similarity 85.7%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFF 7
||:||||
DB 119 KKLVPFF 125
||:||||

RESULT 48
D69355
hypothetical protein AF0844 - *Archaeoglobus fulgidus*
C;Species: *Archaeoglobus fulgidus*
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69355
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.P.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon *Archaeoglobus fulgidus*.
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69355
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-293 <KLE>
A;Cross-references: UNIPROT:O29414; UNIPARC:UPI0000056F64; GB:AE001046; GB:AE000782; N1

Query Match 82.4%; Score 28; DB 2; Length 293;
Best Local Similarity 71.4%; Pred. No. 84;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFF 7
||:||||
DB 139 KKLVPFF 145
||:||||

RESULT 49
H90318
glycerol kinase (glpK-1) [imported] - *Sulfolobus solfataricus*
C;Species: *Sulfolobus solfataricus*
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H90318
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan, J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: *Sulfolobus solfataricus* complete genome.
A;Reference number: A99139
A;Accession: H90318
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <KUR>
A;Cross-references: UNIPROT:Q97XW2; UNIPARC:UPI00000644E6; GB:AE006641; NID:g13814829;
C;Genetics:
A;Gene: glpK-1

```
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: A95039
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: A95039
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333 <KUR>
A:Cross-references: UNIPROT:Q97SK3; UNIPARC:UPI00000C9C8D; GB:AE005672; PIDN:AAK74506.1,
C:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0330

Query Match      82.4%; Score 28; DB 2; Length 333;
Best Local Similarity 83.3%; Pred. No. 94;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFF 6
      ||:|||
DB      143 KKMVFF 148

RESULT 53
B97909
transcription regulator, member of GalR family regR [imported] - Streptococcus pneumonia
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: B97909
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blazczak, L.; Burgett, S.; Dehoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: B97909
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-355 <KUR>
A:Cross-references: UNIPROT:Q8DR72; UNIPARC:UPI00000E3406; GB:AE007317; PIDN:AAK99102.1,
C:Genetics:
A:Gene: regR

Query Match      82.4%; Score 28; DB 2; Length 355;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFF 6
      ||:|||
DB      165 KKMVFF 170

RESULT 54
AF1893
hydrogenase expression/formation protein [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF1893
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF1893
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <KUR>
```

```
Query Match      82.4%; Score 28; DB 2; Length 294;
Best Local Similarity 71.4%; Pred. No. 84;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFF 7
      ||:|||
DB      183 KKMVFFA 189

RESULT 50
A70313
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain nuoM - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: A70313
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: A70313
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-315 <AQF>
A:Cross-references: UNIPROT:O66532; UNIPARC:UPI000005628F; GB:AE000675; NID:g2982863; PI
A:Experimental source: strain VF5
C:Genetics:
A:Gene: nuoM
C:Keywords: NAD; oxidoreductase

Query Match      82.4%; Score 28; DB 2; Length 315;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFF 7
      ||:|||
DB      241 KKLVEFFA 247

RESULT 51
H71729
hypothetical protein RP189 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: H71729
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: H71729
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-321 <AND>
A:Cross-references: UNIPROT:Q9ZDK5; UNIPARC:UPI0000139421; GB:AJ235270; GB:AJ235269; NID
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: RP189
C:Superfamily: Rickettsia prowazekii hypothetical protein RP189

Query Match      82.4%; Score 28; DB 2; Length 321;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 KKLVEFF 7
      ||:|||
DB      178 KLIFFA 183

RESULT 52
A95039
sugar binding transcription regulator RegR [imported] - Streptococcus pneumoniae (strain
C:Species: Streptococcus pneumoniae
```

```
A;Cross-references: UNIPROT:Q8YYZ5, UNIPARC:UPI00000CDE2C; GB:BA000019; PIDN:BA072653.1;
A;Experimental source: strain FCC 7120
C;Genetics:
A;Gene: hupD
C;Superfamily: [NiFe]-hydrogenase maturation factor, HypD type

Query Match      82.4%; Score 28; DB 2; Length 383;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKLVFPA 7
Db      134 KKLVFPA 140
      |||
      |||

RESULT 55
T50330
hypothetical protein SPBC1718.02 [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50330
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
submitted to the EMBL Data Library, February 2000
A;Reference number: 225062
A;Accession: T50330
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-528 <LYN>
A;Cross-references: UNIPROT:Q9P7P2; UNIPARC:UPI000006C7BE; EMBL:AL157874; PIDN:CAB75992.
A;Experimental source: strain 972h(-); cosmid c1718
C;Genetics:
A;Gene: SPDB:SPBC1718.02
A;Map position: 2
A;Introns: 32/2; 81/3; 138/1; 218/2; 348/3; 424/1

Query Match      82.4%; Score 28; DB 2; Length 528;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KKLVFPA 7
Db      18 KKLVFPA 24
      |||
      |||

RESULT 56
T33750
hypothetical protein R11E3.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33750
R;Langston, Z.; Wohldmann, P.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid R11E3.
A;Reference number: 221397
A;Accession: T33750
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-605 <LAN>
A;Cross-references: UNIPROT:Q9TYX2; UNIPARC:UPI00000782CB; EMBL:AF100669; PIDN:AAC68992.
A;Experimental source: strain Bristol N2; clone R11E3
C;Genetics:
A;Gene: CESP:R11E3.7
A;Map position: 4
A;Introns: 272/3; 283/3; 404/2; 450/3; 489/3

Query Match      82.4%; Score 28; DB 2; Length 605;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKLVFPA 7
Db      156 KKLVFPA 162
      |||
      |||
```

RESULT 57

```
JQ0498
genome polyprotein - watermelon mosaic virus 2 (fragment)
N;Contains: 49K protease; coat protein; nuclear inclusion protein NIB
C;Species: watermelon mosaic virus 2, WMV2
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JQ0498
R;Slightom, J.L.
submitted to JIPID, April 1990
A;Description: Watermelon mosaic virus II and zucchini yellow mosaic virus: cloning of
A;Reference number: JQ0498
A;Accession: JQ0498
A;Molecule type: genomic RNA
A;Residues: 1-1016 <QUE>
A;Cross-references: UNIPROT:P18478; UNIPARC:UPI0000131E80
A;Note: readthrough of the terminator codon TGA occurs between residues 267-Ala and 268
```

```
C;Superfamily: tobacco etch virus genome polyprotein
C;Keywords: polyprotein
F;1-219/Product: 49K proteinase (fragment) #status predicted <PRT>
F;220-736/Product: nuclear inclusion protein NIB #status predicted <NIB>
F;737-1016/Product: coat protein #status predicted <COP>
```

```
Query Match      82.4%; Score 28; DB 2; Length 1016;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KKLVFPA 7
Db      561 RRLVFPA 567
      |||
      |||
```

RESULT 58

```
T30302
P-type ATPase - Tetrahymena thermophila
C;Species: Tetrahymena thermophila
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30302
R;Wang, S.; Takeyasu, K.
submitted to the EMBL Data Library, November 1995
A;Description: The starvation-induced P-type ATPase in Tetrahymena thermophila.
```

```
A;Reference number: 220815
A;Accession: T30302
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1133 <WAN>
A;Cross-references: UNIPROT:Q95050; UNIPARC:UPI0000126641; EMBL:U41063; NID:GI545827;
C;Genetics:
A;Genetic code: SGC5
A;Note: TPA9
```

```
Query Match      82.4%; Score 28; DB 2; Length 1133;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KKLVFPA 6
Db      39 KKLVFPA 44
      |||
      |||
```

RESULT 59

```
T07329
hypothetical protein 41e - Chlorella vulgaris chloroplast
```

```
C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07329
R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Teudzuki, J.; Naka
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chl
A;Reference number: 215985; MUID:97303241; PMID:9159184
A;Accession: T07329
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
```

```
A;Residues: 1-41 <WAK>
A;Cross-references: UNIPARC:UPI000011E487; EMBL:AB001684; NID:g2224352; PIDN:BAA57977.1;
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast

Query Match          79.4%; Score 27; DB 2; Length 41;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPF 6
   ||::||
Db 17 KKMIF 22

RESULT 60
H97796
RP534 protein homolog RC0776 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97796
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:2142074; PMID:11557893
A;Accession: H97796
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <KUR>
A;Cross-references: UNIPROT:Q92HJ5; UNIPARC:UPI00000CBECE; GB:AE006914; PIDN:AAL03314.1;
C;Genetics:
A;Gene: RC0776

Query Match          79.4%; Score 27; DB 2; Length 91;
Best Local Similarity 83.3%; Pred. No. 50;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPF 6
   ||::||
Db 18 KKLVPY 23

RESULT 61
AI0493
probable membrane protein YPO4063 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AI0493
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AI0493
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 <KUR>
A;Cross-references: UNIPROT:Q8Z9X4; UNIPARC:UPI00000DC790; GB:AL590842; PIDN:CAC93517.1;
C;Genetics:
A;Gene: YPO4063

Query Match          79.4%; Score 27; DB 2; Length 110;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPF 6
   ||::||
Db 18 KKIIF 23

RESULT 62
T24057
```

```
hypothetical protein R08H2.12 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24057
R;Matthews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19835
A;Accession: T24057
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-147 <WIL>
A;Cross-references: UNIPARC:UPI000007A733; EMBL:Z81575; PIDN:CAB04637.1; GSPDB:GN000023;
A;Experimental source: clone R08H2
C;Genetics:
A;Gene: CESP:R08H2.12
A;Map position: 5
A;Introns: 31/2; 130/1

Query Match          79.4%; Score 27; DB 2; Length 147;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPF 6
   ||::||
Db 127 KRLVPF 132

RESULT 63
D70134
flagellar biosynthesis protein (fliZ) homolog - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: D70134
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: D70134
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-208 <KLE>
A;Cross-references: UNIPROT:Q44904; UNIPARC:UPI00000573FD; GB:AE001137; GB:AE000783; NID
A;Experimental source: strain B31

Query Match          79.4%; Score 27; DB 2; Length 208;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   ||::||
Db 84 KKLIFYS 90

RESULT 64
JC4540
transcription initiation factor IID p30 beta chain - human
N;Alternate names: transcription factor TFIID chain TAFII28
C;Species: Homo sapiens (man)
C;Date: 12-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: JC4540; PC4125; S54780
R;Kuzuhara, T.; Horikoshi, M.
Biol. Pharm. Bull. 19, 122-126, 1996
A;Title: Isolation and characterization of a cDNA encoding a human TFIID subunit contain
A;Reference number: JC4540; MUID:96418138; PMID:8820923
A;Accession: JC4540
A;Molecule type: mRNA
A;Residues: 1-211 <KUZ>
A;Cross-references: UNIPROT:Q15544; UNIPARC:UPI000000106D; DDBJ:D63705; NID:g2645174; PI
A;Accession: PC4125
A;Molecule type: protein
```

A;Residues: 145-211 <K2>
A;Cross-references: UNIPARC:UPI0000178C8D
A;Experimental source: brain
R;Mungus, G.; May, M.; Jacq, X.; Staub, A.; Tora, L.; Chambon, P.; Davidson, I.
EMBO J. 14, 1520-1531, 1995
A;Title: Cloning and characterization of hTAF(II)20 and hTAF(II)28: three su
A;Reference number: S54780; MUID:95246745; PMID:7729427
A;Accession: S54780
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-211 <MEN>
A;Cross-references: UNIPARC:UPI00000106D; EMBL:X83928; NID:g791056; PIDN:CRA58780.1; PI
C;Superfamily: transcription initiation factor IID beta chain
C;Keywords: brain; phosphoprotein; transcription initiation
F;82-85/Region: nuclear location signal
F;108-137,160-194/Region: repeats
F;121-180/Region: histone H4 similarity
F;9,112,114/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status
F;31,33,40,67,68/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status
Query Match 79.4%; Score 27; DB 2; Length 211;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLVPF 6
||:|
Db 206 KKIIF 211
RESULT 65
S74602
hypothetical protein slr1095 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74602
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shingo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74602
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-215 <KAN>
A;Cross-references: UNIPROT:P72739; UNIPARC:UPI00000C0BF5; EMBL:D90900; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein slr1461
Query Match 79.4%; Score 27; DB 2; Length 215;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLVPF 6
||:|
Db 111 KKLVPF 116
RESULT 66
C64703
hypothetical protein HP1467 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: C64703
R;Tombs, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khairak, H.G.; Glodek, A.; McKen
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: C64703

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-231 <TOM>
A;Cross-references: UNIPROT:O26003; UNIPARC:UPI00000C0934; GB:AE000647; GB:AE000511; NI
Query Match 79.4%; Score 27; DB 2; Length 231;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLVPF 6
||:|
Db 3 KKIIF 8
RESULT 67
G97198
HAD superfamily hydrolase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97198
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97198
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-263 <KUR>
A;Cross-references: UNIPROT:O97GB4; UNIPARC:UPI00000CA500; GB:AE001437; PIDN:AAK80378.1
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2423
Query Match 79.4%; Score 27; DB 2; Length 263;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLVPF 6
||:|
Db 3 KKIIF 8
RESULT 68
F97176
HAD superfamily hydrolases, YKRA B. subtilis ortholog [imported] - Clostridium acetobut
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97176
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: F97176
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <KUR>
A;Cross-references: UNIPROT:Q97GX1; UNIPARC:UPI00000CA472; GB:AE001437; PIDN:AAK80201.1
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2244
Query Match 79.4%; Score 27; DB 2; Length 266;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLVPF 6
||:|
Db 3 KKIIF 8
RESULT 69

T26245

hypothetical protein W06G6.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26245
R:McMurray, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20180
A:Accession: T26245
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-300 <WIL>
A:Cross-references: UNIPROT:Q9XUG1; UNIPARC:UPI0000061208; EMBL:Z83129; PIDN:CAB05641.1;
A:Experimental source: clone W06G6
C:Genetics:
A:Gene: CBSP:W06G6.6
A:Map position: 5
A:Introns: 1/1/2; 204/2

Query Match 79.4%; Score 27; DB 2; Length 300;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFFA 7

DB 281 KMVFFA 286

RESULT 70

T25850
hypothetical protein T01B11.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25850
R:Geisel, C.; Stellyes, L.
submitted to the EMBL Data Library, December 1996
A:Description: The sequence of C. elegans cosmid T01B11.
A:Reference number: Z20099
A:Accession: T25850
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-313 <GEI>
A:Cross-references: UNIPROT:P91410; UNIPARC:UPI0000081DDA; EMBL:U80931; PIDN:AAB38001.1;
A:Experimental source: strain Bristol N2; clone T01B11
C:Genetics:
A:Gene: CBSP:T01B11.4
A:Map position: 4
A:Introns: 4/1; 191/2
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 79.4%; Score 27; DB 2; Length 313;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7

DB 223 KKLNPFA 229

RESULT 71

T23207
hypothetical protein K01H12.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23207
R:McMurray, A.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19707
A:Accession: T23207
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-313 <WIL>
A:Cross-references: UNIPROT:Q21103; UNIPARC:UPI0000080D88; EMBL:Z68218; PIDN:CAA92472.1;

A:Experimental source: clone K01H12

C:Genetics:
A:Gene: CBSP:K01H12.2
A:Map position: 4
A:Introns: 4/1; 191/2
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 79.4%; Score 27; DB 2; Length 313;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7

DB 223 KKLNPFA 229

RESULT 72

T28942
hypothetical protein F07C4.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28942
R:Miller, N.; Stellyes, L.
submitted to the EMBL Data Library, January 1997
A:Description: The sequence of C. elegans cosmid F07C4.
A:Reference number: Z20546
A:Accession: T28942
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-315 <MIL>
A:Cross-references: UNIPROT:P91211; UNIPARC:UPI000007D6C2; EMBL:U80023; PIDN:AAC48017.1;
A:Experimental source: strain Bristol N2; clone F07C4
C:Genetics:
A:Gene: CBSP:F07C4.8
A:Map position: 5
A:Introns: 60/2; 221/3

Query Match 79.4%; Score 27; DB 2; Length 315;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7

DB 121 KKLNPFA 127

RESULT 73

S76400
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76400
R:Kaneke, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76400
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-326 <KAN>
A:Cross-references: UNIPROT:P74429; UNIPARC:UPI00000C1025; EMBL:DS0915; GB:AB001339; NIT
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 79.4%; Score 27; DB 2; Length 326;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7

DB 103 KKFVFS 109

Search completed: December 29, 2005, 17:49:06
Job time : 19.129 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.93871 Seconds
(without alignments)
13.656 Million cell updates/sec

Title: US-10-009-122-2
Perfect score: 34
Sequence: 1 KKLFFFA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/2/pubaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubaa/US03_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/2/pubaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	88.2	19	6	US-10-923-605-5
2	30	88.2	19	6	US-10-934-818-5
3	30	88.2	40	7	US-11-016-706-36
4	30	88.2	40	7	US-11-098-674-12
5	30	88.2	42	6	US-10-923-605-1
6	30	88.2	42	6	US-10-934-818-1
7	30	88.2	42	7	US-11-016-706-37
8	30	88.2	43	6	US-10-934-818-6
9	30	88.2	43	6	US-10-250-581-1
10	30	88.2	43	6	US-10-250-581-1
11	30	88.2	770	6	US-10-982-545-15
12	30	88.2	770	6	US-10-789-273-38
13	27	79.4	558	7	US-11-078-189-19
14	27	79.4	708	7	US-11-174-150-25
15	27	79.4	710	7	US-11-078-189-18
16	27	79.4	736	7	US-11-174-150-26
17	27	79.4	736	7	US-11-078-189-9
18	27	79.4	739	7	US-11-078-189-12
19	27	79.4	739	7	US-11-186-284-132
20	26	76.5	1070	7	US-11-147-047-49
21	26	76.5	5	7	US-11-098-674-1
22	25	73.5	47	6	US-10-467-657-5436
23	25	73.5	207	6	US-10-858-730-196
24	25	73.5	443	6	US-10-793-626-1860
25	25	73.5			

26	73.5	528	6	US-10-793-626-1930	Sequence 1930, Ap
27	73.5	660	7	US-11-186-284-125	Sequence 125, App
28	73.5	708	6	US-10-821-234-917	Sequence 917, App
29	70.6	134	6	US-10-793-626-2374	Sequence 2374, Ap
30	70.6	148	6	US-10-467-657-2934	Sequence 2934, Ap
31	70.6	167	6	US-10-967-457-79	Sequence 79, Appl
32	70.6	182	6	US-10-793-626-2836	Sequence 2836, Ap
33	70.6	194	7	US-11-044-899-26	Sequence 26, Appl
34	70.6	196	6	US-10-793-626-630	Sequence 630, App
35	70.6	211	6	US-10-467-657-6932	Sequence 6932, Ap
36	70.6	215	6	US-10-131-826A-4	Sequence 4, Appli
37	70.6	228	6	US-10-467-657-568	Sequence 568, App
38	70.6	228	6	US-10-467-657-4838	Sequence 4838, Ap
39	70.6	233	6	US-10-821-234-1322	Sequence 1322, Ap
40	70.6	249	7	US-11-113-424-30	Sequence 30, Appl
41	70.6	259	6	US-10-512-184-34	Sequence 34, Appl
42	70.6	338	6	US-10-878-556A-19	Sequence 19, Appl
43	70.6	344	6	US-10-131-826A-376	Sequence 376, App
44	70.6	371	6	US-10-512-184-71	Sequence 71, Appl
45	70.6	374	7	US-11-080-991-16	Sequence 16, Appl
46	70.6	396	6	US-10-995-561-1005	Sequence 1005, Ap
47	70.6	453	7	US-11-082-389-198	Sequence 198, App
48	70.6	476	7	US-11-069-642-19	Sequence 19, Appl
49	70.6	481	6	US-10-995-561-959	Sequence 959, App
50	70.6	482	6	US-10-793-626-24	Sequence 24, Appl
51	70.6	598	6	US-10-719-311-16	Sequence 16, Appl
52	70.6	626	6	US-10-512-184-49	Sequence 49, Appl
53	70.6	725	7	US-11-078-189-15	Sequence 15, Appl
54	70.6	734	6	US-10-719-311-4	Sequence 4, Appli
55	70.6	858	6	US-10-613-744-6	Sequence 6, Appli
56	70.6	989	6	US-10-821-234-975	Sequence 975, App
57	70.6	1113	7	US-11-067-811-4	Sequence 4, Appli
58	67.6	21	7	US-11-040-159-20	Sequence 20, Appl
59	67.6	186	6	US-10-467-657-3918	Sequence 3918, Ap
60	67.6	187	6	US-10-980-388-65	Sequence 65, Appl
61	67.6	216	6	US-10-467-657-8102	Sequence 8102, Ap
62	67.6	221	6	US-10-467-657-290	Sequence 290, App
63	67.6	221	6	US-10-467-657-5750	Sequence 5750, Ap
64	67.6	224	6	US-10-793-626-1430	Sequence 1430, Ap
65	67.6	269	6	US-10-467-657-330	Sequence 330, App
66	67.6	271	6	US-10-821-234-1419	Sequence 1419, Ap
67	67.6	272	6	US-10-632-150-46	Sequence 46, Appl
68	67.6	272	7	US-11-073-457-46	Sequence 46, Appl
69	67.6	272	7	US-11-073-460-46	Sequence 46, Appl
70	67.6	337	6	US-10-485-517-234	Sequence 234, App
71	67.6	346	6	US-10-770-726-55	Sequence 55, Appl
72	67.6	370	6	US-10-821-234-1105	Sequence 1105, Ap
73	67.6	400	6	US-10-793-626-1056	Sequence 1056, Ap
74	67.6	402	6	US-10-467-657-9070	Sequence 9070, Ap
75	67.6	463	6	US-10-467-657-6352	Sequence 6352, Ap
76	67.6	463	6	US-10-467-657-7604	Sequence 7604, Ap
77	67.6	522	6	US-10-995-561-1030	Sequence 1030, Ap
78	67.6	600	6	US-10-131-826A-462	Sequence 462, App
79	67.6	615	6	US-10-995-561-940	Sequence 940, App
80	67.6	662	6	US-10-985-561-943	Sequence 943, App
81	67.6	702	6	US-10-995-561-942	Sequence 942, App
82	67.6	745	7	US-11-147-109-2	Sequence 2, Appli
83	67.6	754	6	US-10-995-561-941	Sequence 941, App
84	64.7	104	6	US-10-467-657-6866	Sequence 6866, Ap
85	64.7	113	6	US-10-793-626-1950	Sequence 1950, Ap
86	64.7	134	6	US-10-467-657-8520	Sequence 8520, Ap
87	64.7	153	7	US-11-098-765-2	Sequence 2, Appli
88	64.7	155	6	US-10-467-657-2420	Sequence 2420, Ap
89	64.7	182	6	US-10-980-388-89	Sequence 89, Appl
90	64.7	194	6	US-10-878-556A-130	Sequence 130, App
91	64.7	195	7	US-11-019-955-24	Sequence 24, Appl
92	64.7	200	6	US-10-524-198-2	Sequence 2, Appli
93	64.7	204	6	US-10-980-388-102	Sequence 102, App
94	64.7	209	6	US-10-793-626-304	Sequence 304, App
95	64.7	210	6	US-10-467-657-6318	Sequence 6318, Ap
96	64.7	211	6	US-10-821-234-1372	Sequence 1372, Ap
97	64.7	229	6	US-10-131-826A-410	Sequence 410, App
98	64.7	239	6	US-10-467-657-8743	Sequence 8743, Ap

99	22	64.7	241	7	US-11-019-955-27	Sequence 27, Appl	172	21	61.8	179	6	US-10-467-657-306	Sequence 306, App
100	22	64.7	268	7	US-11-019-955-28	Sequence 28, Appl	173	21	61.8	179	6	US-10-467-657-6422	Sequence 6422, Ap
101	22	64.7	271	6	US-10-793-626-1156	Sequence 1156, Ap	174	21	61.8	190	7	US-10-467-657-3436	Sequence 3436, Ap
102	22	64.7	276	6	US-10-873-528-134	Sequence 134, App	175	21	61.8	194	7	US-11-103-957-57	Sequence 57, Appl
103	22	64.7	310	7	US-11-102-240-140	Sequence 140, App	176	21	61.8	198	6	US-10-131-826A-550	Sequence 550, App
104	22	64.7	327	6	US-10-793-626-1104	Sequence 1104, Ap	177	21	61.8	198	7	US-11-069-642-25	Sequence 25, Appl
105	22	64.7	347	6	US-10-467-657-2014	Sequence 2014, Ap	178	21	61.8	205	6	US-10-873-528-52	Sequence 52, Appl
106	22	64.7	409	6	US-10-821-234-1425	Sequence 1425, Ap	179	21	61.8	216	6	US-10-467-657-5976	Sequence 5976, Ap
107	22	64.7	412	7	US-11-074-176-24	Sequence 24, Appl	180	21	61.8	233	6	US-10-467-657-2300	Sequence 2300, Ap
108	22	64.7	426	6	US-10-467-657-2120	Sequence 2120, Ap	181	21	61.8	241	6	US-10-878-556A-35	Sequence 35, Appl
109	22	64.7	433	6	US-10-652-893-4	Sequence 4, Appl	182	21	61.8	243	6	US-10-512-109-23	Sequence 23, Appl
110	22	64.7	433	6	US-10-821-234-1429	Sequence 1429, Ap	183	21	61.8	243	6	US-10-512-109-48	Sequence 48, Appl
111	22	64.7	445	6	US-10-873-528-30	Sequence 30, Appl	184	21	61.8	248	6	US-10-793-626-3218	Sequence 3218, Ap
112	22	64.7	452	6	US-10-878-556A-151	Sequence 151, App	185	21	61.8	258	6	US-10-793-626-2360	Sequence 2360, Ap
113	22	64.7	461	6	US-10-131-826A-454	Sequence 454, App	186	21	61.8	259	6	US-10-467-657-3410	Sequence 3410, Ap
114	22	64.7	475	7	US-11-174-150-45	Sequence 45, Appl	187	21	61.8	267	6	US-10-467-657-5556	Sequence 5556, Ap
115	22	64.7	524	6	US-10-689-742-13	Sequence 13, Appl	188	21	61.8	298	6	US-10-793-626-1298	Sequence 1298, Ap
116	22	64.7	529	7	US-11-174-150-46	Sequence 46, Appl	189	21	61.8	311	6	US-10-793-626-2450	Sequence 2450, Ap
117	22	64.7	585	6	US-10-967-457-18	Sequence 18, Appl	190	21	61.8	311	7	US-11-179-411-18	Sequence 18, Appl
118	22	64.7	585	6	US-10-939-890-500	Sequence 500, App	191	21	61.8	311	7	US-11-175-766-18	Sequence 18, Appl
119	22	64.7	585	7	US-11-078-663-18	Sequence 18, Appl	192	21	61.8	323	6	US-10-467-657-556	Sequence 556, App
120	22	64.7	585	7	US-11-078-914-18	Sequence 18, Appl	193	21	61.8	346	6	US-10-878-556A-121	Sequence 121, App
121	22	64.7	592	6	US-10-467-657-4888	Sequence 4888, Ap	194	21	61.8	346	7	US-11-069-642-109	Sequence 109, App
122	22	64.7	657	7	US-11-080-591-48	Sequence 48, Appl	195	21	61.8	377	7	US-11-152-892-8	Sequence 8, Appl
123	22	64.7	674	6	US-10-507-275-9	Sequence 9, Appl	196	21	61.8	393	7	US-11-077-712-4	Sequence 4, Appl
124	22	64.7	674	6	US-10-131-826A-230	Sequence 230, App	197	21	61.8	395	6	US-10-793-626-664	Sequence 664, App
125	22	64.7	690	6	US-10-939-890-501	Sequence 501, App	198	21	61.8	413	6	US-10-821-234-989	Sequence 989, App
126	22	64.7	779	7	US-11-128-420-12	Sequence 12, Appl	199	21	61.8	419	6	US-10-821-234-1360	Sequence 1360, Ap
127	22	64.7	856	6	US-10-467-657-8534	Sequence 8534, Ap	200	21	61.8	431	7	US-11-069-642-1	Sequence 1, Appl
128	22	64.7	862	7	US-11-077-550-173	Sequence 173, App	201	21	61.8	437	7	US-11-069-642-92	Sequence 92, Appl
129	22	64.7	1167	6	US-10-601-368-18	Sequence 18, Appl	202	21	61.8	438	7	US-11-069-642-47	Sequence 47, Appl
130	21	61.8	11	6	US-10-914-842A-11	Sequence 11, Appl	203	21	61.8	438	7	US-11-069-642-49	Sequence 49, Appl
131	21	61.8	12	6	US-10-982-891-26	Sequence 26, Appl	204	21	61.8	438	7	US-11-069-642-51	Sequence 51, Appl
132	21	61.8	12	6	US-10-982-891-31	Sequence 31, Appl	205	21	61.8	438	7	US-11-069-642-53	Sequence 53, Appl
133	21	61.8	12	6	US-10-982-891-33	Sequence 33, Appl	206	21	61.8	438	7	US-11-069-642-55	Sequence 55, Appl
134	21	61.8	13	6	US-10-511-559-836	Sequence 836, App	207	21	61.8	438	7	US-11-069-642-59	Sequence 59, Appl
135	21	61.8	13	6	US-10-511-559-837	Sequence 837, App	208	21	61.8	438	7	US-11-069-642-61	Sequence 61, Appl
136	21	61.8	13	6	US-10-511-559-838	Sequence 838, App	209	21	61.8	438	7	US-11-069-642-63	Sequence 63, Appl
137	21	61.8	13	6	US-10-511-559-839	Sequence 839, App	210	21	61.8	446	6	US-10-467-657-930	Sequence 930, App
138	21	61.8	13	6	US-10-511-559-840	Sequence 840, App	211	21	61.8	447	7	US-11-109-156-30	Sequence 30, Appl
139	21	61.8	13	6	US-10-511-559-841	Sequence 841, App	212	21	61.8	448	6	US-10-467-657-1096	Sequence 1096, Ap
140	21	61.8	28	6	US-10-250-581-14	Sequence 14, Appl	213	21	61.8	448	7	US-11-112-882-24	Sequence 24, Appl
141	21	61.8	28	6	US-10-250-581-17	Sequence 17, Appl	214	21	61.8	448	7	US-11-112-882-64	Sequence 64, Appl
142	21	61.8	28	6	US-10-250-581-17	Sequence 17, Appl	215	21	61.8	448	7	US-11-112-882-65	Sequence 65, Appl
143	21	61.8	28	6	US-10-250-581-17	Sequence 17, Appl	216	21	61.8	448	7	US-11-112-882-66	Sequence 66, Appl
144	21	61.8	33	6	US-10-467-657-7026	Sequence 7026, Ap	217	21	61.8	448	7	US-11-112-882-67	Sequence 67, Appl
145	21	61.8	40	6	US-10-250-581-15	Sequence 15, Appl	218	21	61.8	449	6	US-10-467-657-678	Sequence 678, App
146	21	61.8	40	6	US-10-250-581-15	Sequence 15, Appl	219	21	61.8	468	6	US-10-793-626-2242	Sequence 2242, Ap
147	21	61.8	40	6	US-10-250-581-15	Sequence 15, Appl	220	21	61.8	490	6	US-10-793-626-872	Sequence 872, App
148	21	61.8	40	6	US-10-250-581-16	Sequence 16, Appl	221	21	61.8	491	6	US-10-793-626-2770	Sequence 2770, Ap
149	21	61.8	42	6	US-10-250-581-16	Sequence 16, Appl	222	21	61.8	500	6	US-10-957-569-18	Sequence 18, Appl
150	21	61.8	42	6	US-10-250-581-19	Sequence 19, Appl	223	21	61.8	522	7	US-11-080-991-104	Sequence 104, App
151	21	61.8	42	6	US-10-250-581-16	Sequence 16, Appl	224	21	61.8	525	7	US-11-082-389-350	Sequence 350, App
152	21	61.8	42	6	US-10-250-581-19	Sequence 19, Appl	225	21	61.8	525	7	US-11-112-882-27	Sequence 27, Appl
153	21	61.8	48	7	US-11-000-463-388	Sequence 388, App	226	21	61.8	533	6	US-10-467-657-2868	Sequence 2868, Ap
154	21	61.8	48	7	US-11-000-463-860	Sequence 860, App	227	21	61.8	551	7	US-11-109-156-36	Sequence 36, Appl
155	21	61.8	57	6	US-10-467-657-5448	Sequence 5448, Ap	228	21	61.8	553	7	US-11-090-439-18	Sequence 18, Appl
156	21	61.8	57	6	US-10-467-657-6902	Sequence 6902, Ap	229	21	61.8	582	7	US-11-090-439-58	Sequence 58, Appl
157	21	61.8	57	6	US-10-467-657-7888	Sequence 7888, Ap	230	21	61.8	592	6	US-10-623-155-169	Sequence 169, App
158	21	61.8	58	7	US-11-000-463-773	Sequence 773, App	231	21	61.8	601	6	US-10-467-657-7120	Sequence 7120, Ap
159	21	61.8	62	7	US-11-000-463-773	Sequence 773, App	232	21	61.8	626	6	US-10-467-657-1196	Sequence 1196, Ap
160	21	61.8	76	6	US-10-467-657-5690	Sequence 5690, Ap	233	21	61.8	702	6	US-10-467-657-7230	Sequence 7230, Ap
161	21	61.8	79	6	US-10-467-657-2026	Sequence 2026, Ap	234	21	61.8	738	7	US-11-147-047-48	Sequence 48, Appl
162	21	61.8	84	6	US-10-986-501-186	Sequence 186, App	235	21	61.8	757	7	US-11-053-100-47	Sequence 47, Appl
163	21	61.8	98	6	US-10-467-657-4746	Sequence 4746, Ap	236	21	61.8	777	6	US-10-658-986-4	Sequence 4, Appl
164	21	61.8	104	6	US-10-793-626-2512	Sequence 2512, Ap	237	21	61.8	791	6	US-10-623-155-170	Sequence 170, App
165	21	61.8	106	7	US-11-064-174-50	Sequence 50, Appl	238	21	61.8	801	6	US-10-467-657-6470	Sequence 6470, Ap
166	21	61.8	112	6	US-10-467-657-5514	Sequence 5514, Ap	239	21	61.8	881	6	US-10-623-155-430	Sequence 430, App
167	21	61.8	126	6	US-10-467-657-606	Sequence 606, App	240	21	61.8	920	6	US-10-623-155-357	Sequence 357, App
168	21	61.8	133	7	US-11-069-834-2	Sequence 2, Appl	241	21	61.8	921	7	US-11-183-624-2	Sequence 2, Appl
169	21	61.8	138	6	US-10-793-626-1254	Sequence 1254, Ap	242	21	61.8	943	6	US-10-623-155-161	Sequence 161, App
170	21	61.8	135	7	US-11-069-642-97	Sequence 97, Appl	243	21	61.8	949	7	US-11-077-550-68	Sequence 68, Appl
171	21	61.8	160	6	US-10-793-626-750	Sequence 750, App	244	21	61.8	1016	7	US-11-103-957-41	Sequence 41, Appl

```
245 21 61.8 1042 7 US-11-067-811-1
246 21 61.8 1124 7 US-11-195-197-9
247 21 61.8 1170 6 US-10-831-997-2
248 21 61.8 1170 6 US-10-995-561-594
249 21 61.8 1170 6 US-10-995-561-595
250 21 61.8 1170 6 US-10-995-561-596
251 21 61.8 1170 7 US-11-046-456-28
252 21 61.8 1170 7 US-11-046-644-28
253 21 61.8 1389 6 US-10-467-657-334
254 21 61.8 1420 6 US-11-077-550-110
255 21 61.8 1438 6 US-10-511-559-73
256 21 61.8 1467 6 US-10-507-956-1
257 21 61.8 1474 6 US-10-995-561-873
258 21 61.8 1734 6 US-11-192-967-6
259 21 61.8 1734 6 US-11-193-715-6
260 21 61.8 2096 6 US-10-995-561-606
261 21 61.8 2333 7 US-11-096-281-13
262 21 61.8 2339 7 US-11-096-281-11
263 21 61.8 2351 6 US-10-995-561-608
264 21 61.8 3623 6 US-10-995-561-593
265 20.5 60.3 399 7 US-11-147-047-35
266 20 58.8 11 7 US-11-074-176-377
267 20 58.8 12 6 US-10-982-891-29
268 20 58.8 19 6 US-10-467-657-8712
269 20 58.8 27 6 US-10-986-501-347
270 20 58.8 28 6 US-10-250-581-2
271 20 58.8 28 6 US-10-250-581-2
272 20 58.8 40 6 US-10-250-581-3
273 20 58.8 40 6 US-10-250-581-3
274 20 58.8 42 6 US-10-250-581-4
275 20 58.8 42 6 US-10-250-581-4
276 20 58.8 50 6 US-10-467-657-9144
277 20 58.8 53 6 US-10-467-657-6120
278 20 58.8 54 6 US-10-467-657-4978
279 20 58.8 54 6 US-10-467-657-8560
280 20 58.8 56 6 US-10-467-657-1050
281 20 58.8 56 6 US-10-467-657-5386
282 20 58.8 69 7 US-11-000-463-387
283 20 58.8 69 7 US-11-000-463-859
284 20 58.8 71 7 US-11-000-463-765
285 20 58.8 72 6 US-10-467-657-912
286 20 58.8 75 6 US-10-986-501-143
287 20 58.8 78 7 US-11-123-896-431
288 20 58.8 80 7 US-11-123-896-89
289 20 58.8 83 6 US-10-510-386-114
290 20 58.8 90 7 US-11-020-772-33
291 20 58.8 92 6 US-10-467-657-2378
292 20 58.8 96 6 US-10-467-657-2834
293 20 58.8 103 7 US-11-194-246-412
294 20 58.8 105 6 US-10-467-657-9209
295 20 58.8 105 7 US-11-155-775-12
296 20 58.8 106 7 US-11-096-074-4
297 20 58.8 107 6 US-10-485-517-377
298 20 58.8 107 7 US-11-107-028-13
299 20 58.8 107 7 US-11-107-028-14
300 20 58.8 107 7 US-11-107-028-15
```

ALIGNMENTS

```
RESULT 1
US-10-923-605-5
; Sequence 5, Application US/10923605
; Publication No. US2005024972A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
```

```
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-923-605-5

Query Match 88.2%; Score 30; DB 6; Length 19;
Best Local Similarity 85.7%; Pred. No. 0.61;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
Db 3 QKLVFFA 9

RESULT 2
US-10-934-818-5
; Sequence 5, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5

Query Match 88.2%; Score 30; DB 6; Length 19;
Best Local Similarity 85.7%; Pred. No. 0.61;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
Db 3 QKLVFFA 9

RESULT 3
US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
```

; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-36

Query Match 88.2%; Score 30; DB 7; Length 40;
Best Local Similarity 85.7%; Pred. No. 1.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 15 QKLVPFA 21

RESULT 4
US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

Query Match 88.2%; Score 30; DB 7; Length 40;
Best Local Similarity 85.7%; Pred. No. 1.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 15 QKLVPFA 21

RESULT 5
US-10-923-605-1
; Sequence 1, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605

; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-923-605-1

Query Match 88.2%; Score 30; DB 6; Length 42;
Best Local Similarity 85.7%; Pred. No. 1.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 15 QKLVPFA 21

RESULT 6
US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1

Query Match 88.2%; Score 30; DB 6; Length 42;
Best Local Similarity 85.7%; Pred. No. 1.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 15 QKLVPFA 21

RESULT 7
US-11-016-706-37
; Sequence 37, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24

; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patent in Ver. 3.2
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-37

Query Match 88.2%; Score 30; DB 7; Length 42;
Best Local Similarity 85.7%; Pred. No. 1.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 15 QKLVPFA 21

RESULT 8

US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match 88.2%; Score 30; DB 6; Length 43;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 15 QKLVPFA 21

RESULT 9

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 88.2%; Score 30; DB 6; Length 43;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 15 QKLVPFA 21

RESULT 10

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 88.2%; Score 30; DB 6; Length 43;
Best Local Similarity 85.7%; Pred. No. 1.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 15 QKLVPFA 21

RESULT 11

US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease

```
; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; OTHER INFORMATION: Alzheimer's disease amyloid protein
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(40)
; OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40
; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(687)
; OTHER INFORMATION: soluble APP-alpha
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(671)
; OTHER INFORMATION: soluble APP-beta
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(770)
; OTHER INFORMATION: C99
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(713)
; OTHER INFORMATION: beta-amyloid protein 42
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(711)
; OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
; OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(770)
; OTHER INFORMATION: C83
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(713)
; OTHER INFORMATION: P3(42)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(711)
; OTHER INFORMATION: P3(40)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (712)..(770)
; OTHER INFORMATION: gamma-CTF(59)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (714)..(770)
; OTHER INFORMATION: gamma-CTF(57)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (721)..(770)
; OTHER INFORMATION: gamma-CTF(50)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (740)..(770)
; OTHER INFORMATION: C31
; OTHER INFORMATION: C31
US-10-982-545-15
```

```
Query Match      88.2%; Score 30; DB 6; Length 770;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KKLVEFA 7
      :|||||
Db      686 QKLVEFA 692
```

RESULT 12

```
US-10-789-273-38
; Sequence 38, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-273-38
```

```
Query Match      88.2%; Score 30; DB 6; Length 770;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KKLVEFA 7
      :|||||
Db      686 QKLVEFA 692
```

```
RESULT 13
US-10-467-657-7892
; Sequence 7892, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7892
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7892
```

```
Query Match      79.4%; Score 27; DB 6; Length 50;
Best Local Similarity 66.7%; Pred. No. 6.9;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KKLVEFA 6
      :||:|
Db      32 KKLVEFA 37
```

```
RESULT 14
US-11-078-189-19
; Sequence 19, Application US/11078189
; Publication No. US20050277167A1
; GENERAL INFORMATION:
```

; APPLICANT: Bachinger, Hans Peter
; APPLICANT: Vranka, Janice
; TITLE OF INVENTION: PROLYL 3-HYDROXYLASES
; FILE REFERENCE: 08062-020001
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/11/078,189
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/552,409
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
US-11-078-189-19

Query Match 79.4%; Score 27; DB 7; Length 558;
Best Local Similarity 71.4%; Pred. No. 75;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGLVFFA 7
|:|:|
Db 277 KELLFFA 283

RESULT 15
US-11-174-150-25
; Sequence 25, Application US/11174150
; Publication No. US20050260714A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50022
; CURRENT APPLICATION NUMBER: US/11/174,150
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/257,174
; PRIOR FILING DATE: 2002-10-10
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/11797
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/196,603
; PRIOR FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-174-150-25

Query Match 79.4%; Score 27; DB 7; Length 708;
Best Local Similarity 71.4%; Pred. No. 95;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGLVFFA 7
|:|:|
Db 345 KELLFFA 351

RESULT 16
US-11-078-189-18
; Sequence 18, Application US/11078189
; Publication No. US2005027167A1
; GENERAL INFORMATION:
; APPLICANT: Bachinger, Hans Peter
; APPLICANT: Vranka, Janice

; TITLE OF INVENTION: PROLYL 3-HYDROXYLASES
; FILE REFERENCE: 08062-020001
; CURRENT APPLICATION NUMBER: US/11/078,189
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/552,409
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Gallus gallus
US-11-078-189-18

Query Match 79.4%; Score 27; DB 7; Length 710;
Best Local Similarity 57.1%; Pred. No. 95;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGLVFFA 7
|:|:|
Db 356 KLLIYYA 362

RESULT 17
US-11-174-150-26
; Sequence 26, Application US/11174150
; Publication No. US20050260714A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50022
; CURRENT APPLICATION NUMBER: US/11/174,150
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/257,174
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: PCT/US01/11797
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/196,603
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/199,417
; PRIOR FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-174-150-26

Query Match 79.4%; Score 27; DB 7; Length 736;
Best Local Similarity 71.4%; Pred. No. 99;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGLVFFA 7
|:|:|
Db 373 KELLFFA 379

RESULT 18
US-11-078-189-9
; Sequence 9, Application US/11078189
; Publication No. US2005027167A1
; GENERAL INFORMATION:
; APPLICANT: Bachinger, Hans Peter
; APPLICANT: Vranka, Janice
; TITLE OF INVENTION: PROLYL 3-HYDROXYLASES
; FILE REFERENCE: 08062-020001
; CURRENT APPLICATION NUMBER: US/11/078,189
; CURRENT FILING DATE: 2005-03-11

; PRIOR APPLICATION NUMBER: US 60/552,409
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-189-9

Query Match 79.4%; Score 27; DB 7; Length 736;
Best Local Similarity 71.4%; Pred. No. 99;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
|:|:|
Db 373 KELLFFA 379

RESULT 19
US-11-078-189-12
; Sequence 12, Application US/11078189
; Publication No. US20050277167A1
; GENERAL INFORMATION:
; APPLICANT: Bachinger, Hans Peter
; APPLICANT: Vranka, Janice
; TITLE OF INVENTION: PROLYL 3-HYDROXYLASES
; FILE REFERENCE: 08062-020001
; CURRENT APPLICATION NUMBER: US/11/078,189
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/552,409
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-078-189-12

Query Match 79.4%; Score 27; DB 7; Length 739;
Best Local Similarity 71.4%; Pred. No. 99;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
|:|:|
Db 376 KELLFFA 382

RESULT 20
US-11-186-284-132
; Sequence 132, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978

; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-132

Query Match 76.5%; Score 26; DB 7; Length 707;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
|:|:|
Db 577 KKLFFFS 583

RESULT 21
US-11-147-047-49
; Sequence 49, Application US/11147047
; Publication No. US20050260668A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GPS0016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 1070
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-49

Query Match 76.5%; Score 26; DB 7; Length 1070;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 6
|:|:|
Db 1011 KQLVFF 1016

RESULT 22
US-11-098-674-1
; Sequence 1, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use

; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-098-674-1

Query Match 73.5%; Score 25; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFF 6
|:|:|
DB 1 KLVFF 5

RESULT 23

US-10-467-657-5436
; Sequence 5436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Eliseabette
; TITLE OF INVENTION: CONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5436
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5436

Query Match 73.5%; Score 25; DB 6; Length 47;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFF 6
|:|:|
DB 35 KLVFF 40

RESULT 24

US-10-858-730-196
; Sequence 196, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID

; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Coryne-bacterium glutamicum
US-10-858-730-196

Query Match 73.5%; Score 25; DB 6; Length 207;
Best Local Similarity 71.4%; Pred. No. 75;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFF 7
|:|:|
DB 122 KLVFF 128

RESULT 25

US-10-793-626-1860
; Sequence 1860, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1860
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1860

Query Match 73.5%; Score 25; DB 6; Length 443;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFF 6
|:|:|
DB 167 KLVFF 172

RESULT 26

US-10-793-626-1930
; Sequence 1930, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1930
; LENGTH: 528

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1930

Query Match          73.5%; Score 25; DB 6; Length 528;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 KLVVFF 6
Db   477 KLVVFF 481

RESULT 27
US-11-186-284-125
; Sequence 125, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-125

Query Match          73.5%; Score 25; DB 7; Length 660;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  1 KKLIVFFA 7
Db   530 EKAVFFA 536

RESULT 28
US-10-821-234-917
; Sequence 917, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for diagnosis and Treatment of Preecclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07

; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 917
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-917

Query Match          73.5%; Score 25; DB 6; Length 708;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  1 KKLIVFFA 7
Db   578 EKAVFFA 584

RESULT 29
US-10-793-626-2374
; Sequence 2374, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2374
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2374

Query Match          70.6%; Score 24; DB 6; Length 134;
Best Local Similarity 50.0%; Pred. No. 80;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY  1 KKLIVFF 6
Db   6 KKIIYF 11

RESULT 30
US-10-467-657-2934
; Sequence 2934, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2934
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
```

US-10-467-657-2934

Query Match 70.6%; Score 24; DB 6; Length 148;
Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPF 6
DB 21 KKLVPF 26

RESULT 31

US-10-967-457-79
; Sequence 79, Application US/10967457
; Publication No. US2005024931A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF545PCT
; CURRENT APPLICATION NUMBER: US/10/967,457
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: US/09/833,041
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 79
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-967-457-79

Query Match 70.6%; Score 24; DB 6; Length 167;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPF 5
DB 106 KKLVPF 110

RESULT 32

US-10-793-626-2836
; Sequence 2836, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2836
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2836

Query Match 70.6%; Score 24; DB 6; Length 182;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPF 7
DB 13 KKLVPF 19

RESULT 33

US-11-044-899-26
; Sequence 26, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; APPLICANT: Chen, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; TITLE OF INVENTION: THEREON
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 194
; TYPE: PRT
; ORGANISM: C. elegans
US-11-044-899-26

Query Match 70.6%; Score 24; DB 7; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPF 5
DB 101 KKLVPF 105

RESULT 34

US-10-793-626-630
; Sequence 630, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 630
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-630

Query Match 70.6%; Score 24; DB 6; Length 196;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPF 6
DB 125 KKLVPF 130

RESULT 35

US-10-467-657-6932
; Sequence 6932, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6932
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6932

Query Match 70.6%; Score 24; DB 6; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;
QY 3 LVFFA 7
Db 19 LVFFA 23

RESULT 36
US-10-131-826A-4
; Sequence 4, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 4
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-4
Query Match 70.6%; Score 24; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 LVFFA 7
Db 166 LVFFA 170

RESULT 37
US-10-467-657-568
; Sequence 568, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 568
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-568

Query Match 70.6%; Score 24; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 LVFFA 7
Db 156 LVFFA 160

RESULT 38
US-10-467-657-4838
; Sequence 4838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218

```
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838

Query Match          70.6%; Score 24; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 LVFFA 7
Db      156 LVFFA 160

RESULT 39
US-10-821-234-1322
; Sequence 1322, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0
; SEQ ID NO 1322
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1322

Query Match          70.6%; Score 24; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 LVFFA 7
Db      166 LVFFA 170

RESULT 40
US-11-113-424-30
; Sequence 30, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli, et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113.424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075

; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838

; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-30

Query Match          70.6%; Score 24; DB 7; Length 249;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KKLVPFA 7
Db      3 KKLVPFA 9

RESULT 41
US-10-512-184-34
; Sequence 34, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-34

Query Match          70.6%; Score 24; DB 6; Length 259;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KKLVPFA 7
Db      195 KKLVPFA 201

RESULT 42
US-10-878-556A-19
; Sequence 19, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/cn03_human
; DATABASE ENTRY DATE: 2001-10-16
US-10-878-556A-19
```

Query Match 70.6%; Score 24; DB 6; Length 338;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFF 6
||:|
Db 76 KLIFF 80

RESULT 43

US-10-131-826A-376
; Sequence 376, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bereisni, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 376
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-376

Query Match 70.6%; Score 24; DB 6; Length 344;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFF 6
||:|
Db 279 KLIFF 283

RESULT 44
US-10-512-184-71
; Sequence 71, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.v.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising ACE - linker -
; OTHER INFORMATION: scFv PL2.
US-10-512-184-71

Query Match 70.6%; Score 24; DB 6; Length 371;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7
|:|:|
Db 307 KLLVYFA 313

RESULT 45
US-11-080-991-16
; Sequence 16, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-16

Query Match 70.6%; Score 24; DB 7; Length 374;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7
|:|:|
Db 343 KPLIEFA 349

RESULT 46

US-10-995-561-1005
; Sequence 1005, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1005
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1005

Query Match 70.6%; Score 24; DB 6; Length 396;

Best Local Similarity 85.7%; Pred. No. 2.3e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLVFFA 7

Db 78 KLVFFA 84

RESULT 47

US-11-082-389-198

; Sequence 198, Application US/11082389

; Publication No. US2005024935A1

; GENERAL INFORMATION:

; APPLICANT: Pompejus, Markus

; APPLICANT: Kroger, Burkhard

; APPLICANT: Schroder, Hartwig

; APPLICANT: Zelder, Oskar

; APPLICANT: Habethauer, Gregor

; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS

; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE

; FILE REFERENCE: BGI-131CPCN

; CURRENT APPLICATION NUMBER: US/11/082,389

; CURRENT FILING DATE: 2005-03-16

; PRIOR APPLICATION NUMBER: US 09/603024

; PRIOR FILING DATE: 2000-06-23

; PRIOR APPLICATION NUMBER: US 60/141031

; PRIOR FILING DATE: 1999-06-25

; PRIOR APPLICATION NUMBER: US 60/143262

; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: US 60/151281

; PRIOR FILING DATE: 1999-08-27

; PRIOR APPLICATION NUMBER: DE 19930487.4

; PRIOR FILING DATE: 1999-07-01

; PRIOR APPLICATION NUMBER: DE 19930489.0

; PRIOR FILING DATE: 1999-07-01

; PRIOR APPLICATION NUMBER: DE 19931549.3

; PRIOR FILING DATE: 1999-07-08

; PRIOR APPLICATION NUMBER: DE 19931550.7

; PRIOR FILING DATE: 1999-07-08

; PRIOR APPLICATION NUMBER: DE 19932134.5

; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: DE 19941379.7

; PRIOR FILING DATE: 1999-08-31

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 446

; SEQ ID NO 198

; LENGTH: 453

; TYPE: PRT

; ORGANISM: Corynebacterium glutamicum

US-11-082-389-198

Query Match 70.6%; Score 24; DB 7; Length 453;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVFFA 7

Db 401 LVFFA 405

RESULT 48

US-11-069-642-19

; Sequence 19, Application US/11069642

; Publication No. US20050260626A1

; GENERAL INFORMATION:

; APPLICANT: LORENS, JAMES B.

; APPLICANT: PRAY, TODD R.

; APPLICANT: KINSELLA, TODD M.

; APPLICANT: BENNETT, MARK K.

; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR

; TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION

; FILE REFERENCE: RIGI-022CIP3

; CURRENT APPLICATION NUMBER: US/11/069,642

; CURRENT FILING DATE: 2005-02-28

; PRIOR APPLICATION NUMBER: 10/232,758

; PRIOR FILING DATE: 2002-08-30

; PRIOR APPLICATION NUMBER: 10/422,536

; PRIOR FILING DATE: 2003-04-23

; PRIOR APPLICATION NUMBER: 09/800,770

; PRIOR FILING DATE: 2001-03-06

; PRIOR APPLICATION NUMBER: 60/187,130

; PRIOR FILING DATE: 2000-03-06

; NUMBER OF SEQ ID NOS: 168

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 19

; LENGTH: 476

; TYPE: PRT

; ORGANISM: Pyrococcus horikoshii OT3

US-11-069-642-19

Query Match 70.6%; Score 24; DB 7; Length 476;

Best Local Similarity 83.3%; Pred. No. 2.8e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKLVPF 6

Db 346 KKLVPF 351

RESULT 49

US-10-995-561-959

; Sequence 959, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 959

; LENGTH: 481

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-995-561-959

Query Match 70.6%; Score 24; DB 6; Length 481;

Best Local Similarity 66.7%; Pred. No. 2.8e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KLVFFA 7

Db 275 KLVFFA 280

RESULT 50

US-10-793-626-24

; Sequence 24, Application US/10793626

; Publication No. US20050255478A1

```
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-24

Query Match          70.6%; Score 24; DB 6; Length 482;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KKLVEFA 7
      ||::||
DB      387 KKVILFA 393

RESULT 51
US-10-719-311-16
; Sequence 16, Application US/10719311
; Publication No. US20040086490A1
; GENERAL INFORMATION:
; APPLICANT: Chlorini, John A.
;          Kotin, Robert M.
;          Safer, Brian
; TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Needle & Rosenberg
; STREET: 127 Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/719,311
; FILING DATE: 20-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,747
; FILING DATE: 26-Nov-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Selby, Elizabeth
; REGISTRATION NUMBER: 38,298
; REFERENCE/DOCKET NUMBER: 14014.0252
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 598 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: protein
; FEATURE:
; OTHER INFORMATION: AAV4 capsid protein VP2
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-719-311-16
```

```
Query Match          70.6%; Score 24; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVP 5
      |||||
DB      32 KKLVP 36

RESULT 52
US-10-512-184-49
; Sequence 49, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: comprising the leader peptide - chitinase- linker
; OTHER INFORMATION: - scFv PL2 - cmcy/His6.
US-10-512-184-49
```

```
Query Match          70.6%; Score 24; DB 6; Length 626;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KKLVEFA 7
      ||::||
DB      536 KLLVFA 542
```

```
RESULT 53
US-11-078-189-15
; Sequence 15, Application US/11078189
; Publication No. US2005027167A1
; GENERAL INFORMATION:
; APPLICANT: Bachinger, Hans Peter
; APPLICANT: Vranka, Janice
; TITLE OF INVENTION: PROLYL 3-HYDROXYLASES
; FILE REFERENCE: 08062-02001
; CURRENT APPLICATION NUMBER: US/11/078,189
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/552,409
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 725
; TYPE: PRT
; ORGANISM: Gallus gallus
; US-11-078-189-15
```

```
Query Match          70.6%; Score 24; DB 7; Length 725;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFA 7
      ||::||
DB      366 KELLFFS 372
```

RESULT 54


```
US-10-719-311-4
; Sequence 4, Application US/10719311
; Publication No. US20040086490A1
; GENERAL INFORMATION:
; APPLICANT: Chiorini, John A.
;           Kotin, Robert M.
;           Safer, Brian
; TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Needle & Rosenberg
; STREET: 127 Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/719,311
; FILING DATE: 20-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,747
; FILING DATE: 26-Nov-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Selby, Elizabeth
; REGISTRATION NUMBER: 38,298
; REFERENCE/DOCKET NUMBER: 14014.0252
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 734 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: protein
; FEATURE:
; OTHER INFORMATION: AAV4 capsid protein VP1
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-719-311-4
Query Match 70.6%; Score 24; DB 6; Length 734;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVF 5
Db 168 KKLVF 172
|||||

RESULT 55
US-10-613-744-6
; Sequence 6, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: CatIon Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307

US-10-067-811-4
; Sequence 4, Application US/11067811
; Publication No. US20050260688A1
; GENERAL INFORMATION:
; APPLICANT: Morgan, Bruce A
; APPLICANT: Enshell-Sciiffers, David
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HAIR GROWTH
; FILE REFERENCE: 10287-083001
; CURRENT APPLICATION NUMBER: US/11/067,811
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 60/548,272
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1113
; TYPE: PRT
; ORGANISM: Mus Musculus
US-11-067-811-4
Query Match 70.6%; Score 24; DB 7; Length 1113;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;

US-10-821-234-975
; Sequence 975, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 975
; LENGTH: 989
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-975
Query Match 70.6%; Score 24; DB 6; Length 989;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKLVFFA 7
Db 311 KESVFFA 317
|:|||||

RESULT 57
US-11-067-811-4
; Sequence 4, Application US/11067811
; Publication No. US20050260688A1
; GENERAL INFORMATION:
; APPLICANT: Morgan, Bruce A
; APPLICANT: Enshell-Sciiffers, David
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HAIR GROWTH
; FILE REFERENCE: 10287-083001
; CURRENT APPLICATION NUMBER: US/11/067,811
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 60/548,272
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1113
; TYPE: PRT
; ORGANISM: Mus Musculus
US-11-067-811-4
Query Match 70.6%; Score 24; DB 7; Length 1113;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;

US-10-821-234-975
; Sequence 975, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 975
; LENGTH: 989
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-975
Query Match 70.6%; Score 24; DB 6; Length 989;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKLVFFA 7
Db 311 KESVFFA 317
|:|||||

RESULT 57
US-11-067-811-4
; Sequence 4, Application US/11067811
; Publication No. US20050260688A1
; GENERAL INFORMATION:
; APPLICANT: Morgan, Bruce A
; APPLICANT: Enshell-Sciiffers, David
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HAIR GROWTH
; FILE REFERENCE: 10287-083001
; CURRENT APPLICATION NUMBER: US/11/067,811
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 60/548,272
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1113
; TYPE: PRT
; ORGANISM: Mus Musculus
US-11-067-811-4
Query Match 70.6%; Score 24; DB 7; Length 1113;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
```

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
|:|:|
Db 572 KYLMFFA 578

RESULT 58

US-11-040-159-20
; Sequence 20, Application US/11040159
; Publication No. US2005025552A1
; GENERAL INFORMATION:
; APPLICANT: Flynn, Peter
; APPLICANT: Luehrs, Kenneth
; APPLICANT: Balint, Robert F.
; APPLICANT: Her, Jeng-Hong
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Yarranton, Geoffrey I.
; APPLICANT: Kalobios, Inc.
; TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
; FILE REFERENCE: 021167-001730US
; CURRENT APPLICATION NUMBER: US/11/040,159
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US 60/537,364
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/546,216
; PRIOR FILING DATE: 2004-02-23
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:non-natural
; OTHER INFORMATION: synthetic secretion signal peptide designated SP2
US-11-040-159-20

Query Match 67.6%; Score 23; DB 7; Length 21;
Best Local Similarity 71.4%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
|:|:|
Db 4 KQLVVFA 10

RESULT 59

US-10-467-657-3918
; Sequence 3918, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3918
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3918

Query Match 67.6%; Score 23; DB 6; Length 186;

Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
|:|:|
Db 2 KKLIFAA 8

RESULT 60

US-10-980-388-65
; Sequence 65, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-65

Query Match 67.6%; Score 23; DB 6; Length 187;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
|:|:|
Db 178 KRYVYFA 184

RESULT 61

US-10-467-657-8102
; Sequence 8102, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8102
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8102

Query Match 67.6%; Score 23; DB 6; Length 216;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVFFPA 7
|:|:|
Db 18 LIPFA 22

RESULT 62
US-10-467-657-290
; Sequence 290, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 290
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-290

Query Match 67.6%; Score 23; DB 6; Length 221;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVFFPA 7
|:|:|
Db 41 LIPFA 45

RESULT 63
US-10-467-657-5750
; Sequence 5750, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5750
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5750

Query Match 67.6%; Score 23; DB 6; Length 221;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVFFPA 7
|:|:|
Db 41 LIPFA 45

RESULT 64
US-10-793-626-1430
; Sequence 1430, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUB3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1430
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1430

Query Match 67.6%; Score 23; DB 6; Length 224;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
|:|:|
Db 107 KRLIFVA 113

RESULT 65
US-10-467-657-330
; Sequence 330, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 330
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-330

Query Match 67.6%; Score 23; DB 6; Length 269;

Best Local Similarity 80.0%; Pred. No. 2.6e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 4; Conservative 1;

QY 2 KLVFF 6
|:|:|
Db 11 KLVFF 15

RESULT 66
US-10-821-234-1419
; Sequence 1419, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1419
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1419

Query Match 67.6%; Score 23; DB 6; Length 271;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFF 6
|:|:|
Db 109 KLVFF 114

RESULT 67
US-10-632-150-46
; Sequence 46, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiaux, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-46

Query Match 67.6%; Score 23; DB 6; Length 272;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFF 7

Db 211 KLVFF 216
|:|:|

RESULT 68
US-11-073-457-46
; Sequence 46, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-46

Query Match 67.6%; Score 23; DB 7; Length 272;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFF 7
|:|:|
Db 211 KLVFF 216

RESULT 69
US-11-073-460-46
; Sequence 46, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-46

Query Match 67.6%; Score 23; DB 7; Length 272;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLVFF 7
|:|:|
Db 211 KLVFF 216

RESULT 70
US-10-485-517-234
; Sequence 234, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:

```

; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118925.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 234
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-234

Query Match      67.6%; Score 23; DB 6; Length 337;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KKLVPF 6
DB      174 KKVAFP 179

RESULT 71
US-10-770-726-55
; Sequence 55, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-55

Query Match      67.6%; Score 23; DB 6; Length 346;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPF 5
DB      342 KKLIF 346

RESULT 72
US-10-821-234-1105
; Sequence 1105, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Lebat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andermani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047

; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1105
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1105

Query Match      67.6%; Score 23; DB 6; Length 370;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 KLVFFA 7
DB      115 RLFFFA 120

RESULT 73
US-10-793-626-1056
; Sequence 1056, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1056
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1056

Query Match      67.6%; Score 23; DB 6; Length 400;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 KLVFF 6
DB      7 KLVFF 11

RESULT 74
US-10-467-657-9070
; Sequence 9070, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 9070
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9070

```

Query Match 67.6%; Score 23; DB 6; Length 402;
Best Local Similarity 57.1%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
Db 262 RHIVFFA 268

RESULT 75
US-10-467-657-6352
; Sequence 6352, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6352
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6352

Query Match 67.6%; Score 23; DB 6; Length 463;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVVFFA 7
Db 369 LIFFA 373

Search completed: December 29, 2005, 18:50:14
Job time : 4.83871 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 95.4032 Seconds
(without alignments)
32.238 Million cell updates/sec

Title: US-10-009-122-2
Perfect score: 34
Sequence: 1 KKLVPFA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	7	4	AAB48475
2	34	100.0	7	4	AAB82624
3	34	100.0	7	5	AAU96812
4	34	100.0	7	5	AAU11649
5	34	100.0	7	6	AAE35439
6	34	100.0	7	8	ADQ37314
7	34	100.0	7	8	ADQ37263
8	34	100.0	7	9	ADY37922
9	34	100.0	9	6	ABU79063
10	34	100.0	9	7	ABW00197
11	31	91.2	277	7	ADK82706
12	30	88.2	7	2	AAW02312
13	30	88.2	7	2	AAW89376
14	30	88.2	7	5	ABG71007
15	30	88.2	7	5	ABW05155
16	30	88.2	7	8	ADJ64058
17	30	88.2	7	8	ADQ37351
18	30	88.2	7	9	ADZ08903
19	30	88.2	8	2	AAW02310
20	30	88.2	8	2	AAW89374
21	30	88.2	8	5	ABG71005
22	30	88.2	8	5	ABW05153
23	30	88.2	8	8	ADJ64056
24	30	88.2	8	8	ADQ37349

25	30	88.2	9	2	AAR45239	Aar45239	Mutant am
26	30	88.2	9	4	AAB48493	Aab48493	Antifibri
27	30	88.2	9	5	AAU11667	Aau11667	Peptide #
28	30	88.2	9	6	ABP57517	Abp57517	Different
29	30	88.2	9	6	ABU79053	Abu79053	Aggregati
30	30	88.2	9	6	AAE35436	Aae35436	Abeta pep
31	30	88.2	9	7	ABW00187	Abw00187	Peptide #
32	30	88.2	9	8	ADJ135874	Adj135874	Amyloid b
33	30	88.2	9	8	ADQ37260	Adq37260	Vaccine a
34	30	88.2	9	8	ADQ37332	Adq37332	Antifibri
35	30	88.2	10	4	AAB46226	Aab46226	Human APP
36	30	88.2	10	4	AAB46225	Aab46225	Human APP
37	30	88.2	10	4	AAB46224	Aab46224	Human APP
38	30	88.2	10	4	AAB46227	Aab46227	Human APP
39	30	88.2	10	4	AAB82641	Aab82641	All-D pep
40	30	88.2	10	5	AAU96829	Aau96829	Amyloid t
41	30	88.2	10	6	ABP57511	Abp57511	Different
42	30	88.2	10	6	AAE35455	Aae35455	Abeta pep
43	30	88.2	10	8	ADQ37280	Adq37280	Vaccine a
44	30	88.2	10	8	ADQ37371	Adq37371	Amyloid-b
45	30	88.2	10	8	ADQ37374	Adq37374	Amyloid-b
46	30	88.2	10	9	ADY37939	Ady37939	Amyloid-t
47	30	88.2	11	2	AAW32560	Aaw32560	Anti-amyl
48	30	88.2	11	5	AAU99431	Aau99431	Human amy
49	30	88.2	11	5	AAE29504	Aae29504	Amyloid b
50	30	88.2	11	6	ABU79013	Abu79013	Amyloidog
51	30	88.2	11	7	ABR84683	AbR84683	Aggregati
52	30	88.2	11	7	ABW00147	Abw00147	Amyloid-b
53	30	88.2	12	6	AAE35464	Aae35464	Abeta pep
54	30	88.2	12	6	AAE35435	Aae35435	Abeta pep
55	30	88.2	12	6	AAE35466	Aae35466	Abeta pep
56	30	88.2	12	7	ADD20745	Add20745	Human bet
57	30	88.2	12	7	ADZ020744	Adz020744	Human bet
58	30	88.2	12	8	ADJ71476	Adj71476	N-termina
59	30	88.2	12	8	ADQ37407	Adq37407	Amyloid-b
60	30	88.2	12	8	ADQ37289	Adq37289	Vaccine a
61	30	88.2	12	8	ADQ37259	Adq37259	Vaccine a
62	30	88.2	12	9	ADZ08890	Adz08890	Human bet
63	30	88.2	13	6	ADA37467	Ada37467	Human amy
64	30	88.2	13	8	ADJ71477	Adj71477	N-termina
65	30	88.2	13	8	ADJ71464	Adj71464	N-termina
66	30	88.2	14	6	ADA89887	Ada89887	Beta-A4 s
67	30	88.2	14	8	ADJ71452	Adj71452	N-termina
68	30	88.2	14	8	ADJ71465	Adj71465	N-termina
69	30	88.2	14	8	ADJ71478	Adj71478	N-termina
70	30	88.2	14	9	ADZ08889	Adz08889	Human bet
71	30	88.2	15	2	AAW89358	Aaw89358	Beta-amyl
72	30	88.2	15	6	ABU79064	Abu79064	Aggregati
73	30	88.2	15	6	ABU79059	Abu79059	Aggregati
74	30	88.2	15	6	ABU79060	Abu79060	Aggregati
75	30	88.2	15	6	ABU79055	Abu79055	Aggregati
76	30	88.2	15	6	ABU79056	Abu79056	Aggregati
77	30	88.2	15	7	ABU79062	Abu79062	Aggregati
78	30	88.2	15	7	ABW00190	Abw00190	Peptide #
79	30	88.2	15	7	ABW00198	Abw00198	Peptide #
80	30	88.2	15	7	ABW00189	Abw00189	Peptide #
81	30	88.2	15	7	ABW00193	Abw00193	Peptide #
82	30	88.2	15	7	ABW00196	Abw00196	Peptide #
83	30	88.2	15	7	ABW00194	Abw00194	Peptide #
84	30	88.2	15	8	ADJ71466	Adj71466	N-termina
85	30	88.2	15	8	ADJ71453	Adj71453	N-termina
86	30	88.2	15	8	ADJ71479	Adj71479	N-termina
87	30	88.2	15	8	ADJ71440	Adj71440	N-termina
88	30	88.2	16	5	AAE26330	Aae26330	Human bet
89	30	88.2	16	8	ADJ71454	Adj71454	N-termina
90	30	88.2	16	8	ADJ71480	Adj71480	N-termina
91	30	88.2	16	8	ADJ71441	Adj71441	N-termina
92	30	88.2	16	8	ADJ71467	Adj71467	N-termina
93	30	88.2	16	8	ADJ71428	Adj71428	N-termina
94	30	88.2	17	2	AAW54703	Aaw54703	Beta-amyl
95	30	88.2	17	2	AAW18880	Aaw18880	Beta-amyl
96	30	88.2	17	4	AAB91774	Aab91774	Amyloid b
97	30	88.2	17	4	AAB91807	Aab91807	Amyloid b

98	30	88.2	17	4	AAB48346	Aab48346	Beta-amyl	171	30	88.2	28	4	AAB91800	Aab91800	Amyloid b
99	30	88.2	17	5	ABB04911	Abb04911	Human amyl	172	30	88.2	28	4	AAB49396	Aab49396	Human amyl
100	30	88.2	17	6	AAE35468	Aae35468	Beta pep	173	30	88.2	28	5	AAE21439	Aae21439	Human bet
101	30	88.2	17	6	ABB99611	Abb99611	Peptide d	174	30	88.2	28	5	ABB76030	Beta amyl	
102	30	88.2	17	8	ADG93165	Adg93165	Novel exp	175	30	88.2	28	5	AAO18476	Human bet	
103	30	88.2	17	8	ADJ65843	Adj65843	Amyloid B	176	30	88.2	28	5	AAU76484	Amino aci	
104	30	88.2	17	8	ADN02827	Adn02827	Mammalian	177	30	88.2	28	5	ABB04910	Human amyl	
105	30	88.2	17	8	ADQ37291	Adq37291	Vaccine a	178	30	88.2	28	5	AAE26081	Beta amyl	
106	30	88.2	17	8	ADS18447	Ads18447	Amyloid-b	179	30	88.2	28	5	AAM50910	Beta amyl	
107	30	88.2	18	3	AAAB10963	Aab10963	Beta-amyl	180	30	88.2	28	5	ABB77991	Fragment	
108	30	88.2	19	2	AAW18882	Aaw18882	AEDANS-be	181	30	88.2	28	6	AAE35672	Human bet	
109	30	88.2	19	2	AAW18881	Aaw18881	Trp-Beta-	182	30	88.2	28	6	AAE33794	Beta-amyl	
110	30	88.2	19	3	AAAY79935	Aay79935	Beta-amyl	183	30	88.2	28	6	ABG72238	Mutant H6	
111	30	88.2	19	4	AAAB49097	Aab49097	Human amyl	184	30	88.2	28	6	ABG72246	Mutant K2	
112	30	88.2	19	4	AAAB46201	Aab46201	Human APP	185	30	88.2	28	6	ABG72234	Wild-type	
113	30	88.2	19	8	ADU24440	Adu24440	Novel glu	186	30	88.2	28	6	ABG72244	Mutant E2	
114	30	88.2	19	8	ADU24442	Adu24442	Novel glu	187	30	88.2	28	6	ABG72235	Mutant D1	
115	30	88.2	19	8	ADU46714	Adu46714	Amyloid b	188	30	88.2	28	6	ABG72241	Mutant H1	
116	30	88.2	19	8	ADU46716	Adu46716	Gln3 amyl	189	30	88.2	28	6	ABG72240	Mutant E1	
117	30	88.2	19	9	ADZ71366	Adz71366	Human bet	190	30	88.2	28	6	ABG72237	Mutant R5	
118	30	88.2	19	9	ADZ71368	Adz71368	Human bet	191	30	88.2	28	6	ABG72245	Mutant D2	
119	30	88.2	19	9	AEA35401	Aea35401	Novel QC	192	30	88.2	28	6	ABG72242	Mutant H1	
120	30	88.2	19	9	AEA35399	Aea35399	Novel QC	193	30	88.2	28	6	ABG72236	Mutant E3	
121	30	88.2	19	9	AE92572	Aeb92572	Glutaminyl	194	30	88.2	28	6	ABG72239	Mutant D7	
122	30	88.2	19	9	AE92574	Aeb92574	Glutaminyl	195	30	88.2	28	6	AAE35431	Beta pep	
123	30	88.2	20	3	AAAY79934	Aay79934	Beta-amyl	196	30	88.2	28	6	AAE33219	Beta amyl	
124	30	88.2	20	5	ABB06431	Abb06431	Beta-secr	197	30	88.2	28	6	ABU63712	Rat amylo	
125	30	88.2	21	2	AAAY30941	Aay30941	Human sec	198	30	88.2	28	7	AAE38831	Membrane	
126	30	88.2	21	8	ADU24439	Adu24439	Novel glu	199	30	88.2	28	7	ADP55641	Human A b	
127	30	88.2	21	8	ADU46713	Adu46713	Amyloid b	200	30	88.2	28	8	ADO04475	Beta-amyl	
128	30	88.2	21	9	ADV86872	Adv86872	Beta-amyl	201	30	88.2	28	8	ADQ37255	Vaccine a	
129	30	88.2	21	9	ADZ71365	Adz71365	Human bet	202	30	88.2	28	8	ADR16886	A disinte	
130	30	88.2	21	9	AEA35398	Aea35398	Novel QC	203	30	88.2	28	8	ADS15333	Beta-amyl	
131	30	88.2	21	9	AE92571	Aeb92571	Glutaminyl	204	30	88.2	28	9	ADY81768	Human bet	
132	30	88.2	22	8	ADR83670	Aar83670	Amyloidog	205	30	88.2	29	5	AAE26331	Human bet	
133	30	88.2	24	2	AAAS2569	Aar25569	Alzheimer	206	30	88.2	29	9	ADW88083	T668 phos	
134	30	88.2	24	9	ADW88085	Aar88085	T668 phos	207	30	88.2	30	2	AAW81468	Synthetic	
135	30	88.2	24	9	AEBO9195	Aeb09195	Human bet	208	30	88.2	30	5	ABG94392	A beta pe	
136	30	88.2	24	9	AEBO9194	Aeb09194	Human bet	209	30	88.2	30	5	AAU11766	Human amyl	
137	30	88.2	26	2	AAW47229	Aaw47229	Beta-amyl	210	30	88.2	30	5	ABG80717	Mouse Reg	
138	30	88.2	26	2	AAAY33408	Aay33408	Human amyl	211	30	88.2	30	5	ABG80704	Modified	
139	30	88.2	26	6	ABU63718	Abu63718	Rat amylo	212	30	88.2	30	6	ABR42769	Human amyl	
140	30	88.2	26	7	ADP55647	Adp55647	Human a b	213	30	88.2	30	7	ADK82701	Beta-amyl	
141	30	88.2	26	9	ADY72250	Adv72250	N-termina	214	30	88.2	30	8	ADI35870	Amyloid b	
142	30	88.2	27	2	AAAY33409	Aay33409	Human amyl	215	30	88.2	30	8	ADI40718	Beta 1-2	
143	30	88.2	28	1	AAAP70594	Aap70594	Sequence	216	30	88.2	30	9	ADZ59196	Human amyl	
144	30	88.2	28	1	AAAP90381	Aap90381	Synthetic	217	30	88.2	32	4	AAAB8430	Partial s	
145	30	88.2	28	2	AAAR60368	Aar60368	Beta-amyl	218	30	88.2	32	8	ADP73486	Alzheimer	
146	30	88.2	28	2	AAAR54702	Aar54702	Beta-amyl	219	30	88.2	33	2	AAW81469	Synthetic	
147	30	88.2	28	2	AAAR64171	Aar64171	A4-P(1-28	220	30	88.2	33	5	AAU93990	Human bet	
148	30	88.2	28	2	AAAR64164	Aar64164	Generic b	221	30	88.2	33	7	ADE10851	Chimeric	
149	30	88.2	28	2	AAAR64172	Aar64172	A4-B(1-28	222	30	88.2	33	7	ADM39756	B-cell pe	
150	30	88.2	28	2	AAAR64170	Aar64170	A4-O(1-28	223	30	88.2	33	8	ADG63951	Recombina	
151	30	88.2	28	2	AAW01413	Aaw01413	Beta/A4-a	224	30	88.2	33	8	ADP73485	Alzheimer	
152	30	88.2	28	2	AAW01414	Aaw01414	Beta/A4-a	225	30	88.2	33	8	ADR12778	Human bet	
153	30	88.2	28	2	AAAY39805	Aay39805	Beta-amyl	226	30	88.2	35	2	AAW02336	Beta-amyl	
154	30	88.2	28	2	AAW81467	Aaw81467	Synthetic	227	30	88.2	35	2	AAW47228	Beta-amyl	
155	30	88.2	28	4	AAAB35591	Aab35591	Human clo	228	30	88.2	35	2	AAW89361	Beta-amyl	
156	30	88.2	28	4	AAAB35595	Aab35595	Human clo	229	30	88.2	35	2	AAW89357	Beta-amyl	
157	30	88.2	28	4	AAAB35594	Aab35594	Human clo	230	30	88.2	35	2	AAW89356	Beta-amyl	
158	30	88.2	28	4	AAAB35592	Aab35592	Human clo	231	30	88.2	35	2	AAW89359	Beta-amyl	
159	30	88.2	28	4	AAAB35593	Aab35593	Human clo	232	30	88.2	35	4	AAAB91830	Amyloid b	
160	30	88.2	28	4	AAAB35597	Aab35597	Human clo	233	30	88.2	35	4	AAAB91803	Amyloid b	
161	30	88.2	28	4	AAAB35600	Aab35600	Human clo	234	30	88.2	35	5	ABG71016	Long form	
162	30	88.2	28	4	AAAB35596	Aab35596	Human clo	235	30	88.2	35	5	ABB05164	BEVVHHHQ	
163	30	88.2	28	4	AAAB35598	Aab35598	Human clo	236	30	88.2	35	6	AAE35430	Beta pep	
164	30	88.2	28	4	AAAB36202	Aab36202	Human clo	237	30	88.2	35	8	ADJ64067	Human bet	
165	30	88.2	28	4	AAAB35590	Aab35590	Human clo	238	30	88.2	35	8	ADQ37254	Vaccine a	
166	30	88.2	28	4	AAAB36201	Aab36201	Human clo	239	30	88.2	36	2	AAW81471	Synthetic	
167	30	88.2	28	4	AAAB91816	Aab91816	Amyloid b	240	30	88.2	36	5	AAU11776	Synthetic	
168	30	88.2	28	4	AAAB91789	Aab91789	Amyloid b	241	30	88.2	36	5	AAU11771	Synthetic	
169	30	88.2	28	4	AAAB91827	Aab91827	Amyloid b	242	30	88.2	36	6	ABR42779	Amyloid b	
170	30	88.2	28	4	AAAB91783	Aab91783	Amyloid b	243	30	88.2	36	6	ABR42774	Amyloid b	

XX Chalfour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 XX
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 XX disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 XX which elicits production of antibodies to prevent fibrillogenesis and
 XX associated cellular toxicity.
 XX
 XX Disclosure; Page 10; 31pp; English.
 XX
 XX The present sequence is that of an all-D peptide suitable for use for
 XX preparing vaccines for preventing or treating Alzheimer's disease and
 XX other amyloid related disorders in humans. It is based on a portion of
 XX amyloid-beta peptide (see AAB82622), and may be modified by removing or
 XX inserting 1 or more amino acid residues, or by substituting 1 or more
 XX amino acid residues with other amino acid residues or non-amino acid
 XX fragments. Vaccines of the invention are produced using 'non-self'
 XX peptides synthesised from the unnatural D-configuration amino acids to
 XX avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 XX aggregated to be operative or immunogenic. They preferably interact with
 XX at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 XX CAG-binding site region, the amyloid-beta peptide, or their immunogenic
 XX fragments, protein conjugates, immunogenic derivative peptides and
 XX immunogenic peptidomimetics. Examples include all-D peptides
 XX corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 XX 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 XX in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 XX preventing fibrillogenesis and associated cellular toxicity. The amyloid
 XX related diseases may be localised amyloidosis, e.g. diabetes type II,
 XX neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 XX Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 XX prion protein related disorders, or systemic amyloidosis associated with
 XX chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 XX rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 XX amyloidosis found in long-term haemodialysis patients
 XX
 XX Sequence 7 AA;
 XX
 XX Query Match 100.0%; Score 34; DB 4; Length 7;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 KKLVPFFA 7
 XX |||||
 XX Db 1 KKLVPFFA 7
 XX
 XX RESULT 3
 XX AAU96812
 XX ID AAU96812 standard; peptide; 7 AA.
 XX
 XX AC AAU96812;
 XX
 XX 30-JUL-2002 (first entry)
 XX
 XX Amyloid targeting peptide #2.
 XX
 XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 XX transmissible cerebral amyloidosis; transmissible virus dementia;
 XX scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 XX bovine spongiform encephalopathy; inflammation associated amyloid;
 XX primary amyloidosis; feline spongiform encephalopathy;
 XX Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 XX dialysis-related amyloidosis; light chain-related amyloidosis;
 XX cerebral amyloid angiopathy.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX
 XX Misc-difference 1..7 /note= "Preferably D-form residue"
 XX FT

XX WO200207781-A2.
 XX 31-JAN-2002.
 XX
 XX 25-JUL-2001; 2001WO-CA001071.
 XX
 XX 25-JUL-2000; 2000US-0220808P.
 XX
 XX 24-JUL-2001; 2001US-00915092.
 XX
 XX (NEUR-) NEUROCHEM INC.
 XX
 XX Gervais F, Kong X, Chalfour R, Migneault D;
 XX WPI; 2002-371447/40.
 XX
 XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 XX plaques and/or for the treatment of amyloidosis disorders.
 XX
 XX Claim 49; Page 21; 57pp; English.
 XX
 XX The invention relates to an amyloid-targeting imaging agent comprising an
 XX amyloid targeting moiety, a linker moiety and a labelling moiety. The
 XX agent is of general formula A_t-(A_l)_n_k-z-A_l_a_b (I) where z = 0 - 1;
 XX A_t = an amyloid targeting moiety; A_l)_n_k = a linker moiety; and A_l_a_b
 XX = a labelling moiety. Also included are imaging amyloid deposition or
 XX diagnosing an amyloid-related condition in a patient involving
 XX administering (I) to the patient, and ultrasound imaging (I) in the
 XX patient to determine the presence of amyloid or amyloid-related condition
 XX ; and a kit for preparing a radiopharmaceutical preparation comprising
 XX (I), a reducing agent, a buffering agent, a transchelating agent, and
 XX instructions for the preparation and use of the radiopharmaceutical in
 XX the imaging of amyloid or an amyloid-related condition. The agents are
 XX used for imaging amyloid deposition and for diagnosing an amyloid related
 XX condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible
 XX cerebral amyloidosis (transmissible virus dementia), familial CJD,
 XX scrapie, transmissible mink encephalopathy, bovine spongiform
 XX encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 XX primary amyloidosis, Alzheimer's disease, prion-mediated diseases,
 XX cerebral amyloidosis, light chain-related amyloidosis, cerebral
 XX dialysis-related amyloidosis, the agents are capable of crossing the blood-brain
 XX amyloid angiopathy. The agents are capable of binding specifically to amyloid plaques. The
 XX barrier and are capable of binding specifically to amyloid plaques. The
 XX present sequence is a peptide forming the amyloid targeting moiety of the
 XX agent of the invention
 XX
 XX Sequence 7 AA;
 XX
 XX Query Match 100.0%; Score 34; DB 5; Length 7;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 KKLVPFFA 7
 XX |||||
 XX Db 1 KKLVPFFA 7
 XX
 XX RESULT 4
 XX AAU11649
 XX ID AAU11649 standard; peptide; 7 AA.
 XX
 XX AC AAU11649;
 XX
 XX 09-APR-2002 (first entry)
 XX
 XX Peptide #2, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
 XX
 XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 XX CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 XX cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
 XX
 XX Synthetic.
 XX
 XX OS

PN WO200185093-A2.
 XX 15-NOV-2001.
 XX 22-DEC-2000; 2000WO-IB002078.
 XX 23-DEC-1999; 99US-0171877P.
 XX (NEUR-) NEUROCHEM INC.
 XX Green AM, Gervais F;
 XX WPI; 2002-075222/10.
 XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.
 XX
 XX Disclosure; Page 10; 68pp; English.
 XX The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 100.0%; Score 34; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVPFA 7
 |||||
 Db 1 KKLVPFA 7
 RESULT 5
 AAE35439
 ID AAE35439 standard; peptide; 7 AA.
 AC AAE35439;
 XX 17-JUN-2003 (first entry)
 DT
 DE Abeta peptide #10.
 XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 1..7
 FT /note= "D-form residues"
 XX WO200296937-A2.
 XX 05-DEC-2002.
 XX 29-MAY-2002; 2002WO-CA000763.
 XX

PR 29-MAY-2001; 2001US-00867847.
 XX (NEUR-) NEUROCHEM INC.
 XX Gervais F, Hebert L, Chalifour RJ, Kong X;
 XX WPI; 2003-201269/19.
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX
 XX Claim 1; Page 59; 44pp; English.
 XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 100.0%; Score 34; DB 6; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVPFA 7
 |||||
 Db 1 KKLVPFA 7
 RESULT 6
 ADQ37314
 ID ADQ37314 standard; peptide; 7 AA.
 XX ADQ37314;
 AC ADQ37314;
 XX 07-OCT-2004 (first entry)
 DT
 DE Antifibrillogenic amyloidosis inhibiting peptide.
 XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antichyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular condition; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX Synthetic.
 XX WO2004058239-A1.
 PN

CC Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.

XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 34; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
 Db 1 KKLVFPA 7

RESULT 8

ADY37922
 ID ADY37922 standard; peptide; 7 AA.

XX
 AC ADY37922;

DT 19-MAY-2005 (first entry)

XX Amyloid-targeting peptide, SEQ ID NO:2, for use in imaging agent.

XX Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;

XX transmissible spongiform encephalopathy; scrapie; BSE;

XX Alzheimer's disease; neurological disease; amyloidosis;

XX non-insulin dependent diabetes; metabolic disorder.

XX Synthetic.

XX US2005048000-A1.

XX 03-MAR-2005.

XX 03-DEC-2003; 2003US-00728028.

XX 25-JUL-2000; 2000US-0220808P.

XX 24-JUL-2001; 2001US-00915092.

XX 29-JAN-2003; 2003US-0443291P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2005-212201/22.

XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-

XX related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform

XX encephalopathy, primary amyloidosis or Alzheimer's disease.

XX Disclosure; SEQ ID NO 2; 3pp; English.

XX The invention relates to an amyloid-targeting imaging agent. The imaging

XX agent comprises an amyloid targeting moiety (such as a peptide) joined to

XX a labeling moiety via a linking moiety, and is preferably able to cross

XX the blood-brain barrier. The invention also relates to a kit for

XX preparing a radiopharmaceutical preparation from the imaging agent of the

XX invention, a method for imaging amyloid deposition in a patient and a

XX method for diagnosing an amyloid-related condition in a patient. The

CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
 CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
 CC transmissible cerebral amyloidoses (also known as transmissible virus
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
 CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
 CC mediated diseases, dialysis-related amyloidosis, light chain-related
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
 CC patient. The agent does not exhibit excessive toxicity or irritation,
 CC does not induce an allergic response, and permits an earlier diagnosis of
 CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.

XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 34; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
 Db 1 KKLVFPA 7

RESULT 9

ABU79063

ID ABU79063 standard; peptide; 9 AA.

XX
 AC ABU79063;

DT 17-JUN-2003 (first entry)

XX Aggregation blocking peptide #15.

XX Amyloid formation; amyloid-like deposit; Alzheimer's disease;

XX pathological beta-sheet-rich conformation; Down's syndrome;

XX amyloidosis disorder; human prion disease; Kuru; CJD;

XX Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; GSS;

XX prion associated human neurodegenerative disease; animal prion disease;

XX scrapie; spongiform encephalopathy; transmissible mink encephalopathy;

XX chronic wasting disease.

XX Unidentified.

XX US6462171-B1.

XX 08-OCT-2002.

XX 12-DEC-1996; 96US-00766596.

XX 07-JUN-1995; 95US-00478326.

XX 10-APR-1996; 96US-00630645.

XX (UNY) UNIV NEW YORK STATE.

XX Soto-Jara C, Baumann MH, Frangione B;

XX WPI; 2003-379012/36.

XX Novel inhibitory peptides which inhibit and structurally block abnormal

XX PT folding of protein into amyloid or amyloid-like deposit and into

XX pathological beta-sheet rich conformation, useful for treating

XX Alzheimer's disease.

XX Disclosure; Col 51-52; 51pp; English.

XX The invention describes an isolated inhibitory peptide (I) which

XX interacts with a hydrophobic beta-sheet forming cluster of amino acid

XX residues on a protein or peptide for amyloid or amyloid-like deposit

XX formation, and inhibits or structurally blocks the abnormal folding of

CC proteins and peptides into amyloid or amyloid-like deposits and into
 CC pathological beta-sheet-rich conformation. (I) is useful for disorders or
 CC diseases associated with abnormal protein folding into amyloid or amyloid
 CC -like deposits or into pathological beta-sheet-rich precursors of such
 CC deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis
 CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease
 CC (CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated
 CC human neurodegenerative diseases as well as animal prion diseases such as
 CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and
 CC chronic wasting disease of mule deer and elk. (I) is also useful for
 CC detecting and diagnosing the presence or absence of amyloid or amyloid-
 CC like deposits in vivo and its precursors. This is the amino acid sequence
 CC of peptide associated with the inhibition of amyloid or amyloid like
 CC deposits
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 34; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7
 |||||
 Db 1 KKLVEFFA 7

RESULT 10
 ABW00197
 ID ABW00197 standard; peptide; 9 AA.
 XX
 AC ABW00197;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Peptide #15 used in the invention.
 XX
 KW Amyloid-like fibril deposit; prion related encephalopathy; gene therapy;
 KW Alzheimer's disease.
 XX
 OS Unidentified.
 XX
 PN US2003087407-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 06-SEP-2002; 2002US-00235483.
 XX
 PR 07-JUN-1995; 95US-00478326.
 PR 10-APR-1996; 96US-00630645.
 PR 12-DEC-1996; 96US-00766596.
 XX
 PA (UUNY) UNIV NEW YORK STATE.
 XX
 PI Soto-Jara C, Baumann MH, Frangione B;
 XX
 DR WPI; 2003-616149/58.
 XX

XX New inhibitory peptide, useful for preparing a composition for
 PT diagnosing, preventing or treating disorders associated with amyloid-like
 PT fibril deposits, e.g. Alzheimer's disease, or prion related
 PT encephalopathies.
 XX
 XX Claim 1; Page 28; 52pp; English.
 XX
 CC The invention relates to inhibitory peptide comprising a portion of at
 CC least three amino acid residues and a sequence predicted not to adopt a
 CC beta-sheet structure that associates with a hydrophobic beta-sheet
 CC cluster on a protein or peptide involved in the abnormal folding into a
 CC beta-sheet structure, to structurally block the abnormal folding of the
 CC protein or peptide. The inhibitory peptide is useful for preparing a
 CC composition for preventing, treating or detecting disorders or diseases
 CC associated with amyloid-like fibril deposits e.g. Alzheimer's disease and
 CC prion related encephalopathies. The invention is also useful in gene

CC therapy. The present sequence is a peptide used in the invention
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 34; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVEFFA 7
 |||||
 Db 1 KKLVEFFA 7

RESULT 11
 ADK82706
 ID ADK82706 standard; protein; 277 AA.
 XX
 AC ADK82706;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Beta-amyloid peptide antibody sequence #2.
 XX
 KW fusion antibody; senile dementia; beta-amyloid peptide; fibre;
 KW immunocell.
 XX
 OS Unidentified.
 XX
 PN CN1396183-A.
 XX
 PD 12-FEB-2003.
 XX
 PF 13-JUL-2001; 2001CN-00120278.
 XX
 PR 13-JUL-2001; 2001CN-00120278.
 XX
 PA (ZHAN/) ZHANG X.
 XX
 PI Zhang X, Zhang J;
 XX
 DR WPI; 2003-442233/42.
 XX

XX Human fusion antibody for reducing cerebral amyloid fibers associated
 PT with senile dementia.
 XX
 PS Disclosure; Page 8; 26pp; Chinese.
 XX
 CC The invention relates to a human fusion antibody for preventing and
 CC treating senile dementia. The antibody recognises and binds the beta-
 CC amyloid peptide and the fibres generated by it. The human antibody Pc
 CC segment recognized by human immunocells are sequentially contained by its
 CC terminals from N to C. The fusion gene coding for the antibody is also
 CC disclosed. This sequence represents the sequence of a anti-beta-amyloid
 CC peptide antibody.
 XX
 SQ Sequence 277 AA;

Query Match 91.2%; Score 31; DB 7; Length 277;
 Best Local Similarity 85.7%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVEFFA 7
 :|||
 Db 32 RKLVEFFA 38

RESULT 12
 AAW02312
 ID AAW02312 standard; peptide; 7 AA.
 XX
 AC AAW02312;
 XX
 DT 02-MAY-1997 (first entry)

KW Beta-amyloid; amyloid modulator; amyloidogenic protein; amyloidosis;
KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
KW isolated cardiac amyloid; systemic senile amyloidosis; scrapie; myeloma;
KW bovine spongiform encephalopathy; BSE; Creutzfeldt-Jakob disease;
KW adult onset diabetes; Gerstmann-Strausler-Scheinker syndrome;
KW insulinoma; atrial amyloidosis; idiopathic amyloidosis; haemodialysis;
KW macroglobulinemia-associated amyloidosis; reactive amyloidosis;
KW primary localized cutaneous nodular amyloidosis; Sjogren's syndrome;
KW hereditary cerebral haemorrhage with amyloidosis; Muckle-Wells syndrome;
KW hereditary non-neuropathic systemic amyloidosis;
KW familial Mediterranean Fever.
XX Homo sapiens.
XX US2002098173-A1.
XX 25-JUL-2002.
XX 04-OCT-2001; 2001US-00972475.
XX 14-MAR-1995; 95US-00404831.
XX 07-JUN-1995; 95US-00475579.
XX 27-OCT-1995; 95US-00548998.
XX 14-MAR-1996; 96US-00617267.
XX (PRAE-) PRAECIS PHARM INC.
XX Findeis MA, Benjamin H, Garnick MB, Geftter ML, Hundal A;
XX Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;
XX WPI; 2002-697709/75.
XX Amyloid modulator useful for treating a disorder associated with
PT amyloidosis, comprises an amyloidogenic protein and/or a peptide fragment
PT coupled to a modifying group.
XX Example 12; Page 35; 41pp; English.
XX The invention describes an amyloid modulator comprising an amyloidogenic
CC protein and/or peptide fragment coupled to a modifying group so that the
CC compound modulates the aggregation of natural amyloid proteins or
CC peptides. The modulator is used for treating a disorder associated with
CC amyloidosis e.g. familial amyloid polyneuropathy (Portuguese, Japanese
CC and Swedish types), familial amyloid cardiomyopathy (Danish type),
CC isolated cardiac amyloid, systemic senile amyloidosis, scrapie, bovine
CC spongiform encephalopathy, Creutzfeldt-Jakob disease, adult onset
CC diabetes, Gerstmann-Strausler-Scheinker syndrome, insulinoma, isolated
CC atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or
CC macroglobulinemia-associated amyloidosis, primary localized cutaneous
CC nodular amyloidosis associated with Sjogren's syndrome, reactive
CC (secondary) amyloidosis, familial Mediterranean Fever and familial
CC amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome),
CC hereditary cerebral haemorrhage with amyloidosis of Icelandic type,
CC amyloidosis associated with long term haemodialysis, hereditary non-
CC neuropathic systemic amyloidosis (familial amyloid polyneuropathy I),
CC familial amyloidosis of Finnish type, amyloidosis associated with
CC medullary carcinoma of the thyroid, fibrinogen-associated hereditary
CC renal amyloidosis and lysozyme-associated hereditary systemic
CC amyloidosis. The compound is capable of altering and inhibiting beta-
CC amyloid protein (beta-AP) aggregation of natural amyloidogenic proteins
CC or peptides when contacted with a molar excess amount of natural beta-APs
CC relative to the modulator. This sequence represents a fragment of the
CC long form of beta-amyloid used in the creation of an amyloid modulator
XX Sequence 7 AA;

RESULT 15
ABB05155
ID ABB05155 standard; peptide; 7 AA.
XX ABB05155;
AC ABB05155;
XX 02-APR-2002 (first entry)
XX Beta amyloid peptide (15-21) SEQ ID NO: 7.
XX Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta;
KW APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease;
KW neurotropic; neuroprotective; immunosuppressive; antimicrobial; auditory;
KW antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic;
KW amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;
KW amyloidogenic disease; beta amyloid deposition; amyloidosis;
KW hereditary cerebral haemorrhage; familial amyloid polyneuropathy.
XX Homo sapiens.
OS Synthetic.
XX US6319498-B1.
XX 20-NOV-2001.
XX 14-MAR-1996; 96US-00617267.
XX 14-MAR-1995; 95US-00404831.
XX 07-JUN-1995; 95US-00475579.
XX 27-OCT-1995; 95US-00548998.
XX (PRAE-) PRAECIS PHARM INC.
XX Findeis MA, Benjamin H, Garnick MB, Geftter ML, Hundal A;
XX Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;
XX WPI; 2002-146668/19.
XX Amyloid modulator compound useful for treatment of an amyloidogenic
PT disease such as Alzheimer's disease comprises an aggregation core domain
PT and a modifying group attached to it.
XX Disclosure; Col 19; 54pp; English.
XX The present invention describes an amyloid modulator compound (I)
CC comprising an aggregation core domain and a modifying group attached to
CC it. (I) has neurotropic, neuroprotective, immunosuppressive, antimicrobial,
CC antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic
CC and auditory activities, and can be used as a natural amyloid aggregation
CC inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide
CC (beta-AP). (I) are used in the manufacture of a medicament for the
CC diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's
CC disease and other clinical occurrences of beta amyloid deposition such as
CC Down's syndrome individuals and in patients with hereditary cerebral
CC haemorrhage with amyloidosis, and for treating a disorder associated with
CC amyloidosis such as familial amyloid polyneuropathy. (I) reduces the
CC toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)
CC not only reduces the formation of neurotoxic aggregates but also have the
CC ability to reduce the neurotoxicity of performed A-beta fibrils. The
CC present sequence represents a beta-AP peptide, which is used in the
CC exemplification of the present invention
XX Sequence 7 AA;

Query Match 88.2%; Score 30; DB 5; Length 7;
Best Local Similarity 85.7%; Pred. No. 2e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match 88.2%; Score 30; DB 5; Length 7;
Best Local Similarity 85.7%; Pred. No. 2e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
DB 1 QKLVPFA 7

QY 1 KKLVPFA 7
:|||||
DB 1 QKLVPFA 7

Best Local Similarity 85.7%; Pred. NO. 2e+06; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 16
ADJ64058
ID ADJ64058 standard; peptide; 7 AA.
XX
XX
AC ADJ64058;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human beta-amyloid long form peptide fragment #4.
DE
XX
XX
XX Amyloidogenic protein; therapy; amyloidosis;
KW familial amyloid polyneuropathy; cardiomyopathy;
KW systemic senile amyloidosis; bovine spongiform encephalopathy;
KW Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome;
KW diabetes; insulinoma; myeloma; Sjogren's syndrome;
KW familial mediterranean fever; urticaria; deafness;
KW hereditary cerebral haemorrhage; haemodialysis; thyroid;
KW renal amyloidosis; lysosome-associated hereditary systemic amyloidosis;
KW beta-amyloid peptide; human.
XX
XX Homo sapiens.
OS
XX US2004005307-A1.
PN
XX
XX 08-JAN-2004.
XX
XX 17-JUN-2003; 2003US-00463729.
PF
XX
XX 14-MAR-1995; 95US-00404831.
PR
XX 07-JUN-1995; 95US-00475579.
PR
XX 27-OCT-1995; 95US-00548998.
PR
XX 14-MAR-1996; 96US-00617267.
PR
XX 04-OCT-2001; 2001US-00972475.
PR
XX (PRAE-) PRACIS PHARM INC.
XX
XX Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A;
PI Kaaman L, Musso G, Signer ER, Wakefield J, Reed MJ;
PI
XX WPI; 2004-131767/13.
DR
XX
XX New amyloidogenic protein aggregation modulators useful for treating
PT disorder associated with amyloidosis e.g. familial amyloid
PT polyneuropathy, Creutzfeldt-Jakob disease and adult onset diabetes.
PT
XX
XX Example 12; SEQ ID NO 7; 52pp; English.
PS
XX
XX The invention relates to amyloidogenic proteins or peptide fragments
CC aggregation modulators. The invention is used for treating disorder
CC associated with amyloidosis, particularly familial amyloid polyneuropathy
CC (Portuguese, Japanese and Swedish types), familial amyloid cardiomyopathy
CC (Danish type), isolated cardiac amyloid, systemic senile amyloidosis,
CC scrapie, bovine spongiform encephalopathy, Creutzfeldt-Jakob disease,
CC Gerstmann-Strausler-Scheinker syndrome, adult onset diabetes,
CC insulinoma, isolated atrial amyloidosis, idiopathic (primary)
CC amyloidosis, myeloma or macroglobulinemia-associated amyloidosis, primary
CC localized cutaneous nodular amyloidosis associated with Sjogren's
CC syndrome, reactive (secondary) amyloidosis, familial Mediterranean Fever
CC and familial amyloid nephropathy with urticaria and deafness (Muckle-
CC Wells syndrome), hereditary cerebral haemorrhage with amyloidosis of
CC Icelandic type, amyloidosis associated with long term haemodialysis,
CC hereditary non-neuropathic systemic amyloidosis (familial amyloid
CC polyneuropathy III), familial amyloidosis of Finnish type, amyloidosis
CC associated with medullary carcinoma of the thyroid, fibrinogen associated
CC hereditary renal amyloidosis and lysosome-associated hereditary systemic
CC amyloidosis. The present sequence is beta-amyloid peptide fragment used
CC in the exemplification of the invention.
XX
XX Sequence 7 AA;
SQ

Best Local Similarity 85.7%; Pred. NO. 2e+06; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7
:|||||
Db 1 QKLVEFFA 7

RESULT 17
ADQ37351
ID ADQ37351 standard; peptide; 7 AA.
XX
XX AC ADQ37351;
XX
XX 07-OCT-2004 (first entry)
XX
XX Beta-amyloid modulator peptide.
XX
XX amyloid-beta; amyloid-beta related disease;
KW amyloid-beta fibril formation; immune response; nootropic;
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
KW cardiant; antidepressant; endocrine; hypnotic;
KW amyloid-beta fibril formation modulator; immune system modulator;
KW Alzheimer's disease; mild cognitive impairment;
KW mild-to-moderate cognitive impairment; vascular dementia;
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
KW senile dementia; Down's syndrome; inclusion body myositis;
KW age-related macular degeneration; hypothyroidism;
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
KW behavioural dysfunction; neurological condition; psychological condition;
KW vaccine antigen.
XX
XX Synthetic.
XX
XX WO2004058239-A1.
XX
XX 15-JUL-2004.
XX
XX 24-DEC-2003; 2003WO-CA002021.
XX
XX 24-DEC-2002; 2002US-0436379P.
PR
XX 23-JUN-2003; 2003US-0482214P.
XX
XX (NEUR-) NEUROCHEM INT LTD.
XX
XX Gervais F, Bellini F;
PI
XX WPI; 2004-543342/52.
DR
XX
XX Composition for treating e.g. Alzheimer's disease comprises first agent
PT that prevents or treats amyloid-beta related disease and second agent
PT that is either a peptide or peptidomimetic or an immune system modulator.
XX
XX Disclosure; Page 87; 143pp; English.
PS
XX
XX The present invention describes compositions (C) comprising: (a) a first
CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
CC modulates amyloid-beta fibril formation or induces a prophylactic or
CC therapeutic immune response against amyloid-beta fibril formation; or
CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
CC fibril formation. Also described is a kit comprising (C). (C) have
CC nootropic, neuroprotective, cerebroprotective, haemostatic,
CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
CC and can be used as amyloid-beta fibril formation modulators, and as
CC immune system modulators. (C) can be used for preventing or treating an
CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
CC mild-to-moderate cognitive impairment, vascular dementia, cerebral

CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a beta-
 CC amyloid modulator peptide which is used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 7 AA;

Query Match 88.2%; Score 30; DB 8; Length 7;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 :|||||
 Db 1 QKLVPFA 7

RESULT 18

ADZ08903
 ID ADZ08903 standard; peptide; 7 AA.

AC ADZ08903;

XX 16-JUN-2005 (first entry)

DE Human beta-amyloid peptide (SEQ ID No:128) probed with anti-amyloid IgG.

XX amyloid; antibody engineering; antibody production;
 KW amyloid-associated disorder; Alzheimers disease; cancer; allergy;
 KW autoimmune disease; Parkinsons disease;
 KW acquired immune deficiency syndrome; multiple sclerosis; migraine;
 KW dementia; infection; nootropic; neuroprotective; cytostatic;
 KW antiallergic; immunosuppressive; antiparkinsonian; antimigraine;
 KW antimicrobial; anti-HIV; beta-amyloid.

XX Homo sapiens.

XX WO2005028511-A2.

XX 31-MAR-2005.

XX 26-MAR-2004; 2004WO-US009522.

XX 28-MAR-2003; 2003US-0458469P.

PR 28-MAR-2003; 2003US-0458474P.

PR 28-MAR-2003; 2003US-0458509P.

PR 28-MAR-2003; 2003US-0458510P.

XX (CENZ) CENTOCOR INC.

PA (MERC/) MERCKEN M.

PA (BENS/) BENSON J M.

XX Mercken M, Benson JM;

XX WPI; 2005-242565/25.

PT New isolated mammalian anti-amyloid antibodies useful for treating
 PT amyloid-associated disorders, such as Alzheimer's disease, cancer,
 PT allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,
 PT migraine and dementia.

XX Example 4; SEQ ID NO 128; 306pp; English.

XX The invention relates to at least one isolated mammalian amyloid antibody
 CC comprising at least one variable region comprising at least one heavy
 CC chain and at least one light chain, of a fully defined sequence of SEQ ID
 CC NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are:
 CC (i) at least one isolated mammalian amyloid antibody that binds to the
 CC same region of an amyloid polypeptide as an antibody comprising at least
 CC one heavy chain or light chain complementarity determining region (CDR)
 CC having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii)
 CC at least one isolated mammalian amyloid antibody, comprising at least one
 CC human CDR, where the antibody specifically binds at least one epitope
 CC selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined
 CC sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic
 CC acid encoding at least one of any of the isolated mammalian amyloid
 CC antibodies mentioned and having at least one human CDR of a fully defined
 CC sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an
 CC isolated nucleic acid vector comprising an isolated nucleic acid encoding
 CC an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising
 CC an isolated nucleic acid encoding an amyloid antibody, (vi) a method of
 CC producing at least one amyloid antibody, (vii) a composition comprising
 CC at least one of any of the isolated mammalian amyloid antibodies
 CC mentioned, and at least one pharmaceutical carrier or diluent, (viii) an
 CC anti-idiotypic antibody or fragment that specifically binds at least one
 CC of the amyloid antibodies mentioned, (ix) a method of diagnosing or
 CC treating an amyloid related condition in a cell, tissue, organ or animal,
 CC comprising contacting or administering a composition comprising at least
 CC one of the antibodies mentioned, with, or to, the cell, tissue, organ or
 CC animal, (x) a medical device comprising at least one amyloid antibody
 CC mentioned, where the device is suitable for contacting or administering
 CC at least one amyloid antibody, (xi) an article of manufacture for human
 CC pharmaceutical or diagnostic use, comprising packaging material and a
 CC container comprising a solution or a lyophilized form of at least one of
 CC the amyloid antibodies mentioned, and (xii) a method of producing at
 CC least one of the isolated mammalian amyloid antibodies, comprising
 CC providing a host cell or transgenic animal or transgenic plant or plant
 CC cell capable of expressing the antibody in recoverable amounts. The
 CC methods and compositions of the present invention are useful for
 CC producing therapeutic compositions and devices for treating amyloid-
 CC associated disorders, such as Alzheimer's disease, cancer, allergies,
 CC autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis,
 CC migraine, dementia and infections. This sequence represents a peptide
 CC from human beta-amyloid probed with anti-beta-amyloid IgG antibodies.

XX Sequence 7 AA;

Query Match 88.2%; Score 30; DB 9; Length 7;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 :|||||
 Db 1 QKLVPFA 7

RESULT 19

AAW02310

ID AAW02310 standard; peptide; 8 AA.

XX AAW02310;

XX 02-MAY-1997 (first entry)

XX Beta-amyloid modulator peptide #1.

XX Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
 KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
 KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;

KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
 KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
 KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
 KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
 XX Synthetic.
 OS
 PN W09628471-A1.
 XX
 PD 19-SEP-1996.
 XX
 PP 14-MAR-1996; 96WO-US003492.
 XX
 PR 14-MAR-1995; 95US-00404831.
 PR 07-JUN-1995; 95US-00475579.
 PR 27-OCT-1995; 95US-00548998.
 XX
 PA (PHAR-) PHARM PEPTIDES INC.
 XX
 PI Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A;
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ, Molineaux S;
 PI Kubasek W, Chin J, Lee J, Kelley M;
 XX WPI; 1996-433762/43.
 DR
 XX Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
 PT protein coupled (in)directly to at least 1 modifying gp., useful in
 PT treatment of Alzheimer's disease.
 XX
 PS Claim 16; Page 90; 106pp; English.
 XX
 CC AAW02310-W02332 represent the peptide portions of the beta-amyloid
 CC modulator compounds of the invention. Beta-amyloid peptide is a 4
 CC kilodalton peptide that is the major protein component of amyloid
 CC plaques. Amyloid plaques are present both in the brain lesions, and in
 CC the walls of cerebral blood vessels in Alzheimer's disease patients. The
 CC amyloid modulators of the invention comprise an amyloidogenic protein or
 CC peptide (such as this sequence) coupled directly or indirectly to at
 CC least one modifying group. The modifying group is preferably a cyclic,
 CC heterocyclic, or polycyclic group, such as decalin, a cholanyl group, a
 CC biotin containing group, or a fluorescein containing group. These
 CC compounds then modulate the aggregation of these sequences to natural
 CC amyloid proteins or peptides when contacted with the natural
 CC amyloidogenic proteins or peptides. The modulator compounds can be used
 CC in the treatment of disorders associated with amyloidosis, such as
 CC familial amyloid polyneuropathy, familial amyloid cardiomyopathy,
 CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
 CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
 CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
 CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
 CC and other types of amyloidosis. The modulators are also useful for the
 CC treatment of disorders associated with beta-amyloidosis, especially
 CC Alzheimer's disease
 CC
 SQ Sequence 8 AA;

Query Match 88.2%; Score 30; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
 :|||||
 Db 2 QKLVPFA 8

RESULT 20
 AAW89374
 ID AAW89374 standard; peptide; 8 AA.

XX
 AC AAW89374;

XX
 DT 02-MAR-1999 (first entry)

XX

DE Beta-amyloid peptide derivative A-beta-14-21.
 XX
 KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
 KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
 KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;
 KW Creutzfeldt-Jakob disease; BAP.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN US5854204-A.
 XX
 PD 29-DEC-1998.
 XX
 PP 14-MAR-1996; 96US-00612785.
 XX
 PR 14-MAR-1995; 95US-00404831.
 PR 07-JUN-1995; 95US-00475579.
 PR 27-OCT-1995; 95US-00548998.
 XX
 PA (PHAR-) PHARM INC.
 XX
 PI Hundal A, Gefter ML, Kasman L, Musso G, Molineaux S, Benjamin H;
 PI Findeis MA, Chin J, Lee J, Kelley M, Reed M, Wakefield J;
 PI Garnick MB, Kubasek W, Signer ER;
 XX WPI; 1999-094964/08.
 DR
 XX New peptide(s) derived from beta-amyloid peptide that inhibit amyloid
 PT aggregation - and neurotoxicity, specifically for treatment and
 PT prevention of Alzheimer's disease.
 XX
 PS Example 12; Col 64; 52pp; English.
 XX
 CC The present invention describes beta-amyloid peptide (BAP) derivatives.
 CC The BAP derivatives inhibit aggregation of amyloidogenic proteins and
 CC peptides, specifically BAP, and their neurotoxicity, so are useful for
 CC treating and preventing any disease involving amyloidosis, specifically
 CC Alzheimer's disease but also Down's syndrome, familial amyloid
 CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and
 CC Creutzfeldt-Jakob disease. The BAP derivatives are also used to diagnose
 CC these diseases, in vitro or in vivo, by detecting binding of BAP to
 CC labelled BAP derivatives. Some BAP derivatives inhibit BAP aggregation
 CC even when BAP is present in molar excess. The present sequence represents
 CC a BAP derivative
 XX
 SQ Sequence 8 AA;

Query Match 88.2%; Score 30; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
 :|||||
 Db 2 QKLVPFA 8

RESULT 21
 ABG71005
 ID ABG71005 standard; peptide; 8 AA.

XX
 AC ABG71005;

XX
 DT 05-DEC-2002 (first entry)

XX
 DE Long form beta-amyloid protein fragment #2.

XX Beta-amyloid; amyloid modulator; amyloidogenic protein; amyloidosis;
 KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
 KW isolated cardiac amyloid; systemic senile amyloidosis; scrapie; myeloma;
 KW bovine spongiform encephalopathy; BSE; Creutzfeldt-Jakob disease;
 KW adult onset diabetes; Gerstmann-Strausler-Scheinker syndrome;
 KW insulinoma; atrial amyloidosis; idiopathic amyloidosis; haemodialysis;

KW macroglobulinaemia-associated amyloidosis; reactive amyloidosis;
 KW primary localised cutaneous nodular amyloidosis; Sjogren's syndrome;
 KW hereditary cerebral haemorrhage with amyloidosis; Muckle-Wells syndrome;
 KW hereditary non-neuropathic systemic amyloidosis;
 KW familial Mediterranean Fever.
 XX
 OS Homo sapiens.
 XX
 XX US2002098173-A1.
 XX
 XX 25-JUL-2002.
 XX
 XX 04-OCT-2001; 2001US-00972475.
 XX
 XX 14-MAR-1995; 95US-00404831.
 PR 07-JUN-1995; 95US-00475579.
 PR 27-OCT-1995; 95US-00548998.
 PR 14-MAR-1996; 96US-00617267.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX
 XX Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;
 XX
 XX WPI; 2002-697709/75.
 XX
 PT Amyloid modulator useful for treating a disorder associated with
 PT amyloidosis, comprises an amyloidogenic protein and/or a peptide fragment
 PT coupled to a modifying group.
 PT
 PS Example 12; Page 35; 41pp; English.
 XX
 CC The invention describes an amyloid modulator comprising an amyloidogenic
 CC protein and/or peptide fragment coupled to a modifying group so that the
 CC compound modulates the aggregation of natural amyloid proteins or
 CC peptides. The modulator is used for treating a disorder associated with
 CC amyloidosis e.g. familial amyloid polyneuropathy (Portuguese, Japanese
 CC and Swedish types), familial amyloid cardiomyopathy (Danish type),
 CC isolated cardiac amyloid, systemic senile amyloidosis, scrapie, bovine
 CC spongiform encephalopathy, Creutzfeldt-Jakob disease, adult onset
 CC diabetes, Gerstmann-Strausler-Scheinker syndrome, insulinoma, isolated
 CC atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or
 CC macroglobulinaemia-associated amyloidosis, primary localised cutaneous
 CC nodular amyloidosis associated with Sjogren's syndrome, reactive
 CC (secondary) amyloidosis, familial Mediterranean Fever and familial
 CC amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome),
 CC hereditary cerebral haemorrhage with amyloidosis of Icelandic type,
 CC amyloidosis associated with long term haemodialysis, hereditary non-
 CC neuropathic systemic amyloidosis (familial amyloid polyneuropathy III),
 CC familial amyloidosis of Finnish type, amyloidosis associated with
 CC medullary carcinoma of the thyroid, fibrinogen-associated hereditary
 CC renal amyloidosis and lysozyme-associated hereditary systemic
 CC amyloidosis. The compound is capable of altering and inhibiting beta-
 CC amyloid protein (beta-AP) aggregation of natural amyloidogenic proteins
 CC or peptides when contacted with a molar excess amount of natural beta-APs
 CC relative to the modulator. This sequence represents a fragment of the
 CC long form of beta-amyloid used in the creation of an amyloid modulator
 XX
 SQ Sequence 8 AA;

Query Match 88.2%; Score 30; DB 5; Length 8;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFFA 7
 :|||||
 Db 2 QKLVPFFA 8

RESULT 22
 ABB05153
 ID ABB05153 standard; peptide; 8 AA.
 XX

AC ABB05153;
 XX
 DT 02-APR-2002 (first entry)
 XX
 XX Beta amyloid peptide (14-21) SEQ ID NO:5.
 XX
 KW Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta;
 KW APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease;
 KW neurotropic; neuroprotective; immunosuppressive; antimicrobial; auditory;
 KW antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic;
 KW amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;
 KW amyloidogenic disease; beta amyloid deposition; amyloidosis;
 KW hereditary cerebral haemorrhage; familial amyloid polyneuropathy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX US6319498-B1.
 XX
 XX 20-NOV-2001.
 XX
 XX 14-MAR-1996; 96US-00617267.
 XX
 XX 14-MAR-1995; 95US-00404831.
 PR 07-JUN-1995; 95US-00475579.
 PR 27-OCT-1995; 95US-00548998.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX
 XX Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;
 XX
 XX WPI; 2002-146668/19.
 XX
 PT Amyloid modulator compound useful for treatment of an amyloidogenic
 PT disease such as Alzheimer's disease comprises an aggregation core domain
 PT and a modifying group attached to it.
 XX
 PS Disclosure; Col 18; 54pp; English.
 XX
 CC The present invention describes an amyloid modulator compound (I)
 CC comprising an aggregation core domain and a modifying group attached to
 CC it. (I) has neurotropic, neuroprotective, immunosuppressive, antimicrobial,
 CC antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic
 CC and auditory activities, and can be used as a natural amyloid aggregation
 CC inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide
 CC (beta-AP). (I) are used in the manufacture of a medicament for the
 CC diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's
 CC disease and other clinical occurrences of beta amyloid deposition such as
 CC Down's syndrome individuals and in patients with hereditary cerebral
 CC haemorrhage with amyloidosis, and for treating a disorder associated with
 CC amyloidosis such as familial amyloid polyneuropathy. (I) reduces the
 CC toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)
 CC not only reduces the formation of neurotoxic aggregates but also have the
 CC ability to reduce the neurotoxicity of performed A-beta fibrils. The
 CC present sequence represents a beta-AP peptide, which is used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 8 AA;

Query Match 88.2%; Score 30; DB 5; Length 8;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFFA 7
 :|||||
 Db 2 QKLVPFFA 8

RESULT 23
 ADJ64056
 ID ADJ64056 standard; peptide; 8 AA.
 XX

AC ADJ64056;
 XX 06-MAY-2004 (first entry)
 XX Human beta-amyloid long form peptide fragment #2.
 DE
 XX
 KW Amyloidogenic protein; therapy; amyloidosis;
 KW familial amyloid polyneuropathy; cardiomyopathy;
 KW systemic senile amyloidosis; bovine spongiform encephalopathy;
 KW Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome;
 KW diabetes; insulinoma; myeloma; Sjogren's syndrome;
 KW familial mediterranean fever; urticaria; deafness;
 KW hereditary cerebral haemorrhage; haemodialysis; thyroid;
 KW renal amyloidosis; lysosome-associated hereditary systemic amyloidosis;
 KW beta-amyloid peptide; human.
 XX
 OS Homo sapiens.
 XX
 XX US2004005307-A1.
 PN
 XX 08-JAN-2004.
 PD
 XX 17-JUN-2003; 2003US-00463729.
 XX
 XX 14-MAR-1995; 95US-00404831.
 PR 07-JUN-1995; 95US-00475579.
 PR 27-OCT-1995; 95US-00548998.
 PR 14-MAR-1996; 96US-00617267.
 PR 04-OCT-2001; 2001US-00972475.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA
 XX Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A;
 PI Kaaman L, Musso G, Signer ER, Wakefield J, Reed MJ;
 XX WPI; 2004-131767/13.
 DR
 XX New amyloidogenic protein aggregation modulators useful for treating
 PT disorder associated with amyloidosis e.g. familial amyloid
 PT polyneuropathy, Creutzfeldt-Jakob disease and adult onset diabetes.
 XX
 XX Example 12; SEQ ID NO 5; 52pp; English.
 PS
 XX The invention relates to amyloidogenic proteins or peptide fragments
 CC aggregation modulators. The invention is used for treating disorders
 CC associated with amyloidosis, particularly familial amyloid polyneuropathy
 CC (Portuguese, Japanese and Swedish types), familial amyloid cardiomyopathy
 CC (Danish type), isolated cardiac amyloid, systemic senile amyloidosis,
 CC scrapie, bovine spongiform encephalopathy, Creutzfeldt-Jakob disease,
 CC Gerstmann-Strausler-Scheinker syndrome, adult onset diabetes,
 CC insulinoma, isolated atrial amyloidosis, idiopathic (primary)
 CC amyloidosis, myeloma or macroglobulinemia-associated amyloidosis, primary
 CC localized cutaneous nodular amyloidosis associated with Sjogren's
 CC syndrome, reactive (secondary) amyloidosis, familial Mediterranean Fever
 CC and familial amyloid nephropathy with urticaria and deafness (Muckle-
 CC Wells syndrome), hereditary cerebral haemorrhage with amyloidosis of
 CC Icelandic type, amyloidosis associated with long term haemodialysis, of
 CC hereditary non-neuropathic systemic amyloidosis (familial amyloid
 CC polyneuropathy III), familial amyloidosis of Finnish type, amyloidosis
 CC associated with medullary carcinoma of the thyroid, fibrinogen associated
 CC hereditary renal amyloidosis and lysosome-associated hereditary systemic
 CC amyloidosis. The present sequence is beta-amyloid peptide fragment used
 CC in the exemplification of the invention.
 XX
 SQ Sequence 8 AA;
 Query Match 88.2%; Score 30; DB 8; Length 8;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGLVFFA 7
 :|||||
 Db 2 QKLVFFA 8

RESULT 24
 ADQ37349
 ID ADQ37349 standard; peptide; 8 AA.
 XX
 AC ADQ37349;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Beta-amyloid modulator peptide.
 XX
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; nootropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; utropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment; vascular dementia;
 KW mild-to-moderate cognitive impairment; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 XX WO2004058239-A1.
 PN
 XX 15-JUL-2004.
 PD
 XX 24-DEC-2003; 2003WO-CA002021.
 PF
 XX 24-DEC-2002; 2002US-0436379P.
 PR 23-JUN-2003; 2003US-0482214P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 PA
 XX Gervais F, Bellini P;
 PI WPI; 2004-543342/52.
 DR
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 CC that prevents or treats amyloid-beta related disease and second agent
 CC that is either a peptide or peptidomimetic or an immune system modulator.
 PT
 XX Disclosure; Page 87; 143pp; English.
 PS
 XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC utropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, and as
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's

CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a beta-
 CC amyloid modulator peptide which is used in the exemplification of the
 CC present invention.

XX Sequence 8 AA;

Query Match 88.2%; Score 30; DB 8; Length 8;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 :|||||
 Db 2 QKLVPFA 8

RESULT 25

AA45239
 ID AAR45239 standard; peptide; 9 AA.

AC AAR45239;

XX 20-JUN-1994 (first entry)

DE Mutant amyloid precursor protein fragment.

XX Amyloid precursor protein; APP; beta amyloid protein; BAP; detection;
 KW Alzheimer's disease; Down's syndrome.

XX Homo sapiens.

PN AU9338358-A.

XX 04-NOV-1993.

XX 03-MAY-1993; 93AU-00038358.

XX 01-MAY-1992; 92US-00877675.

XX (AMCV) AMERICAN CYANAMID CO.

XX Vitek MP, Jacobson JS;

XX WPI; 1993-406194/51.

DR N-PSDB; AAQ54267.

PT New mutant forms of amyloid precursor protein - for detecting cpds. that
 PT modify activity of enzymes involved in precursor cleavage, also new
 PT nucleic acid encoding them.

XX Disclosure; Page 35; 66pp; English.

XX Recombinant polypeptides produced using the coding sequences of mutant
 CC forms of amyloid precursor proteins comprising from the 5' to the 3' end
 CC a sequence encoding a marker and either (1) a sequence encoding the N-
 CC terminus of an amyloid precursor protein (APP) up to, but not including,
 CC the nucleotides encoding the beta amyloid protein (BAP) domain or (2) the
 CC BAP domain; or the two ligated together, can be used to detect drugs or
 CC compounds that inhibit/augment the activity of proteolytic enzymes which
 CC cleave APP to generate BAP fragments (deposition of which occurs in
 CC patients with Alzheimers disease and Down's syndrome). This is a fragment

CC of amyloid precursor protein containing a mutation which is associated
 CC with diseases involving BAP deposition

XX Sequence 9 AA;

Query Match 88.2%; Score 30; DB 2; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 :|||||
 Db 1 QKLVPFA 7

RESULT 26

AA48493
 ID AAB48493 standard; peptide; 9 AA.

AC AAB48493;

XX 02-MAR-2001 (first entry)

XX Antifibrillogenic peptide #20.

XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 9 /note= "C-terminal amide"

XX WO200068263-A2.

XX 16-NOV-2000.

XX 04-MAY-2000; 2000WO-CA000515.

XX 05-MAY-1999; 99US-0132592P.

XX (NEUR-) NEUROCHEM INC.

XX Chalifour R, Gervais F, Gupta A;

XX WPI; 2001-031852/04.

XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.

XX Claim 7; Page 25; 46pp; English.

XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein

XX Sequence 9 AA;

Query Match 88.2%; Score 30; DB 4; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 :|||||
 Db 3 QKLVPFA 9

RESULT 27
 AAU11667
 ID AAU11667 standard; peptide; 9 AA.
 XX
 AC AAU11667;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Peptide #20, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
 XX
 KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 9 /note= "C-terminal amide"
 FT
 XX WO200185093-A2.
 XX
 XX 15-NOV-2001.
 XX
 XX 22-DEC-2000; 2000WO-IB002078.
 XX
 XX 23-DEC-1999; 99US-0171877P.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 XX Green AM, Gervais F;
 PI
 XX WPI; 2002-075222/10.
 DR
 XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 FT inhibitor.
 PT
 PS Disclosure; Page 10; 68pp; English.
 XX
 CC The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 XX
 SQ Sequence 9 AA;
 Query Match 88.2%; Score 30; DB 5; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KKLVPFA 7
 Db :|||||
 3 QKLVPFA 9
 RESULT 28
 ABP57517
 ID ABP57517 standard; peptide; 9 AA.
 XX
 AC ABP57517;
 XX
 DT 28-APR-2003 (first entry)
 XX
 XX Differentially isotopically labelled (DiMas) peptide #10.
 DE
 XX

KW Mass spectrometry; polymer; analysis; cleavage; substrate specificity;
 KW isotope; protease.
 XX
 OS Synthetic.
 XX
 PN WO2003001206-A1.
 XX
 XX 03-JAN-2003.
 PD
 XX 25-JUN-2002; 2002WO-GB002921.
 XX
 XX 26-JUN-2001; 2001GB-00015581.
 PR
 XX (GLAX) GLAXO GROUP LTD.
 PA
 XX Mckewn SC;
 PI
 XX WPI; 2003-184066/18.
 DR
 XX Analyzing cleavage of polymer, by providing polymer sample, incubating
 PT the sample with labeled isotope for cleavage at potential cleavage site,
 FT and analyzing the masses of any uncleaved fragments by mass spectrometry.
 PT
 XX
 PS Example 3; Page 26; 73pp; English.
 XX
 CC The present invention describes a method (M1) for analysing cleavage of a
 CC polymer. M1 comprises: (a) providing a sample of the polymer, a portion
 CC of the polymer molecules having been labeled at a position on one side of
 CC the potential cleavage site with a first isotopic label and a portion of
 CC the polymer molecules having been labeled at a position on the opposite
 CC side of the potential cleavage site with a second isotopic label; (b)
 CC incubating the sample under conditions suitable for cleavage at the
 CC potential cleavage site; and (c) analysing the mass(es) of any cleaved
 CC fragments by mass spectrometry and thereby determining whether and/or
 CC where cleavage has taken place. M1 is useful for analysing cleavage of a
 CC polymer, where the polymer is a linear polymer, and comprises a peptide
 CC or protein. Methods from the present invention can be used in discovering
 CC new or improved synthetic substrates for both known and unknown enzymes,
 CC e.g. enzymes identified from the human genome. The methods are also
 CC useful to identify the sequence origin, and in screening methods to
 CC identify new substrates for enzymes, in positional peptide scanning
 CC libraries, in *in vivo/ex vivo* in vitro peptide, and in assaying methods
 CC for oligonucleotide or peptide sequencing and in measuring differential
 CC protein expression. The methods are useful for monitoring the cleavage of
 CC polypeptides or polynucleotides, and for determining optimal polymer
 CC substrates. ABP57505 to ABP57605 represent peptides used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 9 AA;
 Query Match 88.2%; Score 30; DB 6; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KKLVPFA 7
 Db :|||||
 3 QKLVPFA 9
 RESULT 29
 ABU79053
 ID ABU79053 standard; peptide; 9 AA.
 XX
 AC ABU79053;
 XX
 DT 17-JUN-2003 (first entry)
 XX
 DE Aggregation blocking peptide #5.
 XX
 KW Amyloid formation; amyloid-like deposit; Alzheimer's disease;
 KW pathological beta-sheet-rich conformation; Down's syndrome;
 KW amyloidosis disorder; human prion disease; kuru; CJD;
 KW Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; GSS;

KW prion associated human neurodegenerative disease; animal prion disease;
 KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;
 KW chronic wasting disease.
 XX Unidentified.
 OS US6462171-B1.
 PN 08-OCT-2002.
 PD 12-DEC-1996; 96US-00766596.
 PF 07-JUN-1995; 95US-00478326.
 PR 10-APR-1996; 96US-00630645.
 XX (UUNY) UNIV NEW YORK STATE.
 PA Soto-Jara C, Baumann MH, Frangione B;
 PI WPI; 2003-379012/36.
 DR Novel inhibitory peptides which inhibit and structurally block abnormal
 PT folding of protein into amyloid or amyloid-like deposit and into
 PT pathological beta-sheet rich conformation, useful for treating
 PT Alzheimer's disease.
 XX Disclosure; Col 47-48; 51pp; English.
 PS The invention describes an isolated inhibitory peptide (I) which
 CC interacts with a hydrophobic beta-sheet forming cluster of amino acid
 CC residues on a protein or peptide for amyloid or amyloid-like deposit
 CC formation, and inhibits or structurally blocks the abnormal folding of
 CC proteins and peptides into amyloid or amyloid-like deposits and into
 CC pathological beta-sheet rich conformation. (I) is useful for disorders or
 CC diseases associated with abnormal protein folding into amyloid or amyloid
 CC -like deposits or into pathological beta-sheet-rich precursors of such
 CC deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis
 CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease
 CC (CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated
 CC human neurodegenerative diseases as well as animal prion diseases such as
 CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and
 CC chronic wasting disease of mule deer and elk. (I) is also useful for
 CC detecting and diagnosing the presence or absence of amyloid or amyloid-
 CC like deposits in vivo and its precursors. This is the amino acid sequence
 CC of peptide associated with the inhibition of amyloid or amyloid like
 CC deposits
 XX
 SQ Sequence 9 AA;
 Query Match 88.2%; Score 30; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVEFF 6
 DB 1 KKLVEFF 6
 RESULT 30
 NAE35436
 ID AAE35436 standard; peptide; 9 AA.
 XX AAE35436;
 AC AAE35436;
 DT 17-JUN-2003 (first entry)
 XX Abeta peptide #7.
 DE All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;

KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX Unidentified.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..9
 FT /note= "D-form residues"
 XX WO200296937-A2.
 XX 05-DEC-2002.
 XX 29-MAY-2002; 2002WO-CA000763.
 XX 29-MAY-2001; 2001US-00867847.
 XX (NEUR-) NEUROCHEM INC.
 PA Gervais F, Hebert L, Chalifour RJ, Kong X;
 PI WPI; 2003-201269/19.
 DR Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX Claim 1; Page 58; 44pp; English.
 PS The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX
 SQ Sequence 9 AA;
 Query Match 88.2%; Score 30; DB 6; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVEFF 7
 DB 3 QKLVEFF 9
 RESULT 31
 ABW00187
 ID ABW00187 standard; peptide; 9 AA.
 XX ABW00187;
 AC ABW00187;
 DT 15-JAN-2004 (first entry)
 XX Peptide #5 used in the invention.
 DE Amyloid-like fibril deposit; prion related encephalopathy; gene therapy;
 KW Alzheimer's disease.
 XX Unidentified.

XX PN US2003087407-A1.
 XX PD 08-MAY-2003.
 XX PF 06-SEP-2002; 2002US-00235483.
 XX PR 07-JUN-1995; 95US-00478326.
 XX PR 10-APR-1996; 96US-00630645.
 XX PR 12-DEC-1996; 96US-00766596.
 XX PA (UJNY) UNIV NEW YORK STATE.
 XX PI Soto-Jara C, Baumann MH, Frangione B;
 XX DR WPI; 2003-616149/58.
 XX PT New inhibitory peptide, useful for preparing a composition for
 PT diagnosing, preventing or treating disorders associated with amyloid-like
 PT fibril deposits, e.g. Alzheimer's disease, or prion related
 PT encephalopathies.
 XX PS Claim 1; Page 25; 52pp; English.
 XX CC The invention relates to inhibitory peptide comprising a portion of at
 CC least three amino acid residues and a sequence predicted not to adopt a
 CC beta-sheet structure that associates with a hydrophobic beta-sheet
 CC cluster on a protein or peptide involved in the abnormal folding into a
 CC beta-sheet structure, to structurally block the abnormal folding of the
 CC protein or peptide. The inhibitory peptide is useful for preparing a
 CC composition for preventing, treating or detecting disorders or diseases
 CC associated with amyloid-like fibril deposits e.g. Alzheimer's disease and
 CC prion related encephalopathies. The invention is also useful in gene
 CC therapy. The present sequence is a peptide used in the invention
 XX SQ Sequence 9 AA;
 Query Match 88.2%; Score 30; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVPF 6
 Db 1 KKLVPF 6
 RESULT 32
 ADI35874
 ID ADI35874 standard; peptide; 9 AA.
 AC ADI35874;
 XX DT 22-APR-2004 (first entry)
 XX DE Amyloid beta peptide SEQ ID NO:28.
 XX KW amyloid beta peptide; vaccine; immunisation; neuroprotective;
 KW Alzheimer's disease.
 XX OS Synthetic.
 XX PN WO2004006861-A2.
 XX PD 22-JAN-2004.
 XX PF 16-JUL-2003; 2003WO-US022280.
 XX PR 17-JUL-2002; 2002US-0396245P.
 XX PA (MIND-) MINDSET BIOPHARMACEUTICALS INC.
 XX PI Chain DG, Fitzer-Attas C;
 XX

DR WPI; 2004-122759/12.
 XX New amyloid beta peptide, useful for preparing a composition for
 PT preventing the formation or progression of amyloid plaques for preventing
 PT or treating Alzheimer's disease.
 XX PS Example 2; SEQ ID NO 28; 69pp; English.
 XX CC The present invention describes an isolated amyloid beta peptide or its
 CC homologue which is selected by a method comprising: (a) determining the
 CC binding value of each amino acid of a subsequence of amyloid beta peptide
 CC upon binding to a HLA class I and/or class II molecule of interest; (b)
 CC determining the resulting score of all amino acids of the subsequence,
 CC based on the binding value of each amino acid obtained in step (1); and
 CC (c) comparing the resulting score to a preselected value. Also described:
 CC (1) a vaccine comprising the isolated amyloid beta peptide and a carrier
 CC or diluent; (2) determining T-cell epitopes within amyloid beta peptide;
 CC (3) predicting the reaction of an individual to a vaccine; (4) matching a
 CC vaccine comprising a beta amyloid or homologue peptide to an individual,
 CC for immunisation of an individual based on the HLA haplotype of the
 CC individual; (5) a kit for matching a vaccine comprising amyloid beta
 CC peptide to an individual based on the HLA haplotype of the individual;
 CC and (6) preventing the formation or progression of amyloid plaques. The
 CC amyloid beta peptide has neuroprotective activity, and can be used in
 CC vaccines. The amyloid beta peptide is useful for preparing a composition
 CC for preventing the formation or progression of amyloid plaques for
 CC preventing or treating Alzheimer's disease. The present sequence
 CC represents an amyloid beta (A-beta) peptide, which is used in an example
 CC from the present invention.
 XX SQ Sequence 9 AA;
 Query Match 88.2%; Score 30; DB 8; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVPFA 7
 Db 3 QKLVPFA 9
 RESULT 33
 ADQ37260
 ID ADQ37260 standard; peptide; 9 AA.
 XX AC ADQ37260;
 XX DT 07-OCT-2004 (first entry)
 XX DE Vaccine antigen amyloid-beta related amino acid sequence.
 XX KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX OS Synthetic.
 XX PF Key Location/Qualifiers
 XX Misc-difference 1...9 /note= "D-form residues"
 XX

PN	WO2004058239-A1.	ID	ADQ37332 standard; peptide; 9 AA.
XX		XX	
PD	15-JUL-2004.	AC	ADQ37332;
XX		XX	
PF	24-DEC-2003; 2003WO-CA002021.	DT	07-OCT-2004 (first entry)
XX		XX	
PR	24-DEC-2002; 2002US-0436379P.	DE	Antifibrillogenic amyloidosis inhibiting peptide.
PR	23-JUN-2003; 2003US-0482214P.	XX	
XX		XX	
PA	(NEUR-) NEUROCHEM INT LTD.	KW	amyloid-beta; amyloid-beta related disease;
XX		KW	amyloid-beta fibril formation; immune response; nootropic;
PI	Gervais F, Bellini F;	KW	neuroprotective; cerebroprotective; haemostatic; ophthalmological;
XX		KW	antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;
XX		KW	anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
XX		KW	cardiant; antidepressant; endocrine; hypnotic;
XX		KW	Alzheimer's disease; immune system modulator;
XX		KW	amyloid-beta fibril formation modulator; mild cognitive impairment;
XX		KW	mild-to-moderate cognitive impairment; vascular dementia;
PT	Composition for treating e.g. Alzheimer's disease comprises first agent	KW	cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
PT	that prevents or treats amyloid-beta related disease and second agent	KW	senile dementia; Down's syndrome; inclusion body myositis;
PT	that is either a peptide or peptidomimetic or an immune system modulator.	KW	age-related macular degeneration; hypothyroidism;
XX		KW	cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
PS	Disclosure; Page 67; 143pp; English.	KW	behavioural dysfunction; neurological condition; psychological condition;
XX		XX	vaccine antigen.
XX		OS	Synthetic.
CC	The present invention describes compositions (C) comprising: (a) a first	XX	
CC	agent (a1) that prevents or treats amyloid-beta related disease; and (b)	XX	
CC	a second agent (a2) that is: (i) a peptide or peptidomimetic that	XX	
CC	modulates amyloid-beta fibril formation or induces a prophylactic or	XX	
CC	therapeutic immune response against amyloid-beta fibril formation; or	XX	
CC	(ii) an immune system modulator that prevents or inhibits amyloid-beta	XX	
CC	fibril formation. Also described is a kit comprising (C). (C) have	XX	
CC	nootropic, neuroprotective, cerebroprotective, haemostatic,	XX	
CC	ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,	XX	
CC	uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,	XX	
CC	neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,	XX	
CC	and can be used as amyloid-beta fibril formation modulators, and as	XX	
CC	immune system modulators. (C) can be used for preventing or treating an	XX	
CC	amyloid-beta related disease e.g. Alzheimer's disease (including sporadic	XX	
CC	(non-hereditary) or familial (hereditary)), mild cognitive impairment,	XX	
CC	mild-to-moderate cognitive impairment, vascular dementia, cerebral	XX	
CC	amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,	XX	
CC	Down's syndrome, inclusion body myositis, age-related macular	XX	
CC	degeneration, or a condition associated with Alzheimer's disease	XX	
CC	(including hypothyroidism, cerebrovascular disease, cardiovascular	XX	
CC	disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,	XX	
CC	aggression, or incontinence), a neurological condition (e.g. Huntington's	XX	
CC	disease, amyotrophic lateral sclerosis, acquired immunodeficiency,	XX	
CC	Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia	XX	
CC	with Lewy bodies, altered muscle tone, seizures, sensory loss, visual	XX	
CC	field deficits, incoordination, gait disturbance, transient ischaemic	XX	
CC	attack or stroke, transient alertness, attention deficit, frequent falls,	XX	
CC	syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural	XX	
CC	haematoma, brain tumour, posttraumatic brain injury, or posthypoxic	XX	
CC	damage), or a psychological condition (e.g. depression, delusions,	XX	
CC	illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep	XX	
CC	disturbance, insomnia, behavioural disinhibition, poor insight, suicidal	XX	
CC	ideation, depressed mood, irritability, anhedonia, social withdrawal, or	XX	
CC	excessive guilt)) in a subject e.g. human having a genomic mutation in an	XX	
CC	amyloid precursor protein gene, an ApoE gene, or a presenilin gene;	XX	
CC	having amyloid-beta deposits. The present sequence represents a peptide	XX	
CC	that can be used as a vaccine antigen in the exemplification of the	XX	
CC	present invention.	XX	
XX		XX	
SQ	Sequence 9 AA;	XX	
	Query Match 88.2%; Score 30; DB 8; Length 9;	XX	
	Best Local Similarity 85.7%; Pred. No. 2e+06;	XX	
	Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	XX	
QY	1 KKLVPFA 7	XX	
	:	XX	
Db	3 QKLVPFA 9	XX	
		XX	
RESULT 34		XX	
ADQ37332		XX	

CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or postrhypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match 88.2%; Score 30; DB 8; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 DB 3 QKLVPFA 9

RESULT 35

AAB46226
 ID AAB46226 standard; peptide; 10 AA.

XX AC AAB46226;

XX DT 04-APR-2001 (first entry)

XX DE Human APP derived immunogenic peptide #22.

XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.

XX OS Homo sapiens.

XX PN WO200072880-A2.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US014810.

XX PR 28-MAY-1999; 99US-00322289.

XX PA (NEUR-) NEURALAB LTD.

XX PI Schenk DB, Bard P, Vasquez NJ, Yednock T;

XX DR WPI; 2001-032104/04.

XX PT Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid specific
 PT antibody.

XX PS Disclosure; Fig 19; 143pp; English.

XX CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective

CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease

XX SQ Sequence 10 AA;

Query Match 88.2%; Score 30; DB 4; Length 10;
 Best Local Similarity 85.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 DB 2 QKLVPFA 8

RESULT 36

AAB46225
 ID AAB46225 standard; peptide; 10 AA.

XX AC AAB46225;

XX DT 04-APR-2001 (first entry)

XX DE Human APP derived immunogenic peptide #21.

XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.

XX OS Homo sapiens.

XX PN WO200072880-A2.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US014810.

XX PR 28-MAY-1999; 99US-00322289.

XX PA (NEUR-) NEURALAB LTD.

XX PI Schenk DB, Bard P, Vasquez NJ, Yednock T;

XX DR WPI; 2001-032104/04.

XX PT Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid specific
 PT antibody.

XX PS Disclosure; Fig 19; 143pp; English.

XX CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease

XX SQ Sequence 10 AA;

Query Match 88.2%; Score 30; DB 4; Length 10;
 Best Local Similarity 85.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7

```

Db      :|||||
        3 QKLVFFA 9

RESULT 37
AAB46224
ID AAB46224 standard; peptide; 10 AA.
XX AC AAB46224;
XX DT 04-APR-2001 (first entry)
XX DE Human APP derived immunogenic peptide #20.
XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
XX KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
XX KW amyloid precursor protein; Alzheimer's disease.
XX OS Homo sapiens.
XX PN WO200072880-A2.
XX PD 07-DEC-2000.
XX PF 26-MAY-2000; 2000WO-US014810.
XX PR 28-MAY-1999; 99US-00322289.
XX PA (NEUR-) NEURALAB LTD.
XX PI Schenk DB, Bard F, Vaequez NJ, Yednock T;
XX PI WPI; 2001-032104/04.
XX PD Preventing or treating a disease associated with amyloid deposits,
XX PT especially Alzheimer's disease, comprises administering amyloid specific
XX PT antibody.
XX PS Disclosure; Fig 19; 143pp; English.
XX CC This invention describes a novel method of preventing or treating a
XX CC disease associated with amyloid deposits of amyloid precursor protein
XX CC (APP) Abeta fragments in the brain of a patient, which comprises
XX CC administering to the patient: (a) an antibody that binds to Abeta, the
XX CC antibody binds to an amyloid deposit and induces a clearing response (Fc
XX CC receptor mediated phagocytosis) against it (b) a polypeptide containing
XX CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
XX CC that induces an immunogenic response against residues 1-3 to 7-11 of
XX CC Abeta. The products of the invention have nootropic and neuroprotective
XX CC activity. The method is also useful for monitoring a course of treatment
XX CC being administered to a patient e.g. active and passive immunization. The
XX CC methods are useful for prophylactic and therapeutic treatment of
XX CC Alzheimer's disease
XX SQ Sequence 10 AA;

Query Match      88.2%; Score 30; DB 4; Length 10;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
Db :|||||
   1 QKLVFFA 7

RESULT 39
AAB82641
ID AAB82641 standard; peptide; 10 AA.
XX AC AAB82641;
XX DT 02-OCT-2001 (first entry)
XX DE All-D peptide used in Alzheimer's disease vaccine.
XX KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
XX KW therapy; antigen.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1..10
XX FT /note= "all D-form residues"
XX PN WO200139796-A2.

```

XX 07-JUN-2001.
 XX 29-NOV-2000; 2000WO-CA001413.
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 XX
 XX Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 XX
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.

PS Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use in
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AA882622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self',
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AA882623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 10 AA;

Query Match 88.2%; Score 30; DB 4; Length 10;
 Best Local Similarity 85.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
 :|||||
 Db 3 QKLVPFA 9

RESULT 40
 AAU96829
 ID AAU96829 standard; peptide; 10 AA.

XX AAU96829;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #19.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;

KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 1..10
 FT /note= "Preferably D-form residue"

XX WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX 25-JUL-2000; 2000US-0220808P.

XX 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid

XX plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 22; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A-t-(A₁-n₁-K₁-A₁-a₁-b₁ (I) where z = 0-1;
 CC A₁ = an amyloid targeting moiety; A₁-n₁-K₁ = a linker moiety; and A₁-a₁-b₁
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (I) to the patient, and ultrasound imaging (I) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC cerebral amyloidosis, light chain-related amyloidosis, cerebral
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX Sequence 10 AA;

Query Match 88.2%; Score 30; DB 5; Length 10;
 Best Local Similarity 85.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
 :|||||
 Db 3 QKLVPFA 9

RESULT 41
 ABP57511
 ID ABP57511 standard; peptide; 10 AA.

XX ABP57511;

XX 28-APR-2003 (first entry)

XX Differentially isotopically labelled (DiMas) peptide #4.
 XX Mass spectrometry; polymer; analysis; cleavage; substrate specificity;
 KW isotope; protease.
 XX Synthetic.
 OS
 XX WO2003001206-A1.
 XX 03-JAN-2003.
 XX 25-JUN-2002; 2002WO-GB002921.
 XX 26-JUN-2001; 2001GB-00015581.
 XX (GLAX) GLAXO GROUP LTD.
 XX Mckesson SC;
 XX WPI; 2003-184066/18.
 XX Analyzing cleavage of polymer, by providing polymer sample, incubating
 PT the sample with labeled isotope for cleavage at potential cleavage site,
 PT and analyzing the masses of any uncleaved fragments by mass spectrometry.
 XX
 PS Example 3; Page 22; 73pp; English.
 XX
 CC The present invention describes a method (M1) for analysing cleavage of a
 CC polymer. M1 comprises: (a) providing a sample of the polymer, a portion
 CC of the polymer molecules having been labeled at a position on one side of
 CC the potential cleavage site with a first isotopic label and a portion of
 CC the polymer molecules having been labeled at a position on the opposite
 CC side of the potential cleavage site with a second isotopic label; (b)
 CC incubating the sample under conditions suitable for cleavage at the
 CC potential cleavage site; and (c) analysing the mass(es) of any cleaved
 CC fragments by mass spectrometry and thereby determining whether and/or
 CC where cleavage has taken place. M1 is useful for analysing cleavage of a
 CC polymer, where the polymer is a linear polymer, and comprises a peptide
 CC or protein. Methods from the present invention can be used in discovering
 CC new or improved synthetic substrates for both known and unknown enzymes,
 CC e.g. enzymes identified from the human genome. The methods are also
 CC useful to identify the sequence origin, and in screening methods to
 CC identify new substrates for enzymes, in positional peptide scanning
 CC libraries, in *in vivo/ex vivo*/in vitro peptide, and in assaying methods
 CC for oligonucleotide or peptide sequencing and in measuring differential
 CC protein expression. The methods are useful for monitoring the cleavage of
 CC polypeptides or polynucleotides, and for determining optimal polymer
 CC substrates. ABP57505 to ABP57605 represent peptides used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 10 AA;
 Query Match 88.2%; Score 30; DB 6; Length 10;
 Best Local Similarity 85.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVPFA 7
 :|||||
 Db 3 QKLVPFA 9
 RESULT 42
 AAE35455
 ID AAE35455 standard; peptide; 10 AA.
 XX
 AC AAE35455;
 XX
 DT 17-JUN-2003 (first entry)
 XX
 DE Abeta peptide #26.
 XX
 KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;

KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1..10
 FT /note= "D-form residues"
 XX
 XX WO200296937-A2.
 XX 05-DEC-2002.
 XX 29-MAY-2002; 2002WO-CA000763.
 XX 29-MAY-2001; 2001US-00867847.
 XX (NEUR-) NEUROCHEM INC.
 XX
 XX Gervais F, Hebert L, Chalifour RJ, Kong X;
 XX WPI; 2003-201269/19.
 XX
 PT Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX
 PS Claim 1; Page 59; 44pp; English.
 CC
 CC The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX
 SQ Sequence 10 AA;
 Query Match 88.2%; Score 30; DB 6; Length 10;
 Best Local Similarity 85.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVPFA 7
 :|||||
 Db 3 QKLVPFA 9
 RESULT 43
 ADQ37280
 ID ADQ37280 standard; peptide; 10 AA.
 XX
 AC ADQ37280;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Vaccine antigen amyloid-beta related amino acid sequence.
 XX

ADV37939
 ID ADV37939 standard; peptide; 10 AA.
 XX AC
 AC ADV37939;
 XX DT
 DT 19-MAY-2005 (first entry)
 XX DE
 DE Amyloid-targeting peptide, SEQ ID NO:19, for use in imaging agent.
 XX
 XX Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
 KW transmissible spongiform encephalopathy; scrapie; BSE;
 KW Alzheimer's disease; neurological disease; amyloidosis;
 KW non-insulin dependent diabetes; metabolic disorder.
 XX
 OS Synthetic.
 XX
 XX US2005048000-A1.
 XX
 XX 03-MAR-2005.
 XX
 XX 03-DEC-2003; 2003US-00728028.
 XX
 XX 25-JUL-2000; 2000US-0220808P.
 XX
 XX 24-JUL-2001; 2001US-00915092.
 XX
 XX 29-JAN-2003; 2003US-0443291P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 XX
 XX Gervais P, Kong X, Chalifour R, Migneault D;
 XX
 XX WPI; 2005-212201/22.
 XX
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
 PT related condition, e.g. Creutzfeldt-Jakob disease, bovine spongiform
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.
 XX
 XX Disclosure; SEQ ID NO 19; 34pp; English.
 XX
 XX The invention relates to an amyloid-targeting imaging agent. The imaging
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
 CC a labeling moiety via a linking moiety, and is preferably able to cross
 CC the blood-brain barrier. The invention also relates to a kit for
 CC preparing a radiopharmaceutical preparation from the imaging agent of the
 CC invention, a method for imaging amyloid deposition in a patient and a
 CC method for diagnosing an amyloid-related condition in a patient. The
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
 CC related conditions such as Creutzfeldt-Jakob disease (CJD), Kuru,
 CC transmissible cerebral amyloidosis (also known as transmissible virus
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
 CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
 CC mediated diseases, dialysis-related amyloidosis, light chain-related
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
 CC patient. The agent does not exhibit excessive toxicity or irritation,
 CC does not induce an allergic response, and permits an earlier diagnosis of
 CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADV37921-ADV37947 and ADV37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.
 XX
 XX Sequence 10 AA;

Query Match 88.2%; Score 30; DB 9; Length 10;
 Best Local Similarity 85.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVFPA 7
 :|||||
 Db 3 QKLVFPA 9

RESULT 47

AAW32560
 ID AAW32560 standard; peptide; 11 AA.
 XX AC
 AC AAW32560;
 XX DT
 DT 21-JAN-1998 (first entry)
 XX DE
 DE Anti-amyloid peptide Abeta inhibiting abnormal protein folding.
 XX
 XX Anti-amyloid peptide; iAbeta; abnormal protein folding inhibitor;
 KW Alzheimer's disease; dementia; Down's syndrome; amyloidosis disorder;
 KW human prion disease; Kuru; Creutzfeldt-Jakob disease;
 KW Gerstmann-Strausler-Scheinker Syndrome; animal prion disease;
 KW prion associated human neurodegenerative disease; scrapie;
 KW spongiform encephalopathy; transmissible mink encephalopathy;
 KW chronic wasting disease; mule; deer; elk; human.
 XX
 XX Homo sapiens.
 OS
 OS Synthetic.
 XX
 XX WO9639834-A1.
 XX
 XX 19-DEC-1996.
 XX
 XX 06-JUN-1996; 96WO-US010220.
 XX
 XX 07-JUN-1995; 95US-00478326.
 XX
 XX 10-APR-1996; 96US-00630645.
 XX
 XX (UANY) UNIV NEW YORK STATE.
 XX
 XX Soto-Jara C, Baumann MH, Frangione B;
 PI
 PI WPI; 1997-051637/05.
 XX
 XX New inhibitors of fibrillogenesis proteins or peptides - used for
 PT preventing, treating or detecting amyloidosis disorders such as
 PT Alzheimer's disease.
 XX
 XX Example 1; Fig 9; 63pp; English.
 XX
 XX A method has been developed for the prevention or treatment of a disorder
 CC or disease associated with the formation of amyloid or amyloid-like
 CC deposits, involving the abnormal folding of a protein or peptide. The
 CC method involves administering an inhibitory peptide which prevents the
 CC abnormal folding or which dissolves existing amyloid or amyloid-like
 CC deposits, where the peptide comprises a sequence of 3-15 amino acid
 CC residues and has a hydrophobic cluster of at least 3 amino acids, where
 CC at least one of the 3 amino acids is a beta-sheet blocking amino acid
 CC residue selected from Pro, Gly, Asn and His. The present sequence
 CC represents an anti-amyloid peptide, Abeta, which inhibits abnormal
 CC protein folding. The inhibitory peptide is capable of associating with a
 CC structural determinant on the protein or peptide to structurally block
 CC and inhibit the abnormal folding into amyloid or amyloid-like deposits.
 CC The method can be used for preventing, treating or detecting e.g.
 CC Alzheimer's dementia or disease, Down's syndrome, other amyloidosis
 CC disorders, human prion diseases such as Kuru, Creutzfeldt-Jakob disease,
 CC Gerstmann-Strausler-Scheinker Syndrome, prion associated human
 CC neurodegenerative diseases or animal prion diseases such as scrapie,
 CC spongiform encephalopathy, transmissible mink encephalopathy and chronic
 CC wasting disease of mule deer and elk
 XX
 XX Sequence 11 AA;

Query Match 88.2%; Score 30; DB 2; Length 11;
 Best Local Similarity 85.7%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVFPA 7
 :|||||
 Db 1 QKLVFPA 7

AC	AAE29504;
XX	27-JAN-2003 (first entry)
DE	Amyloid beta-protein related peptide #1.
XX	Metallopeptide; nontropic; amyloid beta-protein; Alzheimer's disease; AD;
KW	Prion's disease; oxytocin; angiotensin; vasopressin; neuroprotective;
KW	therapy; amyloid beta-protein related peptide.
XX	Unidentified.
XX	WO200264734-A2.
PN	22-AUG-2002.
XX	19-DEC-2001; 2001WO-US050075.
XX	19-DEC-2000; 2000US-0256842P.
PR	11-JUL-2001; 2001US-0304835P.
PR	04-OCT-2001; 2001US-0327835P.
XX	(PALA-) PALATIN TECHNOLOGIES INC.
PA	Sharma SD, Shi Y;
XX	WPI; 2002-740699/80.
PI	Determining secondary structure binding to desired targets within parent
DR	polypeptides that bind to targets, by constructing and complexing
XX	PT peptides to metal ions to form metallopeptides and screening the
PT	metallopeptides.
XX	Claim 194; Page 98; 165pp; English.
PS	The invention relates to a method for identification and determination of
XX	target-specific folding sites in peptides and proteins. The invention of
CC	also relates to a method for determining a secondary structure binding to
CC	desired targets within parent polypeptides that bind to targets, by
CC	constructing and complexing peptides to metal ions to form
CC	metallopeptides and screening the metallopeptides. The method is useful
CC	for determining secondary structure binding to desired target within
CC	parent polypeptide with primary structure that binds to the target, where
CC	the target of interest is a receptor, antibody, toxin, enzyme, hormone,
CC	nucleic acid, intracellular protein domain of biological relevance or
CC	extracellular protein domain of biological relevance. A library of
CC	amyloid beta-protein related peptides is useful for the treatment of
CC	Alzheimer's disease (AD). A library of peptides targeting vasopressin,
CC	oxytocin or angiotensin receptor is useful for treating Prion's disease.
CC	The present sequence is an amyloid beta-protein related peptide
XX	Sequence 11 AA;
SQ	
Query Match	88.2%; Score 30; DB 5; Length 11;
Best Local Similarity	85.7%; Pred. No. 14;
Matches	6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KKLVFFFA 7
	:
Db	2 EKLVFFFA 8
RESULT 50	
ABU79013	
ID	ABU79013 standard; peptide; 11 AA.
XX	AC ABU79013;
XX	DT 17-JUN-2003 (first entry)
XX	Amyloidogenic Amyloid A peptide #3.
XX	Amyloid formation; amyloid-like deposit; Alzheimer's disease;
XX	

AC	AAE29504;
XX	27-JAN-2003 (first entry)
DE	Amyloid beta-protein related peptide #1.
XX	Metallopeptide; nontropic; amyloid beta-protein; Alzheimer's disease; AD;
KW	Prion's disease; oxytocin; angiotensin; vasopressin; neuroprotective;
KW	therapy; amyloid beta-protein related peptide.
XX	Unidentified.
XX	WO200264734-A2.
PN	22-AUG-2002.
XX	19-DEC-2001; 2001WO-US050075.
XX	19-DEC-2000; 2000US-0256842P.
PR	11-JUL-2001; 2001US-0304835P.
PR	04-OCT-2001; 2001US-0327835P.
XX	(PALA-) PALATIN TECHNOLOGIES INC.
PA	Sharma SD, Shi Y;
XX	WPI; 2002-740699/80.
PI	Determining secondary structure binding to desired targets within parent
DR	polypeptides that bind to targets, by constructing and complexing
XX	PT peptides to metal ions to form metallopeptides and screening the
PT	metallopeptides.
XX	Claim 194; Page 98; 165pp; English.
PS	The invention relates to a method for identification and determination of
XX	target-specific folding sites in peptides and proteins. The invention of
CC	also relates to a method for determining a secondary structure binding to
CC	desired targets within parent polypeptides that bind to targets, by
CC	constructing and complexing peptides to metal ions to form
CC	metallopeptides and screening the metallopeptides. The method is useful
CC	for determining secondary structure binding to desired target within
CC	parent polypeptide with primary structure that binds to the target, where
CC	the target of interest is a receptor, antibody, toxin, enzyme, hormone,
CC	nucleic acid, intracellular protein domain of biological relevance or
CC	extracellular protein domain of biological relevance. A library of
CC	amyloid beta-protein related peptides is useful for the treatment of
CC	Alzheimer's disease (AD). A library of peptides targeting vasopressin,
CC	oxytocin or angiotensin receptor is useful for treating Prion's disease.
CC	The present sequence is an amyloid beta-protein related peptide
XX	Sequence 11 AA;
SQ	
Query Match	88.2%; Score 30; DB 5; Length 11;
Best Local Similarity	85.7%; Pred. No. 14;
Matches	6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KKLVFFFA 7
	:
Db	2 EKLVFFFA 8
RESULT 50	
ABU79013	
ID	ABU79013 standard; peptide; 11 AA.
XX	AC ABU79013;
XX	DT 17-JUN-2003 (first entry)
XX	Amyloidogenic Amyloid A peptide #3.
XX	Amyloid formation; amyloid-like deposit; Alzheimer's disease;
XX	

(UNY) UNIV NEW YORK STATE.

Soto-Jara C, Baumann MH, Frangione B;

WPI: 2003-616149/58.

New inhibitory peptide, useful for preparing a composition for diagnosing, preventing or treating disorders associated with amyloid-like fibril deposits, e.g. Alzheimer's disease, or prion related encephalopathies.

Disclosure; Fig 9; 52pp; English.

The invention relates to inhibitory peptide comprising a portion of at least three amino acid residues and a sequence predicted not to adopt a beta-sheet structure that associates with a hydrophobic beta-sheet cluster on a protein or peptide involved in the abnormal folding of the beta-sheet structure, to structurally block the abnormal folding of the protein or peptide. The inhibitory peptide is useful for preparing a composition for preventing, treating or detecting disorders or diseases associated with amyloid-like fibril deposits e.g. Alzheimer's disease and prion related encephalopathies. The invention is also useful in gene therapy. The present sequence is amyloid-beta (Abeta) peptide. This peptide is used in the invention

Sequence 11 AA;

Query Match 88.2%; Score 30; DB 7; Length 11;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
:|||||
DB 1 QKLVFPA 7

RESULT 53
AAE35464
ID AAE35464 standard; peptide; 12 AA.
XX
AC AAE35464;
XX
DT 17-JUN-2003 (first entry)
XX
DE Abeta peptide #35.
XX
KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis; cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis; psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome; Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic; chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotrophic; Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological; ulcer; antiinflammatory; cytostatic; uropathic; therapy.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 7. .12
FT /note= "D-form residues"
XX
PN WO200296937-A2.
XX
PD 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-CA000763.
XX
PR 29-MAY-2001; 2001US-00867847.
XX
PA (NEUR-) NEUROCHEM INC.
XX
PI Gervais F, Hebert L, Chalifour RJ, Kong X;
XX WPI: 2003-201269/19.

(UNY) UNIV NEW YORK STATE.

Soto-Jara C, Baumann MH, Frangione B;

WPI: 2003-616149/58.

New inhibitory peptide, useful for preparing a composition for diagnosing, preventing or treating disorders associated with amyloid-like fibril deposits, e.g. Alzheimer's disease, or prion related encephalopathies.

Disclosure; Fig 9; 52pp; English.

The invention relates to inhibitory peptide comprising a portion of at least three amino acid residues and a sequence predicted not to adopt a beta-sheet structure that associates with a hydrophobic beta-sheet cluster on a protein or peptide involved in the abnormal folding of the beta-sheet structure, to structurally block the abnormal folding of the protein or peptide. The inhibitory peptide is useful for preparing a composition for preventing, treating or detecting disorders or diseases associated with amyloid-like fibril deposits e.g. Alzheimer's disease and prion related encephalopathies. The invention is also useful in gene therapy. The present sequence is amyloid-beta (Abeta) peptide. This peptide is used in the invention

Sequence 12 AA;

Query Match 88.2%; Score 30; DB 6; Length 12;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
:|||||
DB 6 QKLVFPA 12

RESULT 54
AAE35435
ID AAE35435 standard; peptide; 12 AA.
XX
AC AAE35435;
XX
DT 17-JUN-2003 (first entry)
XX
DE Abeta peptide #6.
XX
KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis; cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis; psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome; Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic; chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotrophic; Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological; ulcer; antiinflammatory; cytostatic; uropathic; therapy.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 1. .12
FT /note= "D-form residues"
XX
PN WO200296937-A2.
XX
PD 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-CA000763.
XX
PR 29-MAY-2001; 2001US-00867847.
XX
PA (NEUR-) NEUROCHEM INC.
XX
PI Gervais F, Hebert L, Chalifour RJ, Kong X;
XX WPI: 2003-201269/19.

DR WPI; 2003-201269/19.
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 PS Claim 1; Page 58; 44pp; English.
 XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX
 SQ Sequence 12 AA;

Query Match 88.2%; Score 30; DB 6; Length 12;
 Best Local Similarity 85.7%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 :|||||
 Db 6 QKLVPFA 12

RESULT 55

AAE35466
 ID AAE35466 standard; peptide; 12 AA.

AC AAE35466;

DT 17-JUN-2003 (first entry)

DE Abeta peptide #37.

XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.

OS Unidentified.

PH Key Location/Qualifiers

FT Misc-difference 1..12 /note= "D-form residues"

FN WO200296937-A2.

PD 05-DEC-2002.

XX 29-MAY-2002; 2002WO-CA000763.

XX 29-MAY-2001; 2001US-00867847.

PA (NEUR-) NEUROCHEM INC.

PI Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 PS Claim 1; Page 61; 44pp; English.

XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX

SQ Sequence 12 AA;

Query Match 88.2%; Score 30; DB 6; Length 12;
 Best Local Similarity 85.7%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 :|||||
 Db 3 QKLVPFA 9

RESULT 56

ADD20745

ID ADD20745 standard; peptide; 12 AA.

AC ADD20745;

DT 15-JAN-2004 (first entry)

XX Human beta-amyloid 10-21 H13Q amino acid sequence SEQ ID NO:3.

DE self-assembly; peptide-based structure; beta-amyloid;
 KW self-assembling structure; molecular-level probing; human.

OS Synthetic.

OS Homo sapiens.

XX WO2003082900-A2.

XX 09-OCT-2003.

XX 24-MAR-2003; 2003WO-US009229.

XX 22-MAR-2002; 2002US-0366826P.

XX 23-OCT-2002; 2002US-0420746P.

XX 21-MAR-2003; 2003US-0456641P.

XX (UYEM-) UNIV EMORY.

XX Lynn D, Conticello V, Morgan DA, Dong J;

XX WPI; 2003-804023/75.

XX Controlling self-assembly of peptide-based structures (e.g. nanotubes)
 PT comprises providing a controlled environment and placing segments of beta

PT -amyloids in the controlled environment to generate a self-assembling
 PT structure.
 XX
 PS Claim 1; SEQ ID NO 3; 46pp; English.
 XX
 CC The present invention describes a method (M1) for controlling self-
 CC assembly of self-assembling peptide-based structures by providing a
 CC controlled environment and placing segments of beta-amyloids in the
 CC controlled environment to generate a self-assembling structure. Also
 CC described: (1) a method (M1a) for controlling self-assembly of peptide-
 CC based structures comprising providing a controlled environment adapted to
 CC redirect a self-assembly process, and generating a self-assembling
 CC peptide-based structure by placing the self-assembling peptide in the
 CC controlled environment; and (2) a self-assembling peptide-based structure
 CC comprising beta-amyloid segments, optionally with a conservative amino
 CC acid substitution; and hydrogen bonds formed between the segments of the
 CC beta-amyloid. The method is useful in controlling the self-assembly of
 CC self-assembling peptide-based structures. The self-assembling peptide
 CC structures may be used in generating devices at a molecular level to
 CC permit molecular-level probing. The present sequence represents a human
 CC beta-amyloid 10-21 H13Q variant amino acid sequence, which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 12 AA;

Query Match 88.2%; Score 30; DB 7; Length 12;
 Best Local Similarity 85.7%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 :|||||
 Db 6 QKLVPFA 12

RESULT 57
 ADD20744
 ID ADD20744 standard; peptide; 12 AA.
 XX
 AC ADD20744;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human beta-amyloid 10-21 E11N amino acid sequence SEQ ID NO:2.
 XX
 KW self-assembly; peptide-based structure; beta-amyloid;
 KW self-assembling structure; molecular-level probing; human.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003082900-A2.
 XX
 PD 09-OCT-2003.
 XX
 PF 24-MAR-2003; 2003WO-US009229.
 XX
 PR 22-MAR-2002; 2002US-0366826P.
 PR 23-OCT-2002; 2002US-0420746P.
 PR 21-MAR-2003; 2003US-0456641P.
 XX
 PA (UYEM-) UNIV EMORY.
 XX
 XX Lynn D, Conticello V, Morgan DA, Dong J;
 XX WPI; 2003-804023/75.
 XX
 XX Controlling self-assembly of peptide-based structures (e.g. nanotubes)
 PT comprises providing a controlled environment and placing segments of beta
 PT -amyloids in the controlled environment to generate a self-assembling
 PT structure.
 XX
 PS Claim 1; SEQ ID NO 2; 46pp; English.
 XX

CC The present invention describes a method (M1) for controlling self-
 CC assembly of self-assembling peptide-based structures by providing a
 CC controlled environment and placing segments of beta-amyloids in the
 CC controlled environment to generate a self-assembling structure. Also
 CC described: (1) a method (M1a) for controlling self-assembly of peptide-
 CC based structures comprising providing a controlled environment adapted to
 CC redirect a self-assembly process, and generating a self-assembling
 CC peptide-based structure by placing the self-assembling peptide in the
 CC controlled environment; and (2) a self-assembling peptide-based structure
 CC comprising beta-amyloid segments, optionally with a conservative amino
 CC acid substitution; and hydrogen bonds formed between the segments of the
 CC beta-amyloid. The method is useful in controlling the self-assembly of
 CC self-assembling peptide-based structures. The self-assembling peptide
 CC structures may be used in generating devices at a molecular level to
 CC permit molecular-level probing. The present sequence represents a human
 CC beta-amyloid 10-21 E11N variant amino acid sequence, which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 12 AA;

Query Match 88.2%; Score 30; DB 7; Length 12;
 Best Local Similarity 85.7%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 :|||||
 Db 6 QKLVPFA 12

RESULT 58
 ADJ71476
 ID ADJ71476 standard; peptide; 12 AA.
 XX
 AC ADJ71476;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE N-terminal truncated beta-amyloid peptide, SEQ ID 139.
 XX
 KW Nootropic; Neuroprotective; Vaccine; beta Amyloid;
 KW amyloid precursor protein; APP; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO2004013172-A2.
 XX
 PD 12-FEB-2004.
 XX
 PF 18-JUL-2003; 2003WO-EP007833.
 XX
 PR 24-JUL-2002; 2002EP-00447147.
 PR 06-AUG-2002; 2002US-0401497P.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Delacourte A, Sergeant N;
 XX WPI; 2004-180423/17.
 XX
 PT New beta-amyloid or amyloid precursor protein preparation, useful as a
 PT prophylactic vaccine or a therapeutic for preventing or treating a
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 PT Alzheimer's disease.
 XX
 PS Claim 4; Page 64; 104pp; English.
 XX
 CC The present invention relates to preparations (I) comprising a beta-
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
 CC fragment. The beta-amyloid or APP preparations are useful for
 CC manufacturing a prophylactic vaccine or a therapeutic, or as a
 CC prophylactic vaccine for the prevention, or as a therapeutic for the
 CC treatment of a disease associated with beta-amyloid formation and/or

CC aggregation, such as Alzheimer's disease.
 XX Sequence 12 AA;
 SQ

Query Match 88.2%; Score 30; DB 8; Length 12;
 Best Local Similarity 85.7%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
 Db 6 QKLVPFA 12
 :|||||

RESULT 59
 ADQ37407
 ID ADQ37407 standard; peptide; 12 AA.
 XX
 AC ADQ37407;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Amyloid-beta amino acid sequence.
 XX
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 Key Location/Qualifiers
 FT Misc-difference 7..12 /note= "D-form residues"
 FT
 XX
 PN W02004058239-A1.
 XX
 XX 15-JUL-2004.
 XX
 XX 24-DEC-2003; 2003MO-CA002021.
 XX
 XX 24-DEC-2002; 2002US-0436379P.
 XX
 XX 23-JUN-2003; 2003US-0482214P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 XX
 XX Gervais F, Bellini F;
 XX
 XX WPI; 2004-543342/52.
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 PS Disclosure; Page 68; 143pp; English.
 XX
 CC The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have

CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents an amyloid-
 CC beta amino acid sequence, which can be used as a vaccine antigen in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 12 AA;
 Query Match 88.2%; Score 30; DB 8; Length 12;
 Best Local Similarity 85.7%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
 Db 6 QKLVPFA 12
 :|||||

RESULT 60
 ADQ37289
 ID ADQ37289 standard; peptide; 12 AA.
 XX
 AC ADQ37289;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Vaccine antigen amyloid-beta related amino acid sequence.
 XX
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 Key Location/Qualifiers
 FT Misc-difference 1..12
 FT
 XX
 PN W02004058239-A1.
 XX
 XX 15-JUL-2004.
 XX
 XX 24-DEC-2003; 2003MO-CA002021.
 XX
 XX 24-DEC-2002; 2002US-0436379P.
 XX
 XX 23-JUN-2003; 2003US-0482214P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 XX
 XX Gervais F, Bellini F;
 XX
 XX WPI; 2004-543342/52.
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 PS Disclosure; Page 68; 143pp; English.
 XX
 CC The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have

FT XX /note= "D-form residues"

PN WO2004058239-A1.

XX 15-JUL-2004.

PD 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

PA (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

DR Composition for treating e.g. Alzheimer's disease comprises first agent

PT that prevents or treats amyloid-beta related disease and second agent

PT that is either a peptide or peptidomimetic or an immune system modulator.

XX Disclosure; Page 68; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have

CC nontropic, neuroprotective, cerebroprotective, haemostatic,

CC ophthalmological, antithyroid, vasotropic, cardiovascular, muscular,

CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,

CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,

CC and can be used as amyloid-beta fibril formation modulators, and as

CC immune system modulators. (C) can be used for preventing or treating an

CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic

CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,

CC mild-to-moderate cognitive impairment, vascular dementia, cerebral

CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,

CC Down's syndrome, inclusion body myositis, age-related macular

CC degeneration, or a condition associated with Alzheimer's disease

CC (including hypothyroidism, cerebrovascular disease, cardiovascular

CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,

CC aggression, or incontinence), a neurological condition (e.g. Huntington's

CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,

CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia

CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual

CC field deficits, incoordination, gait disturbance, transient ischaemic

CC attack or stroke, transient alertness, attention deficit, frequent falls,

CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural

CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic

CC damage), or a psychological condition (e.g. depression, delusions,

CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep

CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal

CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or

CC excessive guilt)) in a subject e.g. human having a genomic mutation in an

CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;

CC having amyloid-beta deposits. The present sequence represents a peptide

CC that can be used as a vaccine antigen in the exemplification of the

CC present invention.

XX Sequence 12 AA;

Query Match 88.2%; Score 30; DB 8; Length 12;

Best Local Similarity 85.7%; Pred. No. 16;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7

Db 3 QKLVPFA 9

RESULT 61

ADQ37259

ID ADQ37259 standard; peptide; 12 AA.

XX AC ADQ37259;

XX DT 07-OCT-2004 (first entry)

XX DE Vaccine antigen amyloid-beta related amino acid sequence.

XX KW amyloid-beta; amyloid-beta related disease;

XX KW amyloid-beta fibril formation; immune response; nontropic;

XX KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;

XX KW antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;

XX KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;

XX KW cardiant; antidepressant; endocrine; hypnotic;

XX KW amyloid-beta fibril formation modulator; immune system modulator;

XX KW Alzheimer's disease; mild cognitive impairment;

XX KW mild-to-moderate cognitive impairment; vascular dementia;

XX KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;

XX KW senile dementia; Down's syndrome; inclusion body myositis;

XX KW age-related macular degeneration; hypothyroidism;

XX KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;

XX KW behavioural dysfunction; neurological condition; psychological condition;

XX KW vaccine antigen.

XX Synthetic.

OS Key Location/Qualifiers

FH Misc-difference 1..12 /note= "D-form residues"

FT WO2004058239-A1.

XX 15-JUL-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent

XX that prevents or treats amyloid-beta related disease and second agent

XX that is either a peptide or peptidomimetic or an immune system modulator.

XX Disclosure; Page 67; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have

CC nontropic, neuroprotective, cerebroprotective, haemostatic,

CC ophthalmological, antithyroid, vasotropic, cardiovascular, muscular,

CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,

CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,

CC and can be used as amyloid-beta fibril formation modulators, and as

CC immune system modulators. (C) can be used for preventing or treating an

CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic

CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,

CC mild-to-moderate cognitive impairment, vascular dementia, cerebral

CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,

CC Down's syndrome, inclusion body myositis, age-related macular

CC degeneration, or a condition associated with Alzheimer's disease

CC (including hypothyroidism, cerebrovascular disease, cardiovascular

CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,

CC aggression, or incontinence), a neurological condition (e.g. Huntington's

CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,

CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia

CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual

CC field deficits, incoordination, gait disturbance, transient ischaemic

CC attack or stroke, transient alertness, attention deficit, frequent falls,

CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural

CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic

CC damage), or a psychological condition (e.g. depression, delusions,

CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep

CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal

CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or

CC excessive guilt)) in a subject e.g. human having a genomic mutation in an

CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;

CC having amyloid-beta deposits. The present sequence represents a peptide

CC that can be used as a vaccine antigen in the exemplification of the

CC present invention.

CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic damage), or a psychological condition (e.g. depression, delusions, illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep disturbance, insomnia, behavioural disinhibition, poor insight, suicidal ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt) in a subject e.g. human having a genomic mutation, an amyloid precursor protein gene, an ApoE gene, or a presenilin gene; CC having amyloid-beta deposits. The present sequence represents a peptide CC that can be used as a vaccine antigen in the exemplification of the CC present invention.

XX SQ Sequence 12 AA;

Query Match 88.2%; Score 30; DB 8; Length 12;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 6 QKLVPFA 12

RESULT 62

ADZ08890
ID ADZ08890 standard; peptide; 12 AA.

XX AC ADZ08890;

XX DT 16-JUN-2005 (first entry)

XX DE Human beta-amyloid peptide (SEQ ID No:115) probed with anti-amyloid IgG.

XX KW amyloid; antibody engineering; antibody production;
XX KW amyloid-associated disorder; Alzheimers disease; cancer; allergy;
XX KW autoimmune disease; Parkinsons disease;
XX KW acquired immune deficiency syndrome; multiple sclerosis; migraine;
XX KW dementia; infection; nootropic; neuroprotective; cytostatic;
XX KW antiallergic; immunosuppressive; antiparkinsonian; antimigraine;
XX KW antimicrobial; anti-HIV; beta-amyloid.

XX OS Homo sapiens.

XX FN WO2005028511-A2.

XX PD 31-MAR-2005.

XX PF 26-MAR-2004; 2004WO-US009522.

XX PR 28-MAR-2003; 2003US-0458469P.

XX PR 28-MAR-2003; 2003US-0458474P.

XX PR 28-MAR-2003; 2003US-0458509P.

XX PR 28-MAR-2003; 2003US-0458510P.

XX FA (CENZ) CENTOCOR INC.

XX PA (MERC/) MERCKEN M.

XX PA (BENS/) BENSON J M.

XX PI Mercken M, Benson JM;

XX XX WPI; 2005-242565/25.

XX XX New isolated mammalian anti-amyloid antibodies useful for treating
PT amyloid-associated disorders, such as Alzheimer's disease, cancer,
PT allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,
PT migraine and dementia.

XX Example 4; SEQ ID NO 115; 306pp; English.

XX The invention relates to at least one isolated mammalian amyloid antibody
PS comprising at least one variable region comprising at least one heavy
XX chain and at least one light chain, of a fully defined sequence of SEQ ID
CC NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are:
CC (i) at least one isolated mammalian amyloid antibody that binds to the
CC same region of an amyloid polypeptide as an antibody comprising at least
CC one heavy chain or light chain complementarity determining region (CDR)
CC having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii)
CC at least one isolated mammalian amyloid antibody, comprising at least one
CC human CDR, where the antibody specifically binds at least one epitope
CC selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined
CC sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic
CC acid encoding at least one of any of the isolated mammalian amyloid
CC antibodies mentioned and having at least one human CDR of a fully defined
CC sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an
CC isolated nucleic acid vector comprising an isolated nucleic acid encoding
CC an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising
CC an isolated nucleic acid encoding an amyloid antibody, (vi) a method of
CC producing at least one amyloid antibody, (vii) a composition comprising
CC at least one of the isolated mammalian amyloid antibodies
CC mentioned, and at least one pharmaceutical carrier or diluent, (viii) an
CC anti-idiotypic antibody or fragment that specifically binds at least one
CC of the amyloid antibodies mentioned, (ix) a method of diagnosing or
CC treating an amyloid related condition in a cell, tissue, organ or animal,
CC comprising contacting or administering a composition comprising at least
CC one of the antibodies mentioned, with, or to, the cell, tissue, organ or
CC animal, (x) a medical device comprising at least one amyloid antibody
CC mentioned, where the device is suitable for contacting or administering
CC at least one amyloid antibody, (xi) an article of manufacture for human
CC pharmaceutical or diagnostic use, comprising packaging material and a
CC container comprising a solution or a lyophilized form of at least one of
CC the amyloid antibodies mentioned, and (xii) a method of producing at
CC least one of the isolated mammalian amyloid antibodies, comprising
CC providing a host cell or transgenic animal or transgenic plant or plant
CC cell capable of expressing the antibody in recoverable amounts. The
CC methods and compositions of the present invention are useful for
CC producing therapeutic compositions and devices for treating amyloid-
CC associated disorders, such as Alzheimer's disease, cancer, allergies,
CC autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis,
CC migraine, dementia and infections. This sequence represents a peptide
CC from human beta-amyloid probed with anti-beta-amyloid IgG antibodies.

XX SQ Sequence 12 AA;

Query Match 88.2%; Score 30; DB 9; Length 12;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 6 QKLVPFA 12

RESULT 63

ADA37467

ID ADA37467 standard; peptide; 13 AA.

XX AC ADA37467;

XX XX 20-NOV-2003 (first entry)

XX DE Human amyloid precursor protein fragment.

XX ADAM; a disintegrin and metalloprotease; G-protein coupled receptor;
KW GPCR; beta-amyloid precursor protein; APP; alpha-secretase site;
KW Alzheimer's disease.

OS Homo sapiens.

XX US2003108978-A1.

XX PD 12-JUN-2003.
 XX PF 25-OCT-2002; 2002US-00281458.
 XX PR 25-OCT-2001; 2001US-0337641P.
 XX PA (CIAM/) CIAMBRONE G J.
 XX PI (GIBB/) GIBBONS I.
 XX PI Ciambone GJ, Gibbons I;
 XX WPI; 2003-626205/59.
 XX PT Assaying activity of an a disintegrin and metalloprotease in whole cell
 PT system combining soluble substrate with whole cell system, and
 PT determining amount of product.
 XX PS Disclosure; Page 9; 34pp; English.
 XX CC The invention relates to the activity of a disintegrin and
 CC metalloprotease (ADAM) in a whole cell system assayed by selecting a
 CC soluble substrate that is specifically cleavable by the ADAM, combining
 CC the soluble substrate with the whole cell system under conditions that
 CC allow processing of the substrate to a product by the ADAM and
 CC determining the amount of the product as an indication of the ADAM
 CC activity. Also included is a method of determining the effect of a G-
 CC protein coupled receptor (GPCR) on the activity of an ADAM in a whole
 CC cell system comprising selecting a ligand known to modulate activity of
 CC the GPCR and a soluble substrate that is cleavable by the ADAM, preparing
 CC two mixtures of the whole cell system and the soluble substrate, where
 CC only one of the mixtures contains the ligand, incubating the mixtures
 CC under conditions that allow processing of the substrate to a product by
 CC the ADAM, if the ADAM is active, determining the amount of the product
 CC formed in each mixture and comparing the amount of product formed in
 CC separate mixtures to determine effect of the GPCR on the ADAM activity.
 CC The method may be adapted to assay the effect of a compound on the
 CC cleavage of the Beta-amyloid precursor protein (APP) at its alpha-
 CC secretase site by ADAM 17 or ADAM 10. The invention is used for the
 CC assaying for the activity of an ADAM in a whole cell system. The assay
 CC may be used in the diagnosis of diseases associated with ADAM activities
 CC e.g. Alzheimer's disease. The present sequence is the human APP peptide
 CC fragment containing the alpha-secretase site.
 XX SQ Sequence 13 AA;
 Query Match 88.2%; Score 30; DB 6; Length 13;
 Best Local Similarity 85.7%; Pred. NO. 17;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVFFA 7
 Db :|||||
 5 QKLVFFA 11
 RESULT 64
 ADJ71477
 ID ADJ71477 standard; peptide; 13 AA.
 AC ADJ71477;
 XX DT 06-MAY-2004 (first entry)
 XX DE N-terminal truncated beta-amyloid peptide, SEQ ID 140.
 XX KW Nootropic; Neuroprotective; Vaccine; beta Amyloid;
 KW amyloid precursor protein; APP; Alzheimer's disease.
 XX OS Homo sapiens.
 XX PN WO2004013172-A2.
 XX PD 12-FEB-2004.
 XX PF 18-JUL-2003; 2003WO-EP007833.
 XX PR 24-JUL-2002; 2002EP-00447147.
 XX PR 06-AUG-2002; 2002US-0401497P.
 XX PA (INNO-) INNOGENETICS NV.
 XX PI Delacourte A, Sergeant N;
 XX WPI; 2004-180423/17.
 XX PT New beta-amyloid or amyloid precursor protein preparation, useful as a
 PT prophylactic vaccine or a therapeutic for preventing or treating a
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 PT Alzheimer's disease.

XX PF 18-JUL-2003; 2003WO-EP007833.
 XX PR 24-JUL-2002; 2002EP-00447147.
 XX PR 06-AUG-2002; 2002US-0401497P.
 XX PA (INNO-) INNOGENETICS NV.
 XX PI Delacourte A, Sergeant N;
 XX WPI; 2004-180423/17.
 XX PT New beta-amyloid or amyloid precursor protein preparation, useful as a
 PT prophylactic vaccine or a therapeutic for preventing or treating a
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 PT Alzheimer's disease.
 XX PS Claim 4; Page 64; 104pp; English.
 XX CC The present invention relates to preparations (I) comprising a beta-
 CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
 CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
 CC fragment. The beta-amyloid or APP preparations are useful for
 CC manufacturing a prophylactic vaccine or a therapeutic, or as a
 CC prophylactic vaccine for the prevention, or as a therapeutic for the
 CC treatment of a disease associated with beta-amyloid formation and/or
 CC aggregation, such as Alzheimer's disease.
 XX SQ Sequence 13 AA;
 Query Match 88.2%; Score 30; DB 8; Length 13;
 Best Local Similarity 85.7%; Pred. NO. 17;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVFFA 7
 Db :|||||
 6 QKLVFFA 12
 RESULT 65
 ADJ71464
 ID ADJ71464 standard; peptide; 13 AA.
 XX AC ADJ71464;
 XX DT 06-MAY-2004 (first entry)
 XX DE N-terminal truncated beta-amyloid peptide, SEQ ID 127.
 XX KW Nootropic; Neuroprotective; Vaccine; beta Amyloid;
 KW amyloid precursor protein; APP; Alzheimer's disease.
 XX OS Homo sapiens.
 XX PN WO2004013172-A2.
 XX PD 12-FEB-2004.
 XX PF 18-JUL-2003; 2003WO-EP007833.
 XX PR 24-JUL-2002; 2002EP-00447147.
 XX PR 06-AUG-2002; 2002US-0401497P.
 XX PA (INNO-) INNOGENETICS NV.
 XX PI Delacourte A, Sergeant N;
 XX WPI; 2004-180423/17.
 XX PT New beta-amyloid or amyloid precursor protein preparation, useful as a
 PT prophylactic vaccine or a therapeutic for preventing or treating a
 PT disease associated with beta-amyloid formation and/or aggregation, e.g.
 PT Alzheimer's disease.

XX PS Claim 4; Page 63; 104pp; English.

CC The present invention relates to preparations (I) comprising a beta-amyloid peptide variant or beta-amyloid N-terminal fragment, or N-terminal amyloid precursor protein (APP) soluble fragment or C-terminal fragment. The beta-amyloid or APP preparations are useful for manufacturing a prophylactic vaccine or a therapeutic, or as a prophylactic vaccine for the prevention, or as a therapeutic for the treatment of a disease associated with beta-amyloid formation and/or aggregation, such as Alzheimer's disease.

XX SQ Sequence 13 AA;

Query Match 88.2%; Score 30; DB 8; Length 13;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFFA 7
Db 7 QKLVFFA 13
:|||||

RESULT 66

ADA89887
ID ADA89887 standard; peptide; 14 AA.

AC ADA89887;

XX 20-NOV-2003 (first entry)

XX Beta-A4 second region peptide SEQ ID NO:2.

XX antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; nontropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation, dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; neuronal disorder; aging.

XX Synthetic.

OS Homo sapiens.

XX WO2003070760-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-EP001759.

XX 20-FEB-2002; 2002EP-00003844.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX (MORP-) MORPHOSYS AG.

XX Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretzschmar T; Loehning C, Loetscher H, Nordstedt C, Rothe C;

XX WPI; 2003-663848/62.

XX New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation (e.g. dementia).

XX Claim 1; Page 99; 312pp; English.

CC The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule

CC encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (1), comprising culturing the host cell of (3) under conditions that allow synthesis of (1) and recovering (1) from the culture; (5) a composition comprising (1) or an antibody molecule produced by method (4); (6) a kit comprising (1), nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising (1); (8) testing the resulting Fab optimisation library by panning against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing of selected, optimised clones; (11) preparing a pharmaceutical composition, comprising optimisation of (1), and formulating the optimised antibody/antibody molecule with a carrier; and (12) a pharmaceutical composition prepared by method (8). (1) has neuroprotective, nontropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (I), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the disintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 14 AA;

Query Match 88.2%; Score 30; DB 6; Length 14;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFFA 7
Db 4 QKLVFFA 10
:|||||

RESULT 67

ADJ71452
ID ADJ71452 standard; peptide; 14 AA.

AC ADJ71452;

XX 06-MAY-2004 (first entry)

XX N-terminal truncated beta-amyloid peptide, SEQ ID 115.

XX Nontropic; Neuroprotective; Vaccine; beta Amyloid; amyloid precursor protein; APP; Alzheimer's disease.

XX Homo sapiens.

XX WO2004013172-A2.

XX 12-FEB-2004.

XX 18-JUL-2003; 2003WO-EP007833.

XX 24-JUL-2002; 2002EP-00447147.

XX 06-AUG-2002; 2002US-0401497P.

XX (INNO-) INNOGENETICS NV.

XX Delacourte A, Sergeant N;

XX WPI; 2004-180423/17.

XX New beta-amyloid or amyloid precursor protein preparation, useful as a prophylactic vaccine or a therapeutic for preventing or treating a disease associated with beta-amyloid formation and/or aggregation, e.g. Alzheimer's disease.

```

PS Claim 4; Page 63; 104pp; English.
XX
CC The present invention relates to preparations (I) comprising a beta-
CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
CC fragment. The beta-amyloid or APP preparations are useful for
CC manufacturing a prophylactic vaccine or a therapeutic, or as a
CC prophylactic vaccine for the prevention, or as a therapeutic for the
CC treatment of a disease associated with beta-amyloid formation and/or
CC aggregation, such as Alzheimer's disease.
XX
SQ Sequence 14 AA;

Query Match      88.2%; Score 30; DB 8; Length 14;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7
   :|||||
Db 7 QKLVEFFA 13

RESULT 69
ADJ71478
ID ADJ71478 standard; peptide; 14 AA.
XX
AC ADJ71478;
XX
DT 06-MAY-2004 (first entry)
XX
DE N-terminal truncated beta-amyloid peptide, SEQ ID 141.
XX
KW Nootropic; Neuroprotective; Vaccine; beta Amyloid;
KW amyloid precursor protein; APP; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO2004013172-A2.
XX
PD 12-FEB-2004.
XX
PF 18-JUL-2003; 2003WO-EP007833.
XX
PR 24-JUL-2002; 2002EP-00447147.
PR 06-AUG-2002; 2002US-0401497P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Delacourte A, Sergeant N;
XX
DR WPI; 2004-180423/17.
XX
PT New beta-amyloid or amyloid precursor protein preparation, useful as a
PT prophylactic vaccine or a therapeutic for preventing or treating a
PT disease associated with beta-amyloid formation and/or aggregation, e.g.
PT Alzheimer's disease.
XX
PS Claim 4; Page 64; 104pp; English.
XX
CC The present invention relates to preparations (I) comprising a beta-
CC amyloid peptide variant or beta-amyloid N-terminal fragment, or N-
CC terminal amyloid precursor protein (APP) soluble fragment or C-terminal
CC fragment. The beta-amyloid or APP preparations are useful for
CC manufacturing a prophylactic vaccine or a therapeutic, or as a
CC prophylactic vaccine for the prevention, or as a therapeutic for the
CC treatment of a disease associated with beta-amyloid formation and/or
CC aggregation, such as Alzheimer's disease.
XX
SQ Sequence 14 AA;

Query Match      88.2%; Score 30; DB 8; Length 14;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7
   :|||||
Db 6 QKLVEFFA 12

RESULT 70
ADZ08889
ID ADZ08889 standard; peptide; 14 AA.
XX
AC ADZ08889;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human beta-amyloid peptide (SEQ ID No:114) probed with anti-amyloid IgG.
XX

```

KW	amyloid; antibody engineering; antibody production;
KW	amyloid-associated disorder; Alzheimers disease; cancer; allergy;
KW	autoimmune disease; Parkinsons disease;
KW	acquired immune deficiency syndrome; multiple sclerosis; migraine;
KW	dementia; infection; nootropic; neuroprotective; cytosatic;
KW	antiallergic; immunosuppressive; antiparkinsonian; antimigraine;
KW	antimicrobial; anti-Hiv; beta-amyloid.
XX	
OS	Homo sapiens.
XX	
WO	2005028511-A2.
PN	
XX	
PD	31-MAR-2005.
XX	
XX	26-MAR-2004; 2004WO-US009522.
XX	
PR	28-MAR-2003; 2003US-0458469P.
PR	28-MAR-2003; 2003US-0458474P.
PR	28-MAR-2003; 2003US-0458509P.
PR	28-MAR-2003; 2003US-0458510P.
XX	
XX	(CENZ) CENTOCOR INC.
PA	(MERC/) MERCKEN M.
PA	(BENS/) BENSON J M.
XX	
PI	Mercken M, Benson JM;
DR	WPI; 2005-242565/25.
XX	
PT	New isolated mammalian anti-amyloid antibodies useful for treating
PT	amyloid-associated disorders, such as Alzheimer's disease, cancer,
PT	allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,
PT	migraine and dementia.
XX	
PS	Example 4; SEQ ID NO 114; 306pp; English.
XX	
CC	The invention relates to at least one isolated mammalian amyloid antibody
CC	comprising at least one variable region comprising at least one heavy
CC	chain and at least one light chain, of a fully defined sequence of SEQ ID
CC	NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are:
CC	(i) at least one isolated mammalian amyloid antibody that binds to the
CC	same region of an amyloid polypeptide as an antibody comprising at least
CC	one heavy chain or light chain complementarity determining region (CDR)
CC	having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii)
CC	at least one isolated mammalian amyloid antibody, comprising at least one
CC	human CDR, where the antibody specifically binds at least one epitope
CC	selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined
CC	sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic
CC	acid encoding at least one of any of the isolated mammalian amyloid
CC	antibodies mentioned and having at least one human CDR of a fully defined
CC	sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an
CC	isolated nucleic acid vector comprising an isolated nucleic acid encoding
CC	an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising
CC	an isolated nucleic acid encoding an amyloid antibody, (vi) a method of
CC	producing at least one amyloid antibody, (vii) a composition comprising
CC	at least one of any of the isolated mammalian amyloid antibodies
CC	mentioned, and at least one pharmaceutical carrier or diluent, (viii) an
CC	anti-idiotypic antibody or fragment that specifically binds at least one
CC	of the amyloid antibodies mentioned, (ix) a method of diagnosing or
CC	treating an amyloid related condition in a cell, tissue, organ or animal,
CC	comprising contacting or administering a composition comprising at least
CC	one of the antibodies mentioned, with, or to, the cell, tissue, organ or
CC	animal, (x) a medical device comprising at least one amyloid antibody
CC	mentioned, where the device is suitable for contacting or administering
CC	at least one amyloid antibody, (xi) an article of manufacture for human
CC	pharmaceutical or diagnostic use, comprising packaging material and a
CC	container comprising a solution or a lyophilized form of at least one of
CC	the amyloid antibodies mentioned, and (xii) a method of producing at
CC	least one of the isolated mammalian amyloid antibodies, comprising
CC	providing a host cell or transgenic animal or transgenic plant or plant
CC	cell capable of expressing the antibody in recoverable amounts. The
CC	methods and compositions of the present invention are useful for
CC	producing therapeutic compositions and devices for treating amyloid-

CC associated disorders, such as Alzheimer's disease, cancer, allergies,
CC autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis,
CC migraine, dementia and infections. This sequence represents a peptide
CC from human beta-amyloid probed with anti-beta-amyloid IgG antibodies.
XX

Sequence 14 AA;
Query Match 88.2%; Score 30; DB 9; Length 14;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 KKLVEFA 7
DB 5 QKLVEFA 11

RESULT 71
AAW89358
ID AAW89358 standard; peptide; 15 AA.
XX
XX AAW89358;
XX
XX
DT 02-MAR-1999 (first entry)
XX
XX Beta-amyloid peptide derivative A-beta-11-25.
XX
XX Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
XX aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW familial amyloid polynuropathy; bovine spongiform encephalopathy;
KW Creutzfeldt-Jakob disease; bap.
XX
XX
OS Homo sapiens.
OS Synthetic.
XX
XX US5854204-A.
XX
XX 29-DEC-1998.
XX
XX
XX 14-MAR-1996; 96US-00612785.
XX
XX 14-MAR-1995; 95US-00404831.
PR 07-JUN-1995; 95US-00475579.
PR 27-OCT-1995; 95US-00548998.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX
XX Hundal A, Gefter ML, Kaaman L, Musso G, Molineaux S, Benjamin H;
PI Findels MB, Chin J, Lee J, Kelley M, Reed M, Wakefield J;
PI Garnick W, Kubasek W, Signer ER;
XX
XX WPI; 1999-094964/08.
XX
XX
XX New peptide(s) derived from beta-amyloid peptide that inhibit amyloid
PT aggregation - and neurotoxicity, specifically for treatment and
PT prevention of Alzheimer's disease.
XX
XX
XX Claim 6; Col 81-82; 52pp; English.
XX
XX The present invention describes beta-amyloid peptide (bap) derivatives.
XX The bap derivatives inhibit aggregation of amyloidogenic proteins and
XX peptides, specifically bap, and their neurotoxicity, so are useful for
XX treating and preventing any disease involving amyloidosis, specifically
XX Alzheimer's disease but also Down's syndrome, familial amyloid
XX polynuropathy or cardiomyopathy. bovine spongiform encephalopathy and
XX Creutzfeldt-Jakob disease. The bap derivatives are also used to diagnose
XX these diseases, in vitro or in vivo, by detecting binding of bap to
XX labelled bap derivatives. Some bap derivatives inhibit bap aggregation
XX even when bap is present in molar excess. The present sequence represents
XX a bap derivative
XX
XX Sequence 15 AA;
Query Match 88.2%; Score 30; DB 2; Length 15;

Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 5 QKLVPFA 11

RESULT 72
ABU79064
ID ABU79064 standard; peptide; 15 AA.
XX
AC ABU79064;

17-JUN-2003 (first entry)

Aggregation blocking peptide #16.

KW Amyloid formation; amyloid-like deposit; Alzheimer's disease;
KW pathological beta-sheet-rich conformation; Down's syndrome;
KW amyloidosis disorder; human prion disease; kuru; CJD;
KW Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; GSS;
KW prion associated human neurodegenerative disease; animal prion disease;
KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;
KW chronic wasting disease.

Unidentified.

US6462171-B1.

08-OCT-2002.

12-DEC-1996; 96US-00766596.

07-JUN-1995; 95US-00478326.

10-APR-1996; 96US-00630645.

(UUNY) UNIV NEW YORK STATE.

Soto-Jara C, Baumann MH, Frangione B;

WPI; 2003-379012/36.

Novel inhibitory peptides which inhibit and structurally block abnormal
PT folding of protein into amyloid or amyloid-like deposit and into
PT pathological beta-sheet rich conformation, useful for treating
PT Alzheimer's disease.

Disclosure; Col 51-52; 5lpp; English.

CC The invention describes an isolated inhibitory peptide (I) which
CC interacts with a hydrophobic beta-sheet forming cluster of amino acid
CC residues on a protein or peptide for amyloid or amyloid-like deposit
CC formation, and inhibits or structurally blocks the abnormal folding of
CC proteins and peptides into amyloid or amyloid-like deposits and into
CC pathological beta-sheet-rich conformation. (I) is useful for disorders or
CC diseases associated with abnormal protein folding into amyloid or amyloid
CC -like deposits or into pathological beta-sheet-rich precursors of such
CC deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis
CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease
CC (CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated
CC human neurodegenerative diseases as well as animal prion diseases such as
CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and
CC chronic wasting disease of mule deer and elk. (I) is also useful for
CC detecting and diagnosing the presence or absence of amyloid or amyloid-
CC like deposits in vivo and its precursors. This is the amino acid sequence
CC of peptide associated with the inhibition of amyloid or amyloid like
CC deposits

Sequence 15 AA;

Query Match 88.2%; Score 30; DB 6; Length 15;
Best Local Similarity 85.7%; Pred. No. 19;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 4 QKLVPFA 10

RESULT 73
ABU79059
ID ABU79059 standard; peptide; 15 AA.
XX
AC ABU79059;

17-JUN-2003 (first entry)

Aggregation blocking peptide #11.

KW Amyloid formation; amyloid-like deposit; Alzheimer's disease;
KW pathological beta-sheet-rich conformation; Down's syndrome;
KW amyloidosis disorder; human prion disease; kuru; CJD;
KW Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; GSS;
KW prion associated human neurodegenerative disease; animal prion disease;
KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;
KW chronic wasting disease.

Unidentified.

US6462171-B1.

08-OCT-2002.

12-DEC-1996; 96US-00766596.

07-JUN-1995; 95US-00478326.

10-APR-1996; 96US-00630645.

(UUNY) UNIV NEW YORK STATE.

Soto-Jara C, Baumann MH, Frangione B;

WPI; 2003-379012/36.

Novel inhibitory peptides which inhibit and structurally block abnormal
PT folding of protein into amyloid or amyloid-like deposit and into
PT pathological beta-sheet rich conformation, useful for treating
PT Alzheimer's disease.

Disclosure; Col 49-50; 5lpp; English.

CC The invention describes an isolated inhibitory peptide (I) which
CC interacts with a hydrophobic beta-sheet forming cluster of amino acid
CC residues on a protein or peptide for amyloid or amyloid-like deposit
CC formation, and inhibits or structurally blocks the abnormal folding of
CC proteins and peptides into amyloid or amyloid-like deposits and into
CC pathological beta-sheet-rich conformation. (I) is useful for disorders or
CC diseases associated with abnormal protein folding into amyloid or amyloid
CC -like deposits or into pathological beta-sheet-rich precursors of such
CC deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis
CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease
CC (CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated
CC human neurodegenerative diseases as well as animal prion diseases such as
CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and
CC chronic wasting disease of mule deer and elk. (I) is also useful for
CC detecting and diagnosing the presence or absence of amyloid or amyloid-
CC like deposits in vivo and its precursors. This is the amino acid sequence
CC of peptide associated with the inhibition of amyloid or amyloid like
CC deposits

Sequence 15 AA;

Query Match 88.2%; Score 30; DB 6; Length 15;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
Db :|||||
4 QKLVFPA 10

RESULT 74
ABU79060
ID ABU79060 standard; peptide; 15 AA.
XX
AC
XX ABU79060;
XX
DT 17-JUN-2003 (first entry)
XX
DE Aggregation blocking peptide #12.
XX
KW Amyloid formation; amyloid-like deposit; Alzheimer's disease;
KW pathological beta-sheet-rich conformation; Down's syndrome;
KW amyloidosis disorder; human prion disease; kuru; CJD;
KW Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; GSS;
KW prion associated human neurodegenerative disease; animal prion disease;
KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;
KW chronic wasting disease.
XX
OS Unidentified.
XX
PN US6462171-B1.
XX
PD 08-OCT-2002.
XX
PF 12-DEC-1996; 96US-00766596.
XX
PR 07-JUN-1995; 95US-00478326.
PR 10-APR-1996; 96US-00630645.
XX
PA (UWNY) UNIV NEW YORK STATE.
XX
PI Soto-Jara C, Baumann MH, Frangione B;
XX
DR WPI; 2003-379012/36.
XX
PT Novel inhibitory peptides which inhibit and structurally block abnormal
PT folding of protein into amyloid or amyloid-like deposit and into
PT pathological beta-sheet rich conformation, useful for treating
PT Alzheimer's disease.
XX
PS Disclosure; Col 51-52; 51pp; English.
XX
CC The invention describes an isolated inhibitory peptide (I) which
CC interacts with a hydrophobic beta-sheet forming cluster of amino acid
CC residues on a protein or peptide for amyloid or amyloid-like deposit
CC formation, and inhibits or structurally blocks the abnormal folding of
CC proteins and peptides into amyloid or amyloid-like deposits and into
CC pathological beta-sheet-rich conformation. (I) is useful for disorders or
CC diseases associated with abnormal protein folding into amyloid or amyloid
CC -like deposits or into pathological beta-sheet-rich precursors of such
CC deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis
CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease
CC (CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated
CC human neurodegenerative diseases as well as animal prion diseases such as
CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and
CC chronic wasting disease of mule deer and elk. (I) is also useful for
CC detecting and diagnosing the presence or absence of amyloid or amyloid-
CC like deposits in vivo and its precursors. This is the amino acid sequence
CC of peptide associated with the inhibition of amyloid or amyloid like
CC deposits
XX
SQ Sequence 15 AA;

Query Match 88.2%; Score 30; DB 6; Length 15;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
Db :|||||
4 QKLVFPA 10

RESULT 75
ABU79055
ID ABU79055 standard; peptide; 15 AA.
XX
AC ABU79055;
XX
DT 17-JUN-2003 (first entry)
XX
DE Aggregation blocking peptide #7.
XX
KW Amyloid formation; amyloid-like deposit; Alzheimer's disease;
KW pathological beta-sheet-rich conformation; Down's syndrome;
KW amyloidosis disorder; human prion disease; kuru; CJD;
KW Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; GSS;
KW prion associated human neurodegenerative disease; animal prion disease;
KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;
KW chronic wasting disease.
XX
OS Unidentified.
XX
PN US6462171-B1.
XX
PD 08-OCT-2002.
XX
PF 12-DEC-1996; 96US-00766596.
XX
PR 07-JUN-1995; 95US-00478326.
PR 10-APR-1996; 96US-00630645.
XX
PA (UWNY) UNIV NEW YORK STATE.
XX
PI Soto-Jara C, Baumann MH, Frangione B;
XX
DR WPI; 2003-379012/36.
XX
PT Novel inhibitory peptides which inhibit and structurally block abnormal
PT folding of protein into amyloid or amyloid-like deposit and into
PT pathological beta-sheet rich conformation, useful for treating
PT Alzheimer's disease.
XX
PS Disclosure; Col 49-50; 51pp; English.
XX
CC The invention describes an isolated inhibitory peptide (I) which
CC interacts with a hydrophobic beta-sheet forming cluster of amino acid
CC residues on a protein or peptide for amyloid or amyloid-like deposit
CC formation, and inhibits or structurally blocks the abnormal folding of
CC proteins and peptides into amyloid or amyloid-like deposits and into
CC pathological beta-sheet-rich conformation. (I) is useful for disorders or
CC diseases associated with abnormal protein folding into amyloid or amyloid
CC -like deposits or into pathological beta-sheet-rich precursors of such
CC deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis
CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease
CC (CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated
CC human neurodegenerative diseases as well as animal prion diseases such as
CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and
CC chronic wasting disease of mule deer and elk. (I) is also useful for
CC detecting and diagnosing the presence or absence of amyloid or amyloid-
CC like deposits in vivo and its precursors. This is the amino acid sequence
CC of peptide associated with the inhibition of amyloid or amyloid like
CC deposits
XX
SQ Sequence 15 AA;

Query Match 88.2%; Score 30; DB 6; Length 15;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7

Db :|||||
4 QXLVFFA 10

Search completed: December 29, 2005, 17:33:14
Job time : 99.4032 secs



GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 91.2258 Seconds
(without alignments)
54.137 Million cell updates/sec

Title: US-10-009-122-18

Perfect score: 34

Sequence: 1 KLVFFPAQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	962	2 QANTX2_9DEL	Qantk2 anaeromyxob
2	31	91.2	33	2 QUC33_HUMAN	Quc33 homo sapien
3	31	91.2	42	2 Q56J06_GRAGR	Q56j06 grampus gri
4	31	91.2	42	2 Q56J07_TURTR	Q56j07 turslops tr
5	31	91.2	42	2 Q7M088_CAVPO	Q7m088 cavia porce
6	31	91.2	51	2 Q72A51_DESVH	Q72a51 desulfovibr
7	31	91.2	52	2 Q8WZ99_HUMAN	Q8wz99 homo sapien
8	31	91.2	57	1 A4_UR5MA	Q29149 u alzheimer
9	31	91.2	58	1 A4_CANFA	Q28280 c alzheimer
10	31	91.2	58	1 A4_RABIT	Q28757 o alzheimer
11	31	91.2	58	1 A4_SHEEP	Q28053 b alzheimer
12	31	91.2	59	1 A4_BOVIN	Q35463 cricetus
13	31	91.2	79	2 Q54633_CRIGR	Q54633 chelydra se
14	31	91.2	113	2 Q8JH58_CHESE	Q8jh58 chelydra se
15	31	91.2	213	2 Q4ULC9_RICFE	Q4ulc9 rickettsia
16	31	91.2	218	2 Q8BPV5_MOUSE	Q8bpv5 mus musculu
17	31	91.2	357	2 Q8U118_BRARE	Q8u118 brachydanio
18	31	91.2	375	2 Q8SMFO_HORVU	Q8smfo hordeum vul
19	31	91.2	384	2 Q8BPC7_MOUSE	Q8bpc7 mus musculu
20	31	91.2	417	1 Q865A_DROME	P82982 drosophila
21	31	91.2	471	2 Q33YN7_ARATH	Q33yn7 arabidopsis
22	31	91.2	472	2 Q8UUSO_BRARE	Q8uus0 brachydanio
23	31	91.2	534	2 Q3296_CHICK	Q3296 gallus gall
24	31	91.2	569	2 Q3PVL1_CHICK	Q3pvl1 gallus gall
25	31	91.2	612	2 Q919E7_BRARE	Q919e7 brachydanio
26	31	91.2	678	2 Q7ZZT1_BRARE	Q7zzt1 brachydanio
27	31	91.2	693	2 Q98SG0_XENLA	Q98sg0 xenopus lae
28	31	91.2	695	2 Q5R477_PONPY	Q5r477 pongo pygma
29	31	91.2	695	2 Q5RH29_CANFA	Q5rh29 canis famil
30	31	91.2	695	2 Q56J03_CANFA	Q56j03 canis famil
31	31	91.2	695	2 Q6GR78_MOUSE	Q6gr78 mus musculu

32	31	91.2	695	2 Q9DGJ8_CHICK	Q9dgj8 gallus gall
33	31	91.2	714	2 Q56JK4_CANFA	Q56jk4 canis famil
34	31	91.2	733	2 Q6PQ05_RAT	Q6pq05 rattus norv
35	31	91.2	738	2 Q6NUZ1_BRARE	Q6nuz1 brachydanio
36	31	91.2	738	2 Q9OW28_BRARE	Q9ow28 brachydanio
37	31	91.2	745	2 Q7XZG7_ORYSA	Q7xzg7 oryza sativ
38	31	91.2	747	2 Q91963_9PIPI	Q91963 xenopus ap
39	31	91.2	749	2 Q56JK2_STSCO	Q56jk2 stenella co
40	31	91.2	749	2 Q6NRR1_XENLA	Q6nr1 xenopus lae
41	31	91.2	750	2 Q6DJB6_XENTR	Q6djb6 xenopus tro
42	31	91.2	751	1 A4_SAISC	Q95241 s amyloid b
43	31	91.2	751	2 Q6GSC0_HUMAN	Q6gsc0 homo sapien
44	31	91.2	751	2 Q6RH28_CANFA	Q6rh28 canis famil
45	31	91.2	751	2 Q56JK5_CANFA	Q56jk5 canis famil
46	31	91.2	751	2 Q4R4R8_MACEA	Q4r48 macaca fasc
47	31	91.2	751	2 Q9DGJ7_CHICK	Q9dgj7 gallus gall
48	31	91.2	754	1 CHLD_PEA	O22437 pisum sativ
49	31	91.2	754	2 Q6ATS0_ORYSA	Q6ats0 oryza sativ
50	31	91.2	754	2 Q4RY33_TETNG	Q4ry33 tetraodon n
51	31	91.2	758	1 CHLD_TOBAC	O24133 nicotiana t
52	31	91.2	759	1 CHLD_ARATH	Q98j1 arabidopsis
53	31	91.2	759	2 Q4S0J4_TETNG	Q4s0j4 tetraodon n
54	31	91.2	760	2 Q8VZU7_ARATH	Q8vzu7 arabidopsis
55	31	91.2	770	1 A4_CAVPO	Q60495 c amyloid b
56	31	91.2	770	1 A4_HUMAN	P05067 h amyloid b
57	31	91.2	770	1 A4_MACEA	P53601 m amyloid b
58	31	91.2	770	1 A4_MOUSE	P12023 m amyloid b
59	31	91.2	770	1 A4_PANTR	Q51880 s amyloid b
60	31	91.2	770	1 A4_PIG	P08592 r amyloid b
61	31	91.2	770	1 A4_RAT	Q6rh30 canis famil
62	31	91.2	770	2 Q6RH30_CANFA	Q56jk6 canis famil
63	31	91.2	770	2 Q53ZT3_MOUSE	Q53z3 mus musculu
64	31	91.2	770	2 Q547B7_RAT	Q547b7 rattus norv
65	31	91.2	780	1 A4_TETFL	Q73683 tetraodon f
66	31	91.2	780	2 Q87XV7_PSESM	Q87xv7 pseudomonas
67	30	88.2	355	2 Q4LMP3_9BURK	Q4lmp3 burkholderi
68	30	88.2	364	2 Q54L66_DICDI	Q54l66 dictyosteli
69	30	88.2	421	2 Q4N8N8_THEPA	Q4n8n8 theileria p
70	30	88.2	480	2 Q4UGZ4_THEAN	Q4ugz4 theileria a
71	30	88.2	557	2 Q728F0_DESVH	Q728f0 desulfovibr
72	29	85.3	66	2 Q6D3D0_ERWCT	Q6d3d0 erwinia car
73	29	85.3	81	2 Q8VOR5_ECOLI	Q8vgr5 escherichia
74	29	85.3	95	2 Q6GZK0_ECOLI	Q6gzk0 escherichia
75	29	85.3	97	1 YACC_ECOLI	P23838 escherichia
76	29	85.3	115	2 Q57T88_SALCH	Q57t88 salmonella
77	29	85.3	115	2 Q5PDA6_SALPA	Q5pda6 salmonella
78	29	85.3	115	2 Q7CR72_SALTY	Q7cr72 salmonella
79	29	85.3	115	2 Q8XGD8_SALTI	Q8xgd8 salmonella
80	29	85.3	115	2 Q7UPR1_RHOBA	Q7upr1 rhodospirell
81	29	85.3	137	2 Q9STZ9_ARATH	Q9stz9 arabidopsis
82	29	85.3	152	2 Q7UDR8_SHIFL	Q7udr8 shigella fl
83	29	85.3	156	2 Q8X949_ECOS7	Q8x949 escherichia
84	29	85.3	156	2 Q83SM3_SHIFL	Q83sm3 shigella fl
85	29	85.3	172	2 Q8VY56_ARATH	Q8vy56 arabidopsis
86	29	85.3	229	2 Q9SV79_ARATH	Q9sv79 arabidopsis
87	29	85.3	231	2 Q9XGY6_SIMCH	Q9xgy6 simmondsia
88	29	85.3	352	2 Q8U460_PYRFU	Q8u460 pyrococcus
89	29	85.3	357	2 Q4WJL8_ASPFU	Q4wj18 aspergillus
90	29	85.3	358	2 Q8PPL1_XANAC	Q8ppl1 xanthomonas
91	29	85.3	366	2 Q4NSU7_THEPA	Q4nsu7 theileria p
92	29	85.3	391	2 Q5L117_GEOKA	Q5l117 geobacillus
93	29	85.3	403	2 Q4UY55_XANCP	Q4uy55 xanthomonas
94	29	85.3	404	2 Q8P597_XANCP	Q8p597 xanthomonas
95	29	85.3	428	2 Q9MIQ8_ARATH	Q9miq8 arabidopsis
96	29	85.3	428	2 Q89329_9POTV	Q89329 zucchini ye
97	29	85.3	461	2 Q7T910_9POTV	Q7t910 zucchini ye
98	29	85.3	470	2 Q6C854_YARLI	Q6c854 yarrowia li
99	29	85.3	485	2 Q8NQ52_CORGL	Q8nq52 corynebacte
100	29	85.3	485	2 Q52NV6_9POTV	Q52nv6 zucchini ye
101	29	85.3	488	2 Q7T911_9POTV	Q7t911 zucchini ye
102	29	85.3	490	2 Q7T912_9POTV	Q7t912 zucchini ye
103	29	85.3	490	2 Q5K4D4_9POTV	Q5k4d4 soybean mos
104	29	85.3	493		

105	29	85.3	493	2	Q5K4D5_9POTV	Q5k4d5 soybean mos	178	28	82.4	685	2	Q5A951_CANAL	Q5a951 candida alb
106	29	85.3	505	2	Q6M5A9_CORGL	Q6m5a9 corynebacte	179	28	82.4	690	2	Q83IB2_TROW8	Q83ib2 tropheryma
107	29	85.3	508	2	Q5GV55_XANOR	Q5gv55 xanthomonas	180	28	82.4	691	2	Q9H7V0_HUMAN	Q9h7v0 homo sapien
108	29	85.3	512	1	CADC_ECOLI	P23g90 escherichia	181	28	82.4	691	2	Q5R745_PONPY	Q5r745 pongo pygma
109	29	85.3	512	2	Q8VR66_ECOLI	Q8vr66 escherichia	182	28	82.4	698	2	Q83GW3_TROWT	Q83gw3 tropheryma
110	29	85.3	512	2	Q8FAT2_ECOL6	Q8fat2 escherichia	183	28	82.4	699	2	Q7L1C9_HUMAN	Q7l1c9 homo sapien
111	29	85.3	512	2	Q8XDS2_ECO57	Q8xds2 escherichia	184	28	82.4	746	2	Q8NDA0_HUMAN	Q8nda0 homo sapien
112	29	85.3	513	2	Q8ZMP6_SALTY	Q8zmp6 salmonella	185	28	82.4	771	2	Q4WPG0_ASFFU	Q4wpg0 aspergillus
113	29	85.3	570	2	Q4FTR5_9GAMM	Q4ftr5 psychobact	186	28	82.4	881	2	Q6BM22_DBBHA	Q6bm22 debaryomyce
114	29	85.3	615	2	Q50285_ENTHI	Q50z85 entamoeba h	187	28	82.4	946	2	Q8WY25_HUMAN	Q8wy25 homo sapien
115	29	85.3	623	2	Q9VEB8_DROME	Q9vzb8 drosophila	188	28	82.4	957	2	Q7T3T7_OREMO	Q7t3t7 oreochromis
116	29	85.3	638	2	Q5BZV4_EMENI	Q5bzv4 aspergillus	189	28	82.4	971	2	Q9VECS_DROME	Q9vecs drosophila
117	29	85.3	663	2	Q5BCB9_ASERGILL	Q5bcb9 aspergillus	190	28	82.4	1035	2	Q5T224_HUMAN	Q5t224 homo sapien
118	29	85.3	695	2	Q98SF9_XENLA	Q98sf9 xenopus lae	191	28	82.4	1049	2	Q81ZA0_HUMAN	Q81za0 homo sapien
119	29	85.3	695	2	Q7XQ00_XENLA	Q7xq00 xenopus lae	192	28	82.4	1049	2	Q6PJJ7_HUMAN	Q6pjj7 homo sapien
120	29	85.3	737	1	A4_FURFU	Q93z79 fugu rubrip	193	28	82.4	1049	2	Q5RFR6_PONPY	Q5rfr6 pongo pygma
121	29	85.3	776	2	Q9SH68_ARATH	Q9sh68 arabidopsis	194	28	82.4	1058	2	Q5T225_HUMAN	Q5t225 homo sapien
122	29	85.3	851	2	Q6C4R4_YARLI	Q6c4r4 yarrowia li	195	28	82.4	1080	2	Q8DT75_STRMU	Q8dt75 streptococc
123	29	85.3	955	2	Q8ORZ2_VIPOTV	Q8orz2 calla lily	196	28	82.4	1215	2	Q6L2N7_PICTO	Q6l2n7 pictophilus
124	29	85.3	1016	2	Q05912_9POTV	Q05912 zucchini ye	197	28	82.4	1676	2	Q8A6R7_BACTN	Q8a6r7 bacteroides
125	29	85.3	1056	2	Q6FKH6_CANGA	Q6fkh6 candida gla	198	28	79.4	15	2	Q9TWFS_9CRUS	Q9twfs artemia (br
126	29	85.3	1916	2	Q8OKU4_9POTV	Q8oku4 zucchini ye	199	27	79.4	46	2	Q8EXM4_LEPIN	Q8exm4 leptospira
127	29	85.3	3080	1	POLG_ZTWC	P18479 z genome po	200	27	79.4	91	2	Q5TT27_ANOGA	Q5tt27 anopheles g
128	29	85.3	3080	2	Q6WN47_9POTV	Q6wn47 zucchini ye	201	27	79.4	118	2	Q58M43_9CAUD	Q58m43 cyanophage
129	29	85.3	3080	2	Q6WN48_9POTV	Q6wn48 zucchini ye	202	27	79.4	132	2	Q4YR43_PLABE	Q4yr43 plasmodium
130	29	85.3	3080	2	Q6WN49_9POTV	Q6wn49 zucchini ye	203	27	79.4	164	2	Q73N39_TREDE	Q73n39 treponema d
131	29	85.3	3080	2	Q6Y2U7_9POTV	Q6y2u7 zucchini ye	204	27	79.4	165	2	Q6APD6_DSPPS	Q6apd6 desulfotale
132	29	85.3	3080	2	Q7T908_9POTV	Q7t908 zucchini ye	205	27	79.4	175	2	Q4UGG7_THEAN	Q4ugg7 theileria a
133	29	85.3	3080	2	Q7T914_9POTV	Q7t914 zucchini ye	206	27	79.4	175	2	Q4N989_THEPA	Q4n989 theileria p
134	29	85.3	3083	1	POLG_ZTWS	Q36979 z genome po	207	27	79.4	177	2	Q81JC9_PLAF7	Q81jc9 plasmodium
135	29	85.3	3105	2	Q70XR2_9POTV	Q70xr2 soybean mos	208	27	79.4	177	2	Q4YCB6_PLABE	Q4ycb6 plasmodium
136	28	82.4	22	2	Q5C064_SCHJA	Q5c064 schistosoma	209	27	79.4	182	2	Q4XDG5_PLACH	Q4xdg5 plasmodium
137	28	82.4	49	2	Q4XA79_PLACH	Q4xp83 plasmodium	210	27	79.4	185	2	Q92588_STRCO	Q92588 streptomyce
138	28	82.4	57	2	Q4XP83_PLACH	P30748 escherichia	211	27	79.4	193	2	Q89NA0_BRAJA	Q89na0 bradyrhizob
139	28	82.4	81	1	MOAD_ECOLI	Q9app7 uncultured	212	27	79.4	214	2	Q7RCA7_PLAYO	Q7rca7 plasmodium
140	28	82.4	81	2	Q9APP7_9BACT	Q9app7 uncultured	213	27	79.4	214	2	Q9LZY2_ARATH	Q9lzy2 arabidopsis
141	28	82.4	81	2	Q5TRF2_SALCH	Q5trf2 salmonella	214	27	79.4	223	2	Q7P7S8_FUSNN	Q7p7s8 fusobacteri
142	28	82.4	81	2	Q65TTO_MANSM	Q65tto manheimia	215	27	79.4	223	2	Q8RDM7_FUSNN	Q8rdm7 fusobacteri
143	28	82.4	81	2	Q7N6P4_PHOLL	Q7n6p4 photorhabdu	216	27	79.4	247	2	Q4V236_PLACH	Q4v236 plasmodium
144	28	82.4	81	2	Q8DB97_VIBU	Q8db97 vibrio vuln	217	27	79.4	257	2	Q72V35_LEPIC	Q72v35 leptospira
145	28	82.4	81	2	Q9KT78_VIECH	Q9kt78 vibrio chol	218	27	79.4	257	2	Q8EZT1_LEPIN	Q8ezt1 leptospira
146	28	82.4	81	2	Q8S3S8_SHIFL	Q8s3s8 shigella fl	219	27	79.4	272	2	Q54BA3_DICDI	Q54ba3 dictyostell
147	28	82.4	81	2	Q7MM72_VIBVY	Q7mm72 vibrio vuln	220	27	79.4	276	2	Q962V2_TRISP	Q962v2 trichinella
148	28	82.4	81	2	Q8X807_ECO57	Q8x807 escherichia	221	27	79.4	296	2	Q8XRDB_RALSO	Q8xrd8 ralstonia s
149	28	82.4	83	2	Q8ZQO0_SALTY	Q8zqg0 salmonella	222	27	79.4	300	2	Q9XU61_CAEBL	Q9xu61 caenorhabdi
150	28	82.4	85	2	Q87MY3_VIBPA	Q87my3 vibrio para	223	27	79.4	314	2	Q9Z2H7_MOUSE	Q9z2h7 m semaf cyt
151	28	82.4	105	2	Q64CV5_9ARCH	Q64cv5 uncultured	224	27	79.4	315	2	Q74N48_NANEQ	Q74n48 nanorarchaeu
152	28	82.4	132	2	Q7VL67_HAEDU	Q7vl67 haemophilus	225	27	79.4	316	1	TRUB_PHOPR	Q6luj0 photobacter
153	28	82.4	182	2	Q835H4_ENTFA	Q835h4 enterococcu	226	27	79.4	329	1	EBAA3_FLAME	P36913 flavobacter
154	28	82.4	223	2	Q89219_CLOTE	Q89219 clostridium	227	27	79.4	330	1	SYW_DEIRA	Q9twv7 deinococcus
155	28	82.4	270	2	Q7MW75_PORGI	Q7mw75 porphyromon	228	27	79.4	331	2	Q6BMW6_DBBHA	Q6bmw6 debaryomyce
156	28	82.4	276	2	Q4XE69_PLACH	Q4xe69 plasmodium	229	27	79.4	341	1	Y665_METJA	Q58079 methanococc
157	28	82.4	279	2	Q4YWA7_PLABE	Q4ywa7 plasmodium	230	27	79.4	342	2	Q86QF4_TRISP	Q86qp4 trichinella
158	28	82.4	284	2	Q4XAZ2_PERSY	Q4xaz2 pseudomonas	231	27	79.4	349	2	Q9XU59_CAEBL	Q9xu59 caenorhabdi
159	28	82.4	306	2	Q9AZG0_9CAUD	Q9azg0 bacterioph	232	27	79.4	350	2	Q552M0_DICDI	Q552m0 dictyostell
160	28	82.4	306	2	Q9CEB2_LACIA	Q9ceb2 lactococcus	233	27	79.4	364	2	Q93CU7_SHIBO	Q93cu7 shigella bo
161	28	82.4	321	1	Y189_RICPR	Q9zdx5 rickettsia	234	27	79.4	387	2	Q81FH5_BACCR	Q81fh5 bacillus ce
162	28	82.4	336	2	Q94155_ORYSA	Q94155 oryza sativ	235	27	79.4	399	2	Q5WPU9_LUTLO	Q5wpu9 lutzonvial
163	28	82.4	346	2	Q9SYB5_ARATH	Q9syb5 arabidopsis	236	27	79.4	410	2	Q8L2B4_PICTO	Q8l2b4 picophilus
164	28	82.4	353	2	Q961C3_HUMAN	Q961c3 homo sapien	237	27	79.4	421	2	Q6G1K7_BARHE	Q6g1k7 bartonella
165	28	82.4	357	2	Q4R803_MACFA	Q4r803 macaca fasc	238	27	79.4	432	2	Q5U3S9_BRARE	Q5u3s9 brachydanio
166	28	82.4	439	2	Q7SFH1_NEUCR	Q7sfh1 neurospora	239	27	79.4	436	2	Q4YRG0_PLABE	Q4yrg0 plasmodium
167	28	82.4	449	2	Q6NKH0_CORDI	Q6nkh0 corynebacte	240	27	79.4	437	1	DNAA_MYCKA	P35888 mycoplasma
168	28	82.4	450	2	Q5WFB7_BACSK	Q5wfb7 bacillus cl	241	27	79.4	437	2	Q5KUT3_GROKA	Q5kut3 geobacillus
169	28	82.4	473	1	CYSG_BUCAL	P57500 b siroheme	242	27	79.4	450	2	Q4TRF8_9SPHN	Q4trf8 erythrobaet
170	28	82.4	479	2	Q9QDL5_9POTV	Q9qdl5 sarcophilus	243	27	79.4	456	2	Q6GVJ4_9BURK	Q6gvj4 burkholderi
171	28	82.4	479	2	Q4F979_9POTV	Q4f979 eustrephus	244	27	79.4	464	2	Q4S4T5_TETNG	Q4s4t5 tetraodon n
172	28	82.4	491	2	Q8N2B3_HUMAN	Q8n2b3 homo sapien	245	27	79.4	470	2	Q8EUD7_WCPSE	Q8eud7 mycoplasma
173	28	82.4	583	2	Q9XZ66_CAEBL	Q9xz66 caenorhabdi	246	27	79.4	477	2	Q817Z9_CRAGI	Q817z9 crassostrea
174	28	82.4	639	2	Q96JJO_HUMAN	Q96jj0 homo sapien	247	27	79.4	496	2	Q5K4D0_9POTV	Q5k4d0 daheen mos
175	28	82.4	651	2	Q9PYV4_GVXN	Q9pyv4 xestia c-ni	248	27	79.4	498	2	Q5NX24_AZOSE	Q5nx24 azoarcus sp
176	28	82.4	681	2	Q5WLL8_BACSK	Q5wll8 bacillus cl	249	27	79.4	498	2	Q5NWB1_AZOSE	Q5nwb1 azoarcus sp
177	28	82.4	685	1	MDU1_CANAL	P97998 candida alb	250	27	79.4	517	1	SEST_CAEBL	Q9n4d6 caenorhabdi

251 27 79.4 531 2 065536 ARATH
 252 27 79.4 532 2 Q9PTB2 ICTPU
 253 27 79.4 571 2 Q97KU8 CLOAB
 254 27 79.4 606 2 Q91VU5 MOUSE
 255 27 79.4 624 2 05E684 VIBF1
 256 27 79.4 627 2 057E48 BRUAB
 257 27 79.4 627 2 08G1M1 BRUSU
 258 27 79.4 646 2 08YGA2 BRUCELLA
 259 27 79.4 663 2 Q6RUU2 MUSCULU
 260 27 79.4 667 2 05B3H6 EMENI
 261 27 79.4 667 2 04U8H8 THEAN
 262 27 79.4 679 2 04WXW0 ASPFU
 263 27 79.4 685 2 05AGS1 DICDI
 264 27 79.4 711 2 Q99YJ3 STRPY
 265 27 79.4 711 2 Q8K670 STRF3
 266 27 79.4 721 2 06AG25 LEIIX
 267 27 79.4 729 2 05XAK5 STRP6
 268 27 79.4 729 2 08NZK4 STRP8
 269 27 79.4 741 2 05NHQ1 FRATT
 270 27 79.4 808 2 Q8DK23 SYNEL
 271 27 79.4 810 2 059JZ3 CANAL
 272 27 79.4 810 2 05ABW6 CANAL
 273 27 79.4 810 2 05AC87 CANAL
 274 27 79.4 810 2 09P852 CANAL
 275 27 79.4 811 2 05A8N0 CANAL
 276 27 79.4 811 2 05AC07 CANAL
 277 27 79.4 811 2 05ACC8 CANAL
 278 27 79.4 819 2 04JCD0 SULAC
 279 27 79.4 821 2 06ZRO2 HUMAN
 280 27 79.4 933 2 06ZU08 HUMAN
 281 27 79.4 1013 2 Q6BNQ9 DEBHA
 282 27 79.4 1054 2 067430 AQUAE
 283 27 79.4 1105 2 Q9VX31 DROME
 284 27 79.4 1179 2 015206 HUMAN
 285 27 79.4 1191 2 0756U3 ASHGO
 286 27 79.4 1265 2 06Z091 MOUSE
 287 27 79.4 1273 2 09UFH2 HUMAN
 288 27 79.4 1412 2 Q5F3M1 CHICK
 289 27 79.4 1492 2 Q83Y21 FEWBP
 290 27 79.4 1566 2 07RIX3 PLAYO
 291 27 79.4 1661 2 069223 MOUSE
 292 27 79.4 1775 2 06CT24 KLULA
 293 27 79.4 2584 2 Q65Z23 MONAN
 294 27 79.4 4488 2 09QZ81 MOUSE
 295 27 79.4 4511 2 07PXX5 ANOGE
 296 26 76.5 40 2 087MN1 VIBPA
 297 26 76.5 41 2 04YAX8 PLABE
 298 26 76.5 61 2 Q4XX51 FLACH
 299 26 76.5 70 2 Q6HN03 BACHK
 300 26 76.5 75 2 Q81UQ0 BACAN

ALIGNMENTS

RESULT 1
 Q4NTK2_9DELTA PRELIMINARY; PRT; 962 AA.
 ID Q4NTK2_9DELTA PRELIMINARY; PRT; 962 AA.
 AC Q4NTK2_9DELTA PRELIMINARY; PRT; 962 AA.
 DT 13-SEP-2005 (TREMELREL. 31, Created)
 DT 13-SEP-2005 (TREMELREL. 31, Last sequence update)
 DT 13-SEP-2005 (TREMELREL. 31, Last annotation update)
 DE Pyruvate, phosphate dikinase (BC 2.7.9.1).
 GN ORFNames=AdhDRAFT_2040;
 OS Anaeromyxobacter dehalogenans 2CP-C.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
 CC Cytophactineae; Myxococcaceae; Anaeromyxobacter.
 OX NCBI_TaxID=290397;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=2CP-C;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,

RA Hammon N., Israeli S., Pitluck S., Richardson P.;
 RT "Sequencing of the draft genome assembly of Anaeromyxobacter
 RT dehalogenans 2CP-C.";
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=2CP-C;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Anaeromyxobacter
 RT dehalogenans 2CP-C.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AAHD01000017; EAL78925.1; -; Genomic_DNA.
 DR Kinase; Pyruvate; Transferase.
 KW KINASE; PYRUVATE; TRANSFERASE.
 SQ SEQUENCE 962 AA; 104247 MW; CP843895DC5C3790 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 962;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
 Db 420 KLVFFPAQ 426

RESULT 2

Q9UC33_HUMAN PRELIMINARY; PRT; 33 AA.
 ID Q9UC33_HUMAN PRELIMINARY; PRT; 33 AA.
 AC Q9UC33;
 DT 01-MAY-2000 (TREMELREL. 13, Created)
 DT 01-MAY-2000 (TREMELREL. 13, Last sequence update)
 DT 01-MAY-2004 (TREMELREL. 26, Last annotation update)
 DE Beta-amyloid peptide (Fragment).
 DE Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RL MEDLINE=93024877; PubMed=1406936; DOI=10.1038/359325a0;
 RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
 RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
 RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
 RT biological fluids";
 RL Nature 359:325-327(1992).
 DR HSSP; Q16019; 1BA4.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR SEQUENCE 33 AA; 3674 MW; BIDEFE2F4167ABD0 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 33;
 Best Local Similarity 85.7%; Pred. No. 9.7;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFPAQ 7
 Db 16 KLVFFPAE 22

RESULT 3

Q56JG6 GRAGR
 ID Q56JG6 GRAGR PRELIMINARY; PRT; 42 AA.
 AC Q56JG6;
 DT 10-MAY-2005 (TREMELREL. 30, Created)
 DT 10-MAY-2005 (TREMELREL. 30, Last sequence update)
 DT 10-MAY-2005 (TREMELREL. 30, Last annotation update)

```

DE Amyloid beta protein (Fragment).
OS Grampus griseus (Risso's dolphin).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Grampus.
OX NCBI_TaxID=83653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY926589; AAX81918.1; -; mRNA.
RL NON_TER 1
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match          91.2%; Score 31; DB 2; Length 42;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 16 KLVFFAE 22

RESULT 4
ID Q56JJ7 TURTR PRELIMINARY; PRT; 42 AA.
AC Q56JJ7;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Tursiops truncatus (Atlantic bottlenose dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Tursiops.
OX NCBI_TaxID=9739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY926588; AAX81917.1; -; mRNA.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match          91.2%; Score 31; DB 2; Length 42;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 16 KLVFFAE 22

RESULT 5
ID Q7M088 CAVPO PRELIMINARY; PRT; 42 AA.
AC Q7M088;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid protein (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93290653; PubMed=7685598;

```

```

RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,
RA Kamiya H., Ohno M.;
RT "Receptor-mediated specific biological activity of a beta-amyloid
RT protein fragment for NK-1 substance p receptors.";
RL Biochem. Biophys. Res. Commun. 193:624-630(1993).
DR PIR; P0512; P0512.
DR HSP; Q16019; 11YT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match          91.2%; Score 31; DB 2; Length 42;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 16 KLVFFAE 22

RESULT 6
ID Q72A51 DESVH PRELIMINARY; PRT; 51 AA.
AC Q72A51;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=DVU2146;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS 8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15077118; DOI=10.1038/nbt959;
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Meche B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidson T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough.";
RL Nat. Biotechnol. 22:554-559(2004).
DR EMBL; AB017316; AAS96619.1; -; Genomic_DNA.
DR TIGR; DVU2146; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 51 AA; 6205 MW; E7F69C0D8432B7F5 CRC64;

Query Match          91.2%; Score 31; DB 2; Length 51;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 18 KLVFFAQ 24

RESULT 7
ID Q8WZ99 HUMAN PRELIMINARY; PRT; 52 AA.
AC Q8WZ99;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

```

```

DE Amyloid protein (Fragment).
GN Name=APP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15201367; DOI=10.1136/jnmp.2003.010611;
RA Wakutani Y., Watanabe K., Adachi Y., Wada-Isoe K., Urakami K.,
RA Ninomiya H., Salido T.C., Hashimoto T., Iwatsubo T., Nakashima K.;
RT "Novel amyloid precursor protein gene missense mutation (D678N) in
RL J. Neuro. Neurosurg. Psychiatr. 75:1039-1042(2004).
DR EMBL; AB066441; BAB71958.2; -; mRNA.
DR GO; GO:0016021; C:binding; IEA.
DR GO; GO:0005488; C:integral to membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR FT NON_TER 1 52
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 5597 MW; 3F08E9EC18011AD CRC64;

Query Match 91.2%; Score 31; DB 2; Length 52;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7
DB 16 KLVPFAE 22

RESULT 8
A4_URSWA
ID A4_URSWA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (fragment).
GN Name=APP;
OS Ursus maritimus (Polar bear) (Thalassos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
OC Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

```

```

DR EMBL; X56128; CAA39593.1; -; mRNA.
DR FIR; B60045; B60045.
DR HSP; P08592; INMU.
DR InterPro; IPR001255; A4_APP.
DR InterPro; PTHR10083:SP6; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >57 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >57 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >57 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT NON_TER 1 57
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D8EB82DFA CRC64;

Query Match 91.2%; Score 31; DB 1; Length 57;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7
DB 21 KLVPFAE 27

RESULT 9
A4_CANFA
ID A4_CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (fragment).
GN Name=APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RX "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR EMBL; X56125; CAA39590.1; -; mRNA.
DR HSP; P08592; INMU.

```

```

DR Ensembl; ENSCAFG0000008557; Canis familiaris.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PRO0204; BETAAMYLOID.
DR PROSITE; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PRO0204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT CHAIN 7 >58 CTF-alpha (By similarity).
FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
FT CHAIN 47 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 34 Extracellular (Potential).
FT TRANSMEM 35 58 Potential.
FT NON_TER 1 1
FT NON_TER 58 58
FT SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 91.2%; Score 31; DB 1; Length 58;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 22 KLVFFAE 28

RESULT 10
A4 RABBIT
ID A4 RABBIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
fragment 57)] (Fragment).
GN Name=APP;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
intracellular signaling pathway through the GTP-binding protein
G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
DR EMBL; X56129; CAA39594.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4 APP.
DR PANTHER; PTHR10083:SF6; Beta-APP.
DR InterPro; IPR001255; Beta-APP.

```

```

DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PRO0204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
FT SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 91.2%; Score 31; DB 1; Length 58;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 21 KLVFFAE 27

RESULT 11
A4 SHEEP
ID A4 SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
fragment 57)] (Fragment).
GN Name=APP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
intracellular signaling pathway through the GTP-binding protein
G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
DR EMBL; X56130; CAA39595.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.

```

```

DR PRINTS: PR00204; BETAMYLOID
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA92D CRC64;

Query Match 91.2%; Score 31; DB 1; Length 58;
Best Local Similarity 85.7%; Pred. No. 16; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;

QY 1 KLVFFAQ 7
Db 21 KLVFFAE 27

RESULT 12
A4_BOVIN
ID A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DE 10-NOV-1997 (Rel. 35, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
fragment 57)] (Fragment).
GN Name=APP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=32017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G1O (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X56124; CAA39589.1; -; mRNA.
CC EMBL; X56126; CAA39591.1; -; mRNA.
CC HSSP; P08592; 1NMJ.
CC InterPro; IPR008155; A4 APP.
CC InterPro; IPR001255; Beta-APP.
CC PANTHER; PTHR10083:SF6; Beta-APP; 1.
CC Pfam; PF03494; Beta-APP; 1.
CC PRINTS; PR00204; BETAMYLOID.

```

```

DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT CHAIN 7 >59 CTF-alpha (By similarity).
FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
FT CHAIN 47 >59 Gamma-CTF(59) (By similarity).
FT CHAIN 49 >59 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 34 Extracellular (Potential).
FT TRANSMEM 35 58 Potential.
FT TOPO_DOM 59 >59 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 91.2%; Score 31; DB 1; Length 59;
Best Local Similarity 85.7%; Pred. No. 17; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;

QY 1 KLVFFAQ 7
Db 22 KLVFFAE 28

RESULT 13
O35463 CRIGR PRELIMINARY; PRT; 79 AA.
ID O35463;
AC O35463;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alzheimer's amyloid beta protein (fragment).
GN Name=beta APP;
OS Cricetus lagurus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetinae; Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sambamurti K., Pinnix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030413; AAB86608.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAMYLOID.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 79;
Best Local Similarity 85.7%; Pred. No. 22; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;

QY 1 KLVFFAQ 7
Db 36 KLVFFAE 42

RESULT 14
O8JH58 CHESE PRELIMINARY; PRT; 113 AA.
ID O8JH58;
AC O8JH58;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Amyloid beta protein (fragment).
DE Chelydra serpentina serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Testudines; Cryptodira; Testudinoidae; Chelydridae; Chelydra.
OX NCBI_TaxID=134619;
RN NUCLEOTIDE SEQUENCE.
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RX MEDLINE=21876906; PubMed=11882478;
RT "Octylphenol (OP) alters the expression of members of the amyloid
RT protein family in the hypothalamus of the snapping turtle, Chelydra
RT serpentina serpentina.";
RL Environ. Health Perspect. 110:269-275(2002).
DR EMBL; AF541917; RAN04908.1; -; mRNA.
DR HSSP; Q16019; 11VT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta_APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match          91.2%; Score 31; DB 2; Length 113;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
   |||||
Db 30 KLVFFAE 36

RESULT 15
Q4ULC9 RICFE
ID Q4ULC9_RICFE PRELIMINARY; PRT; 213 AA.
AC Q4ULC9
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Uncharacterized phage-associated protein.
GN OrderedLocustNames=RF_0793;
OS Rickettsia felis (Rickettsia azadi).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia; spotted fever group.
OX NCBI_TaxID=42862;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=URRWKCal2.
RX PubMed=15984913; DOI=10.1371/journal.pbio.0030248;
RA Ogata H., Renesto P., Audic S., Robert C., Blanc G., Fournier P.-E.,
RA Parinello H., Claverie J.-M., Raoult D.;
RT "The genome sequence of Rickettsia felis identifies the first putative
RT conjugative plasmid in an obligate intracellular parasite.";
RL PLoS Biol. 3:E248-E248(2005).
DR EMBL; CP000053; AY61644.1; -; Genomic_DNA.
SQ Complete proteome.
SQ SEQUENCE 213 AA; 24651 MW; 35852F551672389E CRC64;

Query Match          91.2%; Score 31; DB 2; Length 213;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
   |||||
Db 38 KLVYFAQ 44

RESULT 16
QBPPV5 MOUSE
ID QBPPV5_MOUSE PRELIMINARY; PRT; 218 AA.
AC QBPPV5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

```

```

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
DE library, clone:D430025B14 product:amyloid beta (A4) protein, full
DE insert sequence. (Fragment).
CN Name=App;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RT Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Mateu Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
RA Blake J., Boirelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA The FANTOM Consortium,
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed sequencing.";
RL Genome Res. 10:1757-1771(2000).

```



```

FT  NON TER      1
SQ  SEQUENCE    357 AA;  40962 MW;  07D999EEF6C55B2D8 CRC64;

Query Match      91.2%;  Score 31;  DB 2;  Length 357;
Best Local Similarity  85.7%;  Pred. No. 91;
Matches 6;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0

Qy  1  KLVFFFAQ 7
    |||||:
Db   274  KLVFFFAE 280

RESULT 18
Q9SMF0 HORVU PRELIMINARY;      PRT;   375 AA.
AC  Q9SMF0;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
MG  Mg-protoporphylin IX (Fragment).
GN  Name=xantha-g;
OS  Hordeum vulgare (Barley).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC  Triticeae; Hordeum.
OX  NCBI_TaxID=4513;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RA  Petersen B.L., Morrell J., Moeller M.G., Jensen P.E., Henningsen K.W.;
RL  Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AJ011926; CAB58179.1; -; mRNA.
DR  InterPro; IPR002035; VWF A.
DR  PRINTS; PR00453; VWFADOMAIN.
DR  SMART; SM00327; VWA; 1.
DR  PROSITE; PS50234; VWFA; 1.
FT  NON TER      1
SQ  SEQUENCE    375 AA;  41123 MW;  563BC063F425DCF3 CRC64;

Query Match      91.2%;  Score 31;  DB 2;  Length 375;
Best Local Similarity  85.7%;  Pred. No. 95;
Matches 6;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0

Qy  1  KLVFFFAQ 7
    |||||
Db   84  KLVFFFAQ 90

RESULT 19
Q9BPC7 MOUSE PRELIMINARY;      PRT;   384 AA.
AC  Q9BPC7;
DT  01-MAR-2003 (TrEMBLrel. 23, Created)
DT  01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
DE  library, clone:4833432109 product:amyloid beta (A4) protein, full
DE  insert sequence. (Fragment).
GN  Name=App;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=C57BL/6J; TISSUE=Head;
RX  MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA  Carninci P., Hayashizaki Y.;
RT  "High-efficiency full-length cDNA cloning.";
RL  Meth. Enzymol. 303:19-44(1999).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=C57BL/6J; TISSUE=Head;

```

DR	GO: 0005515; F:protein binding; IPI.
DR	GO: 0030199; P:extracellular matrix organization and bioge. . ; IO
DR	InterPro: IPR008155; A4 APP.
DR	Pfam: IPR001255; Beta-APP.
DR	Pfam: PF03494; Beta-APP, 1.
DR	PRINTS: PR00203; AMYLOIDA4.
DR	PRINTS: PR00204; BETAAMYLOID.
DR	PROSITE: PS00320; A4_INTRA; 1.
FT	NON_TER 1
SQ	SEQUENCE 384 AA; 43990 MW; A81BIAD8AE683173 CRC64;
Query Match 91.2%; Score 31; DB 2; Length 384;	
Best Local Similarity 85.7%; Pred. No. 97;	
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps	
Qy	1 KLVFFAQ 7
Db	301 KLVFFAE 307
RESULT 20	
OR65A_DROME	
ID	OR65A_DROME STANDARD; PRT; 417 AA.
AC	P82982;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	13-SEP-2005 (Rel. 48, Last annotation update)
DE	Putative odorant receptor 65a.
GN	Name=OR65a; ORFNames=CG32401;
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxId=7227;
RN	[1]
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC	STRAIN=Berkelley;
RP	MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RX	Adams M.D., Celniker S.E., Holt R.A., Evans C.A. Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutten G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	Balaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA	Hosin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA	Jalali M., Kalush C., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleib J.M.,
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA	Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA	Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA	Ye J., Yeh R.-J., Zaveri J.S., Zhan M., Zhu S., Zhao Q., Zheng L.,
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP GENOME REANNOTATION.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Milera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Battencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 CC -1- FUNCTION: Probable role in the odorant response, being an odorant
 CC receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor Dr-or
 CC family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AE003563; AAN12091.1; -, Genomic DNA.
 CC Ensembl; CG32401; *Drosophila melanogaster*.
 CC FlyBase; FBgn0041625; Or65a.
 CC GO; GO:0016021; C:integral to membrane; ISS.
 CC GO; GO:0004984; F:olfactory receptor activity; ISS.
 CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; ISS.
 CC GO; GO:0007608; P:perception of smell; ISS.
 CC DR InterPro; IPR004117; 7tm6_olfrrecept.
 CC Pfam; PF02949; 7tm6_6; 1.
 CC KW G-protein coupled receptor; Hypothetical protein; Multigene family;
 KW Olfaction; Receptor; Sensory transduction; Transducer; Transmembrane.
 FT TOPO_DOM 1 62 Extracellular (Potential).
 FT TRANSMEM 63 83 1 (Potential).
 FT TOPO_DOM 84 98 Cytoplasmic (Potential).
 FT TRANSMEM 99 119 2 (Potential).
 FT TOPO_DOM 120 152 Extracellular (Potential).
 FT TRANSMEM 153 173 3 (Potential).
 FT TOPO_DOM 174 206 Cytoplasmic (Potential).
 FT TRANSMEM 207 227 4 (Potential).
 FT TOPO_DOM 228 290 Extracellular (Potential).
 FT TRANSMEM 291 311 5 (Potential).
 FT TOPO_DOM 312 316 Cytoplasmic (Potential).
 FT TRANSMEM 317 337 6 (Potential).
 FT TOPO_DOM 338 393 Extracellular (Potential).
 FT TRANSMEM 394 414 7 (Potential).
 FT TOPO_DOM 415 417 Cytoplasmic (Potential).
 SQ SEQUENCE 417 AA; 48730 MW; 2112BE9E1E356059 CRC64;
 Query Match 91.2%; Score 31; DB 1; Length 417;
 Best Local Similarity 85.7%; Pred. No. 1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KLVFVFAQ 7
 Db 111 RLVFVFAQ 117
 RESULT 21
 Q93YN7 ARATH
 ID Q93YN7 ARATH PRELIMINARY; PRT; 471 AA.
 AC Q93YN7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Magnesium-chelate subunit Chld-like protein.

GN Name=T27G7.20;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OC NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY059906; AAL24388.1; -, mRNA.
 DR EMBL; AY114693; AAM48012.1; -, mRNA.
 DR GO; GO:0016851; F:magnesium chelate activity; IEA.
 DR GO; GO:0015995; P:chlorophyll biosynthesis; IEA.
 DR GO; GO:0015979; P:photosynthesis; IEA.
 DR InterPro; IPR011776; Bchd-Chld.
 DR InterPro; IPR012174; Mgchl-Chld.
 DR InterPro; IPR000523; Mg_chelate_chiI.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF01078; Mg_chelate; 1.
 DR PIRSF; PIRSF036550; Mgchl Chld; 1.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00327; VWA; 1.
 DR TIGRFAMs; TIGR02031; Bchd-Chld; 1.
 DR PROSITE; PS0234; VWF; 1.
 SQ SEQUENCE 471 AA; 52064 MW; 90E3B59F510DB9F4 CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 471;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KLVFVFAQ 7
 Db 180 KLLVFFAQ 186
 RESULT 22
 Q8UUS0 BRARE
 ID Q8UUS0 BRARE PRELIMINARY; PRT; 472 AA.
 AC Q8UUS0;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative membrane protein (Fragment).
 GN Name=appa;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX PubMed=11862463; DOI=10.1007/s00427-001-0189-9;
 RA Musa A., Lehrach H., Russo V.E.A.;
 RT "Distinct expression patterns of two zebrafish homologues of the human
 RT APP gene during embryonic development.";
 RL Dev. Genes Evol. 211:563-567(2001).
 DR EMBL; AJ315636; CAC85733.1; -, mRNA.

RESULT 24
O9PVL1 CHICK

```
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON TER 1
SQ SEQUENCE 612 AA; 69710 MW; 59A9ACBDF9C59EFF CRC64;

Query Match
Best Local Similarity 91.2%; Score 31; DB 2; Length 612;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 529 KLVFFAE 535

RESULT 26
Q7ZT1_BRARE
ID Q7ZT1_BRARE PRELIMINARY; PRT; 678 AA.
AC Q7ZT1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Amyloid protein a variant 2.
GN Name=appa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN 1
RP NUCLEOTIDE SEQUENCE.
RA Groth C., Lardelli M.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY271746; AAP22958.1; -; mRNA.
DR HSP; Q16019; LH23.
DR SMR; Q7ZT1; 29-124, 383-491.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4 EXTRA; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 678 AA; 76755 MW; 94163778444FD0BC CRC64;

Query Match
Best Local Similarity 91.2%; Score 31; DB 2; Length 678;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 595 KLVFFAE 601

RESULT 27
Q98SGO_XENLA
ID Q98SGO_XENLA PRELIMINARY; PRT; 693 AA.
AC Q98SGO;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid precursor protein A.
GN Name=app;
OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN 1
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE-21610087; PubMed-11741158; DOI=10.1016/S0169-328X(01)00279-0;
RX van den Hurk W.H., Bloemen M., Martens G.J.M.;
RA "Expression of the gene encoding the beta-amyloid precursor protein
RT APP in Xenopus laevis.";
RL Brain Res. Mol. Brain Res. 97:13-20(2001).
RN 2
RP NUCLEOTIDE SEQUENCE.
RA Van den Hurk W.H.;
RL thesis (2001), Department of Biological Sciences, University of
RL Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298150; CAC37193.1; -; mRNA.
DR HSP; Q16019; LH23.
DR SMR; Q98SGO; 27-122, 383-492.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4 EXTRA; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW SIGNAL.
FT SIGNAL 1 19 Potential.
SQ SEQUENCE 693 AA; 78567 MW; CAF1DF655CIAB653 CRC64;

Query Match
Best Local Similarity 91.2%; Score 31; DB 2; Length 693;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 610 KLVFFAE 616

RESULT 28
Q5R477_PONPY
ID Q5R477_PONPY PRELIMINARY; PRT; 695 AA.
AC Q5R477;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp459D212.
GN Name=DKFZp459D212;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN 1
RP NUCLEOTIDE SEQUENCE.
RA TISSUR=Cortex;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Pobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR861380; CH93439.1; -; mRNA.
DR SMR; Q5R477; 28-123, 124-189, 385-494.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
```

DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome_c_r.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4 EXTRA; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
KW Hypothetical protein_

SQ SEQUENCE 695 AA; 78626 MW; 0B5DD9BA2213E49 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 695;

Best Local Similarity 85.7%; Pred. No. 1.7e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7

|||||:

Db 612 KLVFFFAE 618

RESULT 29

Q6RH29 CANFA

ID Q6RH29 CANFA PRELIMINARY; PRT; 695 AA.

AC Q6RH29;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Beta amyloid protein isoform APP695.

GN Name=Beta APP;

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;

OC Canis.

OX NCBI_TaxID=9615;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Nakata M.;

RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY498707; AAR9727.1; -; mRNA.

DR SRR; O16019; 1BA4.

DR HMP; Q6RH29; 28-123, 124-189, 385-494.

DR Ensembl; ENSCAP0000008557; Canis familiaris.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR InterPro; IPR008155; A4 APP.

DR InterPro; IPR008154; A4 extra.

DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF02177; A4 EXTRA; 1.

DR Pfam; PF03494; Beta-APP; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00204; BETAAMYLOID.

DR SMART; SM00006; A4 EXTRA; 1.

DR PROSITE; PS00319; A4 EXTRA; 1.

DR PROSITE; PS00320; A4 INTRA; 1.

SQ SEQUENCE 695 AA; 78649 MW; 718CA42A9F986C10 CRC64;

Query Match

Best Local Similarity 91.2%; Score 31; DB 2; Length 695;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7

|||||:

Db 612 KLVFFFAE 618

RESULT 30

Q56JK3 CANFA

ID Q56JK3 CANFA PRELIMINARY; PRT; 695 AA.

AC Q56JK3;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Beta-amyloid protein 695.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RL "Relationship between canine dementia and Alzheimer's disease."; Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926582; AAX81911.1; -; mRNA.
SQ SEQUENCE 695 AA; 78748 MW; 5A253E0DB677875A CRC64;

Query Match 91.2%; Score 31; DB 2; Length 695;

Best Local Similarity 85.7%; Pred. No. 1.7e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7

|||||:

Db 612 KLVFFFAE 618

RESULT 31

Q6GR78 MOUSE

ID Q6GR78 MOUSE PRELIMINARY; PRT; 695 AA.

AC Q6GR78;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Amyloid beta (A4) protein.

GN Name=App;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6; TISSUE=Brain;

EX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6; TISSUE=Brain;

RA Strausberg R.;

RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC070409; AAH70409.1; -; mRNA.

SQ SEQUENCE 695 AA; 78442 MW; 0DE93FAS6FB20F3A CRC64;

Query Match

Best Local Similarity 91.2%; Score 31; DB 2; Length 695;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 612 KLVFFAE 618

RESULT 32
Q9DGJ8_CHICK
ID Q9DGJ8_CHICK PRELIMINARY; PRT; 695 AA.
AC Q9DGJ8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid protein 695 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]

NUCLEOTIDE SEQUENCE.
RP Sarasa M., Rodolose A., Sorribas V.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RE EMBL; AF289218; AAC00593.1; -; mRNA.
DR HSP; Q16019; 11YT.
DR SMR; Q9DGJ8; 28-123, 124-189, 385-494.
DR Ensembl; ENSGALG00000015770; Gallus gallus.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF021177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4 EXTRA; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 695;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 612 KLVFFAE 618

RESULT 33
Q56JK4_CANFA
ID Q56JK4_CANFA PRELIMINARY; PRT; 714 AA.
AC Q56JK4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Beta-amyloid protein 714.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
NUCLEOTIDE SEQUENCE.
RP Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease."
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RE EMBL; AY926581; AAX81910.1; -; mRNA.
SQ SEQUENCE 714 AA; 80826 MW; 50DDE51FB9B930EC5 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 714;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAQ 7
Db 631 KLVFFAE 637

RESULT 34
Q6P6Q5_RAT
ID Q6P6Q5_RAT PRELIMINARY; PRT; 733 AA.
AC Q6P6Q5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE App protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
NUCLEOTIDE SEQUENCE.
RP TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
NUCLEOTIDE SEQUENCE.
RP TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC062082; AAH62082.1; -; mRNA.
DR HSSP; Q16019; 1AAP.
DR SMR; Q6P6Q5; 28-123, 124-189, 287-342, 441-550.
DR Ensembl; ENSRNOG00000006997; Rattus norvegicus.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR GO; GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF021177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4 EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.

```
SQ SEQUENCE 733 AA; 82797 MW; 8538F36FF73762F1 CRC64;
Query Match 91.2%; Score 31; DB 2; Length 733;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFPAQ 7
Db 650 KLVFFPAE 656
|||||:

RESULT 35
Q6NUZ1 BRARE
ID Q6NUZ1 BRARE PRELIMINARY; PRT; 738 AA.
AC Q6NUZ1;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Amyloid beta (A4) protein a.
GN Name=appa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RT TISSUE=Embryo;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Director MGC Project;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC068375; AAH68375.1; -; mRNA.
DR HSSP; Q16019; 1BA4.
DR SMR; Q6NUZ1; 29-124, 443-551.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00203; AMYL0IDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4 EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00203; AMYL0IDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
```

```
DR SMART; SM00006; A4 EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 738 AA; 83577 MW; 3A02A6C158AF57B1 CRC64;
Query Match 91.2%; Score 31; DB 2; Length 738;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFPAQ 7
Db 655 KLVFFPAE 661
|||||:

RESULT 36
Q90W28 BRARE
ID Q90W28 BRARE PRELIMINARY; PRT; 738 AA.
AC Q90W28;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Amyloid protein.
GN Name=appa; Synonyms=app;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Groth C., Lardelli M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF389401; AAK64495.1; -; mRNA.
DR HSSP; Q16019; 1H23.
DR SMR; Q90W28; 29-124, 443-551.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00203; AMYL0IDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00006; A4 EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 738 AA; 83577 MW; AF480F6D308FD298 CRC64;
Query Match 91.2%; Score 31; DB 2; Length 738;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFPAQ 7
Db 655 KLVFFPAE 661
|||||:

RESULT 37
Q7XZG7_ORYSA
```



```

ID QTXZG7 ORYSA PRELIMINARY; PRT; 745 AA.
AC QTXZG7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative magnesium chelatase subunit chld.
GN Name=OSUNB003J23.6;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Rhamnoidae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Teitlin T., Kim M.M., Bera J.J., Jin S.S.,
RA Padrosh D.W., Tallon L.J., Koo H., Ziemann V., Heiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RA Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP Buell R.;
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC137507; AAP73850.1; -; Genomic DNA.
DR HSSP; P26239; IG8P.
DR Gramene; QTXZG7; -.
DR GO; GO:0016851; F:magnesium chelatase activity; IEA.
DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0015995; P:chlorophyll biosynthesis; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011776; BchD-ChlD.
DR InterPro; IPR012174; Mgchl Chld.
DR InterPro; IPR000523; Mg_chelatase_chII.
DR InterPro; IPR002035; VNF_A.
DR Pfam; PF01078; Mg_chelatase; 1.
DR PIRSF; PIRSF036550; Mgchl Chld; 1.
DR PRINTS; PR00453; VNFADOMAIN.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00327; VWA; 1.
DR TIGRFAMs; TIGR02031; BchD-Chld; 1.
DR PROSITE; PS02034; VWFA; 1.
SQ SEQUENCE 745 AA; 80846 MW; 4A347B2PB9PC6646 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 745;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 455 KLVFFAQ 461

RESULT 38
Q91963_9PIPI PRELIMINARY; PRT; 747 AA.
AC Q91963;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE APP747.
GN Name=APP747;
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae.
OX NCBI_TaxID=8353;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93129227; PubMed=1282805;

ID Q91963_9PIPI PRELIMINARY; PRT; 747 AA.
AC Q91963;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE APP747.
GN Name=APP747;
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae.
OX NCBI_TaxID=8353;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93129227; PubMed=1282805;

```

```

RA Okado H., Okamoto H.;
RT "A xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression.";
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; S52417; AAB24853.1; -; mRNA.
DR HSSP; Q16019; 1H23.
DR SMR; Q91963; 26-119, 283-338, 437-546.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 747;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 664 KLVFFAQ 670

RESULT 39
Q56JK2 STECO PRELIMINARY; PRT; 749 AA.
AC Q56JK2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Beta-amyloid protein 749.
OS Stenella coeruleoalba (Striped dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Stenella.
OX NCBI_TaxID=9737;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY926583; AAX81912.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020637; F:heme binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
SQ SEQUENCE 749 AA; 84542 MW; 42659987C2A95D6 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 749;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 666 KLVFFAQ 672

```

DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 749 AA; 84766 MW; 33478C6B6A8C295D CRC64;

Query Match 91.2%; Score 31; DB 2; Length 749;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLWFFFA 7
|||||:
DB 666 KLWFFFAE 672

RESULT 41
Q6DJB6_XENTR PRELIMINARY; PRT; 750 AA.

ID Q6DJB6_XENTR PRELIMINARY; PRT; 750 AA.
AC Q6DJB6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Amyloid beta (A4) protein (protease nexin-II, Alzheimer disease).
GN Name=app-prov;
OS Xenopus tropicalis (Western clawed frog) (*Silurana tropicalis*).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenoportidae; Xenopus; *Silurana*.
NCBI_TaxID=8364;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Whole body;
RC MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zengerg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Whole body;
RC Klein S., Gerhard D.S.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC075266; AAH75266.1; -; mRNA.
DR SNR; Q6DJB6; 27-122, 285-340, 440-549.
DR GO; GO016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta_APP.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLQIDA4.
DR

DR PRINTS; PRO0759; BASICTASE.
 DR PRINTS; PRO0204; BETAAMYLOID.
 DR PRODOM; SM000222; Prot Inh_Kunz-m; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Protease.
 SQ SEQUENCE 750 AA; 84927 MW; 4222350843147CAF CRC64;

Query Match 91.28; Score 31; DB 2; Length 750;
 Best Local Similarity 85.74; Pred. NO. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
 |||||
 667 KLVFFAE 673

Db

RESULT 42
 A4_SAISC
 ID_ A4_SAISC STANDARD; PRT; 751 AA.
 AC Q95241;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
 DE protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
 DE APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
 DE Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
 DE CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 GN Name=APP;
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
 OC Cebinae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney, and Liver;
 RX MEDLINE=96108492; PubMed=8532114; DOI=10.1016/0197-4580(95)00090-2;
 RA Levy E., Amorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral
 RT amyloid angiopathy.";
 RL Neurobiol. Aging 16:805-808 (1995).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell motility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/rip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(o) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metallated APP induces neuronal
 CC death directly or is potentiated through Cu(2+)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal

CC apoptosis (By similarity).
 CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IBI, KNS2
 CC (via its TPR domain) (By similarity), APPBP2 (via BAGS) and DDB1.
 CC In vitro, it binds MAPT via the WT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=Q95241-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=Q95241-2; Sequence=Not described;
 CC -1- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -1- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC protein, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at App-720 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

use as long as its content is in no way modified and this statement is not removed.

EMBL; S81024; AAD14347.1; -; mRNA.
 PDB; 1RW6; X-ray; A=346-551.
 SMR; Q95241; 28-123, 124-189, 287-342.
 InterPro; IPR008155; A4_APP.
 InterPro; IPR008154; A4_extra.
 InterPro; IPR001255; Beta-APP.
 InterPro; IPR002223; Prot inh Kunz-m.
 PANTHER; PTHR10083.SF6; Beta-APP; 5.
 Pfam; PF02177; A4_EXTRA; 1.
 Pfam; PF03494; Beta-APP; 1.
 Pfam; PF00014; Kunitz BPTI; 1.
 PRINTS; PR00203; AMYLOIDA4.
 PRINTS; PR00759; BASICPTASE.
 PRINTS; PR00204; BETAAMYLOID.
 ProDom; PD000222; Prot Inh Kunz-m; 1.
 SMART; SM00006; A4_EXTRA; 1.
 SMART; SM00131; KU; 1.
 PROSITE; PS00319; A4_EXTRA; 1.
 PROSITE; PS00320; A4_INTRA; 1.
 PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 3D-structure; Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron; Metal-binding; Notch signaling pathway; Phosphorylation; Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal; Transmembrane; Zinc.
 SIGNAL 1 17 By similarity.
 CHAIN 18 751 Amyloid beta A4 protein.
 CHAIN 18 668 Soluble APP-alpha (Potential).
 CHAIN 18 652 Soluble APP-beta (Potential).
 CHAIN 653 751 C99 (Potential).
 CHAIN 653 694 Beta-amyloid protein 42 (Potential).
 CHAIN 653 692 Beta-amyloid protein 40 (Potential).
 CHAIN 669 751 C93 (Potential).
 PEPTIDE 669 694 P3(42) (Potential).
 PEPTIDE 669 692 P3(40) (Potential).
 CHAIN 693 751 Gamma-CTF(59) (Potential).
 CHAIN 695 751 Gamma-CTF(57) (Potential).
 CHAIN 702 751 Gamma-CTF(50) (Potential).
 CHAIN 721 751 C31 (Potential).
 TOPO_DOM 18 680 Extracellular (Potential).
 TRANSMEM 681 704 Potential.
 TOPO_DOM 705 751 Cytoplasmic (Potential).
 DOMAIN 291 341 BPTI/Kunitz inhibitor.
 REGION 96 110 Heparin-binding (By similarity).
 REGION 181 188 Zinc-binding (By similarity).
 REGION 316 344 Heparin-binding (By similarity).
 REGION 363 428 Heparin-binding (By similarity).
 REGION 504 521 Collagen-binding (By similarity).
 REGION 713 732 Interaction with G(o)-alpha (By similarity).
 MOTIF 705 715 Basolateral sorting signal (By similarity).
 MOTIF 740 743 NPXY motif.
 COMPBIAS 230 260 Asp/Glu-rich (acidic).
 METAL 137 137 Poly-Thr.
 METAL 147 147 Copper (By similarity).
 METAL 149 149 Copper (By similarity).
 METAL 151 151 Copper (By similarity).
 METAL 658 658 Copper or zinc (By similarity).
 METAL 662 662 Copper or zinc (By similarity).
 METAL 665 665 Copper or zinc (By similarity).
 METAL 666 666 Copper or zinc (By similarity).
 SITE 144 144 Required for Cu(2+) reduction (By similarity).
 SITE 301 302 Reactive bond.
 SITE 652 653 Cleavage (by beta-secretase) (By similarity).
 SITE 653 654 Cleavage (by caspase-6) (By similarity).

FT SITE 668 669 Cleavage (by alpha-secretase) (By similarity).
 FT SITE 685 685 Implicated in free radical propagation (By similarity).
 Query Match 91.2%; DB 1; Length 751;
 Best Local Similarity 85.7%; Pred. NO. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFAQ 7
 Db 668 KLVFFAE 674
 RESULT 43
 QGSC0 HUMAN
 ID Q6GSC0_HUMAN PRELIMINARY; PRT; 751 AA.
 AC Q6GSC0;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Amyloid beta A4 protein,, isoform b.
 GN Name=APP;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RG NIH MGC Project;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR EMBL; BC065529; AA065529.1; -; mRNA.
 DR SMR; QGSC0; 28-123, 124-189, 287-342, 441-550.
 DR Ensembl; ENSG00000142192; Homo sapiens.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0020037; F:heme binding; IEA.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR01255; Beta-APP.
 DR InterPro; IPR012282; Cytochrome c R.
 DR InterPro; IPR002223; Prot inh Kunz-m.
 Pfam; PF02177; A4_EXTRA; 1.
 Pfam; PF03494; Beta-APP; 1.

RESULT 46	
Q4R4R8	MACFA
ID	Q4R4R8 MACFA PRELIMINARY; PRT; 751 AA.
AC	Q4R4R8;
DT	13-SEP-2005 (TrEMBLrel. 31, Created)
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE	Brain cDNA, clone: Q14-13524, similar to human amyloid beta (A4)
DE	protein (protease nexin-II, Alzheimer disease) (APP), transcript
DE	variant 2,
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey) .
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC	Cercopitheidae; Cercopithecinae; Macaca.
NCBI_Taxid	95541;
	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	International consortium for macaque cDNA sequencing, analysis;
FT	"DNA sequences of macaque genes expressed in brain or testis and

evolutionary implications.";

[2]

Nucleotide SEQUENCE.

Osada N., Hirata M., Tanuma R., Kueuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.: "Substitution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs."; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

-/- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

EMBL; AB169826; BA01907.1; -; mRNA.

InterPro; IPR008155; A4_APP.

InterPro; IPR008154; A4_extra.

InterPro; IPR001255; Beta_APP.

InterPro; IPR012282; Cytochrome_c.R.

InterPro; IPR002223; Prot_inh_Kunz-m.

Pfam; PF02177; A4_EXTRA; 1.

Pfam; PF03494; Beta_APP; 1.

Pfam; PF00014; Kunitz_BPTI; 1.

PRINTS; PR00203; AMYLOIDA4.

PRINTS; PR00759; BASICTPASE.

PRINTS; PR00204; BETAAMYLOID.

ProDom; PD000222; Prot_inh_Kunz-m; 1.

SMART; SM00006; A4_EXTRA; 1.

SMART; SM00131; KU; 1.

PROSITE; PS00319; A4_EXTRA; 1.

PROSITE; PS00320; A4_INTRA; 1.

PROSITE; PS00280; BPTI_KUNITZ_1; 1.

PROSITE; PS00279; BPTI_KUNITZ_2; 1.

SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 751;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFAQ 7
Db 668 KLVPFAE 674

RESULT 48

CHLD_PEA STANDARD; PRT; 754 AA.

ID CHLD_PEA AC O22437;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Magnesium-chelatease subunit chld, chloroplast precursor (EC 6.6.1.1)
GN Name=CHLD;
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;
OC rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Spring; TISSUE=Leaf;
RA Luo M., Weinstein J.D.;
RT Cloning and sequencing of a cDNA encoding the putative Mg-chelatease subunit b from pea (Pisum sativum L. cv. Spring).";
RL (er) Plant Gene Register PGR97-139.
CC -/- FUNCTION: Involved in chlorophyll biosynthesis; introduces a magnesium ion into protoporphyrin IX to yield Mg-protoporphyrin IX.
CC -/- CATALYTIC ACTIVITY: ATP + protoporphyrin IX + Mg(2+) + H(2)O = ADP + phosphate + Mg-protoporphyrin IX + 2 H(+).
CC -/- PATHWAY: Chlorophyll biosynthesis.
CC -/- SUBCELLULAR LOCATION: Chloroplast stroma.
CC -/- SIMILARITY: Belongs to the Mg-chelatease subunits D/I family.
CC -/- SIMILARITY: Contains 1 WFA domain.

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

EMBL; AF014399; AAB72194.1; -; mRNA.
PIR; T06249; T06249.
HSP; P26239; 1G8P.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR011776; Bchd-Chld.
InterPro; IPR000523; Mg_chelatease_chiI.
InterPro; IPR012174; Mgchl_Chld.
InterPro; IPR002035; WVF_A.
Pfam; PF01078; Mg_chelatease; 1.
PIRSF; PIRSF036550; Mgchl_Chld; 1.
PRINTS; PM00453; WVFADOMAIN.
SMART; SM00382; AAA; 1.
SMART; SM00327; WVA; 1.
TIGRFAMs; TIGR02031; Bchd-Chld; 1.

Qy 1 KLVPFAQ 7
Db 668 KLVPFAE 674

RESULT 47

ID QDGJ7_CHICK PRELIMINARY; PRT; 751 AA.

AC QDGJ7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amylolid protein 751 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

NCBI_TaxID=9031;
[1]

Nucleotide SEQUENCE.

Sarasa M., Rodolose A., Sorribas V.;
Ensembl; ENSGALG0000015770; Gallus_gallus.
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

-/- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

EMBL; AF289219; AAG00594.1; -; mRNA.
HSP; Q16019; 1IYT.
SMR; Q9DGJ7; 28-123, 124-189, 287-342, 441-550.
Ensembl; ENSGALG0000015770; Gallus_gallus.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005488; F:binding; IEA.
GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
InterPro; IPR008155; A4_APP.
InterPro; IPR008154; A4_extra.
InterPro; IPR001255; Beta_APP.
InterPro; IPR002223; Prot_inh_Kunz-m.
Pfam; PF02177; A4_EXTRA; 1.
Pfam; PF03494; Beta_APP; 1.
Pfam; PF00014; Kunitz_BPTI; 1.

DR PROSITE; PS0234; VWFA; 1.
 KW ATP-binding; Chlorophyll biosynthesis; Chloroplast; Ligase;
 FT Nucleotide-binding; Photosynthesis; Translational;
 TRANSIT 1 ? Chloroplast (Potential).
 FT CHAIN ? 754 Magnesium-chelatase subunit chld.
 FT DOMAIN 551 751 VWFA.
 FT COMPIAS 398 449 Glu/Pro-rich.
 FT COMPIAS 405 412 Poly-Pro.
 FT COMPIAS 423 432 Poly-Glu.
 SQ SEQUENCE 754 AA; 82865 MW; 1D56BA3139080A90 CRC64;

Query Match 91.2%; Score 31; DB 1; Length 754;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFAQ 7
 ||:||||
 Db 462 KLVPFAQ 468

RESULT 49

Q6ATS0 ORYSA
 ID Q6ATS0 ORYSA PRELIMINARY; PRT; 754 AA.
 AC Q6ATS0; 2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Putative magnesium chelatase.
 GN Name=OSJNBa0028P23.2;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 ON NCBI_TaxID=39947;
 RN NUCLEOTIDE SEQUENCE.
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
 RA Overton II L.L., Teitron T., Kim M.M., Bera J.J., Jin S.S.,
 RA Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
 RA Vanaken S.S., Riedmuller S.B., Uterback T.T., Feldblyum T.V.,
 RA Yang Q.O., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
 RA White O., Salzberg S.L., Fraser C.M.;
 RT "Oryza sativa chromosome 3 BAC OSJNBa0028P23 genomic sequence.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 [2]

NUCLEOTIDE SEQUENCE.

RA Buell R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC135595; AAT77900.1; -; Genomic_DNA.
 DR Gramene; Q6ATS0; -.
 DR GO; GO:0016851; P:magnesium chelatase activity; IEA.
 DR GO; GO:0017111; P:nucleoside-triphosphatase activity; IEA.
 DR GO; GO:0000166; P:nucleotide binding; IEA.
 DR GO; GO:0015995; P:chlorophyll biosynthesis; IEA.
 DR GO; GO:0015979; P:photosynthesis; IEA.
 DR InterPro; IPR003593; AAA_Arpase.
 DR InterPro; IPR011776; BchD-Chld.
 DR InterPro; IPR012174; Mgchl Chld.
 DR InterPro; IPR000523; Mg chelatase_chII.
 DR InterPro; IPR002035; VWFA.
 DR Pfam; PF01078; Mg_chelatase; 1.
 DR PIRSF; PIRSF036550; Mgchl Chld; 1.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00382; AAA; 1.
 DR SMART; SM00327; VWFA; 1.
 DR TIGRFAm6; TIGR02031; BchD-Chld; 1.
 DR PROSITE; PS0234; VWFA; 1.
 SQ SEQUENCE 754 AA; 81878 MW; 8B9PFAA055401164D CRC64;

Query Match 91.2%; Score 31; DB 2; Length 754;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFAQ 7
 ||:||||
 Db 464 KLVPFAQ 470

RESULT 50

Q4RY33 TETNG
 ID Q4RY33 TETNG PRELIMINARY; PRT; 754 AA.
 AC Q4RY33;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 3 SCAF14978, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00027170001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontoidea; Tetraodontidae; Tetraodon.
 ON NCBI_TaxID=99883;
 RN NUCLEOTIDE SEQUENCE.

RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McSwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crullius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 [2]

NUCLEOTIDE SEQUENCE.

RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; CRAE01014978; CAG06699.1; -; Genomic_DNA.
 DR NON_TER 1 1
 FT NON_TER 754 754
 FT NON_TER 754 754
 SQ SEQUENCE 754 AA; 84740 MW; 4A37B051A9FAD777 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 754;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFAQ 7
 ||:||||
 Db 671 KLVPFAE 677

RESULT 51

CHLD_TOBAC
 ID CHLD_TOBAC STANDARD; PRT; 758 AA.
 AC O24133;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Magnesium-chelatase subunit chld, chloroplast precursor (EC 6.6.1.1)
 DE (Mg-protoporphyrin IX chelatase) (Mg-chelatase subunit D).
 GN Name=CHLD;
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; lamids; Solanales; Solanaceae; Nicotiana.

```

OX NCBI_TaxID=4097;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Papanbrock J., Graefe S., Kruse E., Haesel F., Grimm B.;
RA "Mg-chelate of tobacco: identification of a chl D cDNA sequence
RT encoding a third subunit, analysis of the interaction of the three
RT subunits with the yeast two-hybrid system, and reconstitution of the
RT enzyme activity by co-expression of recombinant CHL D, CHL H and CHL
RT I.";
RL Plant J. 12:981-990(1997).
CC -!- FUNCTION: Involved in chlorophyll biosynthesis; introduces a
CC magnesium ion into protoporphyrin IX to yield Mg-protoporphyrin
CC IX.
CC -!- CATALYTIC ACTIVITY: ATP + protoporphyrin IX + Mg(2+) + H(2)O = ADP
CC + phosphate + Mg-protoporphyrin IX + 2 H(+).
CC -!- PATHWAY: Chlorophyll biosynthesis.
CC -!- SUBCELLULAR LOCATION: Chloroplast stroma.
CC -!- SIMILARITY: Belongs to the Mg-chelatase subunits D/I family.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Y10022; CAA71128.1; -; mRNA.
DR PIR; T02925; T02925.
DR HSSP; P26239; IG8P.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011776; BchD-Chld.
DR InterPro; IPR000523; Mg_chelatase_chII.
DR InterPro; IPR012174; MgChl_Chld.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01078; Mg_chelatase; 1.
DR FIRSF; FIRSF036550; Mgchl_Chld; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00327; VWA; 1.
DR TIGRFAMs; TIGR02031; BchD-Chld; 1.
DR PROSITE; PS50234; VWFA; 1.
KW ATP-binding; Chlorophyll biosynthesis; Chloroplast; Ligase;
KW Nucleotide-binding; Photosynthesis; Transit peptide.
FT TRANSIT 1 62 Chloroplast (Potential).
FT CHAIN 63 758 Magnesium-chelatase subunit chld.
FT DOMAIN 556 752 VWFA.
FT COMPIAS 399 445 Glu/Pro-rich.
FT COMPIAS 409 416 Poly-Pro.
FT COMPIAS 427 434 Poly-Glu.
SQ SEQUENCE 758 AA; 83013 MW; ED531E85D5FAFEF8 CRC64;

Query Match 91.2%; Score 31; DB 1; Length 758;
Best Local Similarity 85.7%; Pred.No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KLVFFAQ 7
Db 467 KLVFFAQ 473

RESULT 52
CHLD ARATH
ID CHLD ARATH STANDARD; PRT; 759 AA.
AC Q9SJ61; Q9SJ61;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Magnesium-chelatase subunit chld, chloroplast
DE (Mg-protoporphyrin IX chelatase) (Mg-chelatase subunit D).
GN Name=CHLD; OrderedLocNames=At1g08520; ORFNames=T27G7.20;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

```

OC OC
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=9418040;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Hill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Guntler J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.-H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Miltcher J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 32-759.
RC STRAIN=cv. C24;
RA Green J., Jensen P.E., Gibson L.C.D., Hunter C.N.;
RT "Characterization of the magnesium protoporphyrin chelatase chld
RT subunit from Arabidopsis thaliana cv. C24.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in chlorophyll biosynthesis; introduces a
CC magnesium ion into protoporphyrin IX to yield Mg-protoporphyrin
CC IX.
CC -!- CATALYTIC ACTIVITY: ATP + protoporphyrin IX + Mg(2+) + H(2)O = ADP
CC + phosphate + Mg-protoporphyrin IX + 2 H(+).
CC -!- PATHWAY: Chlorophyll biosynthesis.
CC -!- SUBCELLULAR LOCATION: Chloroplast stroma.
CC -!- SIMILARITY: Belongs to the Mg-chelatase subunits D/I family.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AC006932; AAF22895.1; ALT SEQ; Genomic_DNA.
DR EMBL; AF083555; AAD52031.1; -; mRNA.
DR HSSP; P26239; IG8P.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011776; BchD-Chld.
DR InterPro; IPR000523; Mg_chelatase_chII.
DR InterPro; IPR012174; MgChl_Chld.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01078; Mg_chelatase; 1.
DR FIRSF; FIRSF036550; Mgchl_Chld; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00327; VWA; 1.
DR TIGRFAMs; TIGR02031; BchD-Chld; 1.
DR PROSITE; PS50234; VWFA; 1.
KW ATP-binding; Chlorophyll biosynthesis; Chloroplast; Ligase;
KW Nucleotide-binding; Photosynthesis; Transit peptide.
FT TRANSIT 1 759 Magnesium-chelatase subunit chld.
FT CHAIN 557 753 VWFA.
FT DOMAIN 411 418 Poly-Pro.
FT COMPIAS 425 438 Poly-Glu.

```


FT CONFLICT 70 70 D -> B (in Ref. 2).
 FT CONFLICT 150 150 D -> N (in Ref. 2).
 FT CONFLICT 270 270 G -> S (in Ref. 2).
 FT CONFLICT 285 286 Missing (in Ref. 2).
 FT CONFLICT 314 314 R -> S (in Ref. 2).
 FT CONFLICT 379 379 E -> K (in Ref. 2).
 FT CONFLICT 426 426 E -> D (in Ref. 2).
 SQ SEQUENCE 759 AA; 83155 MW; A4169319E1247BD1 CRC64;

Query Match 91.2%; Score 31; DB 1; Length 759;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
 ||:||||
 Db 468 KLVFFAQ 474

RESULT 53
 Q4S0J4_TETNG PRELIMINARY; PRT; 759 AA.
 ID Q4S0J4_TETNG PRELIMINARY; PRT; 759 AA.
 AC Q4S0J4;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 2 SCAF14781, whole genome shotgun sequence.
 GN ORFNAMES=GSTENG00025991001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OC NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Maudet E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet M., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Blemont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,
 RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissenbach J., Roest Crollius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]

NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR EMBL; CAAB01014781; CAG05838.1; -; Genomic_DNA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Prot. inh. Kunz-m.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYL0IDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR ProDom; PD000222; Prot. inh. Kunz-m; 1.
 DR SMART; SM00006; A4_EXTEA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 SQ SEQUENCE 759 AA; 85017 MW; 5EEF9B8B6C273233 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 759;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
 ||:||||
 Db 676 KLVFFAQ 682

RESULT 54
 Q8VZU7_ARATH PRELIMINARY; PRT; 760 AA.
 ID Q8VZU7_ARATH PRELIMINARY; PRT; 760 AA.
 AC Q8VZU7;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Putative Mg-chelatease.
 GN Name=At1g08520;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.,
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]

NUCLEOTIDE SEQUENCE.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
 RA Davis R.W., Ecker J.R., Theologis A.,
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY063821; AAL36177.1; -; mRNA.
 DR EMBL; AY091402; AAM14341.1; -; mRNA.
 DR HSSP; P26239; 1G8P.
 DR GO; GO:0016851; P:magnesium chelatease activity; IEA.
 DR GO; GO:0017111; P:nucleoside-triphosphatase activity; IEA.
 DR GO; GO:0000166; P:nucleoside binding; IEA.
 DR GO; GO:0015995; P:chlorophyll biosynthesis; IEA.
 DR GO; GO:0015979; P:photosynthesis; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR011776; BchD-Chld.
 DR InterPro; IPR012174; Mgchl_Chld.
 DR InterPro; IPR00523; Mg_chelatease_chII.
 DR InterPro; IPR002035; VWF_A.
 DR PIRSF; PIRSF036550; Mgchl_Chld; 1.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00382; AAA; 1.
 DR SMART; SM00327; VWA; 1.
 DR TIGRFAMs; TIGR02031; BchD-Chld; 1.
 DR PROSITE; PS0234; VWFA; 1.
 SQ SEQUENCE 760 AA; 83283 MW; A3A2D92DF93D4F43 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 760;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
 ||:||||
 Db 469 KLVFFAQ 475

RESULT 55
 A4 CAVPO STANDARD; PRT; 770 AA.
 AC Q60495; Q60496;
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) (Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
 GN Name=APP;
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 OC Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Liver;
 RX MEDLINE=97236426; PubMed=9116031; DOI=10.1016/S0167-4781(96)00232-1;
 RA Beck M., Mueller D., Bigl V.;
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 RT alternative splicing";
 RL Biochim. Biophys. Acta 1351:17-21(1997).
 RN [2]
 RP INTERACTION OF BETA-APP40 WITH APOE.
 RX MEDLINE=98007700; PubMed=9349544;
 RA Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
 RA Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
 RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
 RT cerebral capillary sequestration and blood-brain barrier transport of
 RT circulating Alzheimer's amyloid beta.";
 RL J. Neurochem. 69:1995-2004(1997).
 RN [3]
 RP PROCESSING.
 RX MEDLINE=20084499; PubMed=10619481; DOI=10.1016/S0306-4522(99)00390-5;
 RA Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
 RA Bigl V.;
 RT "Guinea-pig primary cell cultures provide a model to study expression
 RT and amyloidogenic processing of endogenous amyloid precursor
 RT protein.";
 RL Neuroscienc 95:243-254(2000).
 RN [4]
 RP GAMMA-SECRETASE PROCESSING.
 RX MEDLINE=20576391; PubMed=11035007; DOI=10.1074/jbc.M005968200;
 RA Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
 RA Ziani-Cherif C., Onstead L., Sambamurti K.;
 RT "A novel gamma -secretase assay based on detection of the putative C-
 RT terminal fragment-gamma of amyloid beta protein precursor.";
 RL J. Biol. Chem. 276:481-487(2001).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APPB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metallated APP

induces neuronal death directly or is potentiated through Cu(2+)-
 mediated low-density lipoprotein oxidation (By similarity). Can
 regulate neurite outgrowth through binding to components of the
 extracellular matrix such as heparin and collagen I and IV (By
 similarity). The splice isoforms that contain the BPTI domain
 possess protease inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
 CC and apolipoproteins E and J in the CSF and to HDL particles in
 CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
 CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK3IP1, SHC1 and Numb and Dab1 (By similarity). Also
 CC interacts with GPCR-like protein BPP, PPRL1, APPBP1, IB1, KNS2
 CC (via its TPR domains), APPBP2 (via BASS) and DDB1 (By similarity).
 CC Associates with microtubules in the presence of ATP and in a
 CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
 CC all three isoforms of APOE, in vitro and in vivo. When lipidated,
 CC ApoE3 appears to be the preferred amyloid binding isoform, while
 CC the apoE4 isoform-beta-APP40 complex is capable of being
 CC transported across the blood-brain barrier.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated pits
 CC (By similarity). During maturation, the immature APP (N-
 CC glycosylated in the endoplasmic reticulum) moves to the Golgi
 CC complex where complete maturation occurs (O-glycosylated and
 CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
 CC APP is released into the extracellular space and the C-terminal is
 CC internalized to endosomes and lysosomes (By similarity). Some APP
 CC accumulates in secretory transport vesicles leaving the late Golgi
 CC compartment and returns to the cell surface (By similarity). APP
 CC sorts to the basolateral surface in epithelial cells (By
 CC similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms, missing exons 7,8 and 15, seem to
 CC exist. The L-isoforms, missing exon 15, are referred to as
 CC appicans;
 CC Name=APP770;
 CC IsoId=Q60495-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
 CC -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
 CC brain. The longer isoforms containing the BPTI domain are
 CC predominantly expressed in peripheral organs such as muscle and
 CC liver.
 CC -!- INDUCTION: Increased levels during neuronal differentiation.
 CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells.
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue (By similarity). The NPXY site is also involved in
 CC clathrin-mediated endocytosis.
 CC -!- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
 CC gamma-secretase yields P3 peptides. This is the major secretory

CC pathway and is nonamyloidogenic. Alternatively,
 CC presenilin/nicastrin-mediated gamma-secretase processing of CTF-
 CC beta releases the amyloid beta proteins, amyloid-beta 40 (Aβeta40)
 CC and amyloid-beta 42 (Aβeta42), major components of amyloid
 CC plaques, and the corresponding cytotoxic C-terminal fragments
 CC (CTFs).
 CC -1- PTM: Proteolytically cleaved by caspase-3 during neuronal
 CC apoptosis (By similarity).
 CC -1- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
 CC the L-APP isoforms produces the APP proteoglycan core proteins,
 CC the appicans (By similarity).
 CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific (By similarity).
 CC Phosphorylation can affect APP processing, neuronal
 CC differentiation and interaction with other proteins.
 CC -1- PTM: Extracellular binding and reduction of copper, results in a
 CC corresponding oxidation of Cys-144 and Cys-158, and the formation
 CC of a disulfide bond (By similarity).
 CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates.
 CC -1- SIMILARITY: Belongs to the APP family.

CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC -----
 DR EMBL; X97631; CAA66230.1; -; mRNA.
 DR EMBL; X99198; CAA67589.1; -; mRNA.
 DR HSSP; P08592; INMJ.
 DR SMR; Q60495; 28-123, 124-189, 287-342, 460-569.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Prot inh Kunz-m.
 DR PANTHER; PTHR10083:SF6; Beta-APP; 6.
 DR Pfam; PF021177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR ProDom; PD000222; Prot inh Kunz-m; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 DR KW Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits;
 KW Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron;
 KW Metal-binding; Notch signaling pathway; Phosphorylation;
 KW Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal;
 KW Transmembrane; Zinc.
 FT SIGNAL 1 17 By similarity.
 FT CHAIN 18 770 Amyloid beta A4 protein.
 FT CHAIN 18 687 Soluble APP-alpha (By similarity).
 FT CHAIN 18 671 Soluble APP-beta (By similarity).
 FT CHAIN 672 770 CTF-alpha (By similarity).
 FT CHAIN 672 713 Beta-amyloid protein 42 (By similarity).
 CC -----

Query Match 91.2%; Score 31; DB 1; Length 770;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KLVFFAQ 7
 |||||
 Db 687 KLVFFAE 693

RESULT 56

A4_HUMAN STANDARD; PRT; 770 AA.
 ID AC P05067; P09000; P78438; Q13764; Q13793; Q16011; Q16014;
 AC Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCB8; Q9UCD1; Q9UQS5;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
 DE nexin-II) (PN-II) (APP1) (PreA4) [Contains: Soluble APP-alpha (S-APP-
 DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
 DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
 DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
 DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
 DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
 DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
 DE (Amyloid intracellular domain 50) (AID(50)); C31].
 GN Name-APP; Synonyms=A4, AD1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87144572; PubMed=2881207; DOI=10.1038/325733a0;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 RT cell-surface receptor.";
 RL Nature 325:733-736(1987).
 RN [2]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=88122639; PubMed=2893289; DOI=10.1038/331525a0;
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 RT proteinase inhibitors.";
 RL Nature 331:525-527(1988).
 RN [3]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Baynes R.M.,
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The preA4 (695) precursor protein of Alzheimer's disease A4 amyloid is
 RT encoded by 16 exons.";
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP770).
 RX MEDLINE=90236318; PubMed=2110105; DOI=10.1016/0378-1119(90)90310-N;
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 RN [5]
 RP ERRATUM.
 RX PubMed=1908403; DOI=10.1016/0378-1119(91)90093-Q;
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RL Gene 102:291-292(1991).
 RN [6]
 RP NUCLEOTIDE SEQUENCE (ISOFORM L-APP733).
 RC TISSUE=Leukocyte;
 RX MEDLINE=92268136; PubMed=1587857;
 RA Koenig G., Moening U., Czech C., Prior R., Banati R.,
 RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells.";
 RL J. Biol. Chem. 267:10804-10809(1992).

RN NUCLEOTIDE SEQUENCE (ISOFORM APP770).
 RP MEDLINE=97263807; PubMed=9108164; DOI=10.1093/nar/25.9.1802;
 RA Hattori M., Teukahara F., Furuhata Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 [8]
 RN NUCLEOTIDE SEQUENCE (ISOFORM APP639).
 RP TISSUE=Brain;
 RC MEDLINE=22744650; PubMed=12859342;
 RX DOI=10.1046/j.1460-9568.2003.02731.x;
 RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
 RT "Identification of a novel alternative splicing isoform of human
 RT amyloid precursor protein gene, APP639.";
 RL Eur. J. Neurosci. 18:102-108(2003).
 [9]
 RN NUCLEOTIDE SEQUENCE (GENOMIC DNA), AND VARIANT LYS-501.
 RP Livingston R.J., Rieder M.J., Rajkumar N., Downing T.K., Olson A.N.,
 RA Nguyen C.P., Gildersleeve H., Cassidy C.M., Johnson E.J.,
 RA Swanson J.E., McFarland I., Yool B., Park C., Nickerson D.A.;
 RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department
 RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 [10]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS APP305 AND APP751).
 RP TISSUE=Eye, and Pancreas;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [11]
 RN NUCLEOTIDE SEQUENCE OF 1-10.
 RP TISSUE=Liver;
 RC MEDLINE=89016647; PubMed=3140222;
 RX Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 [12]
 RN ERRATUM, AND SEQUENCE REVISION.
 RP Schon E.A., Mita S., Sadlock J., Herbert J.;
 RA Nucleic Acids Res. 16:11402-11402(1988).
 [13]
 RN NUCLEOTIDE SEQUENCE OF 1-75.
 RP MEDLINE=89165870; PubMed=2538123;
 RA La Pauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene.";
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 [14]
 RN PROTEIN SEQUENCE OF 18-50.
 RP TISSUE=Fibroblast;
 RC MEDLINE=87250462; PubMed=3597385;
 RX van Nostrand W.E., Cunningham D.D.;

RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 [15]
 RN PROTEIN SEQUENCE OF 18-40.
 RP TISSUE=Platelet;
 RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
 RA Thomas G.R., Vandekerckhove J.;
 RT "Exploring proteomes and analyzing protein processing by mass
 RT spectrometric identification of sorted N-terminal peptides.";
 RL Nat. Biotechnol. 21:566-569(2003).
 [16]
 RN PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP751).
 RP TISSUE=Brain;
 RC MEDLINE=89346754; PubMed=2569763;
 RX de Sauvage F., Octave J.N.;
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein.";
 RL Science 245:651-653(1989).
 [17]
 RN PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RP TISSUE=Brain;
 RC MEDLINE=87231971; PubMed=30355574;
 RX Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 [18]
 RN NUCLEOTIDE SEQUENCE OF 286-366.
 RP MEDLINE=88122640; PubMed=2893290; DOI=10.1038/331528a0;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 [19]
 RN NUCLEOTIDE SEQUENCE OF 287-367.
 RP MEDLINE=88122641; PubMed=2893291; DOI=10.1038/331530a0;
 RX Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows protease
 RT inhibitory activity.";
 RL Nature 331:530-532(1988).
 [20]
 RN NUCLEOTIDE SEQUENCE OF 507-770.
 RP TISSUE=Brain cortex;
 RC MEDLINE=88124954; PubMed=2893379;
 RX Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 [21]
 RN PROTEIN SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RP MEDLINE=96139497; PubMed=8576160; DOI=10.1074/jbc.271.3.1613;
 RA Behr D., Hesse L., Masters C.L., Multhaup G.;
 Query Match 91.2%; Score 31; DB 1; Length 770;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLIVFFAQ 7
 Db 687 KLIVFFAE 693
 RESULT 57
 A4 MACFA STANDARD; PRT; 770 AA.
 ID A4 MACFA
 AC P53601; Q60HH7; Q95KN7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31].
DE Name=APP; ORFNames=QCC8-1594;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RN NUCLEOTIDE SEQUENCE (ISOFORMS APP695 AND APP770).
RP TISSUE=Cerebellum;
RC MEDLINE=91273117; PubMed=1905108;
RA Podlany M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435 (1991).
RL [2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RP TISSUE=Brain cortex;
RA Kusuda J., Oeada N., Tanuma R., Hirata M., Sugano S., Hashimoto K.;
RT "Isolation and characterization of cDNA for macaque neurological
RT disease genes";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Functions as a cell surface receptor and performs a
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction. In vitro, copper-metallated APP induces neuronal
CC death directly or is potentiated through Cu(2+)-mediated low-
CC density lipoprotein oxidation (By similarity). Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPTI domain
CC possess protease inhibitor activity (By similarity).
CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -1- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK8IP1, and SHC1. Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPP, FPR1L, APPBP1, IBL, KNS2
CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DBP1.
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm

CC and nuclei of neurons (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=APP770;
CC IsoID=PS3601-1; Sequence=Displayed;
CC Name=APP695;
CC IsoID=PS3601-2; Sequence=VSP_000010, VSP_000011;
CC Name=3;
CC IsoID=PS3601-3; Sequence=VSP_013360, VSP_013361;
CC -1- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).
CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue. The NPXY site is also involved in clathrin-mediated
CC endocytosis (By similarity).
CC -1- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC C83 and C99. Subsequent processing of C83 by gamma-secretase
CC yields P3 peptides. This is the major secretory pathway and is
CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC gamma-secretase processing of C99 releases the amyloid beta
CC proteins, amyloid-beta 40 (Abeta40), and amyloid-beta 42 (Abeta42),
CC major components of amyloid plaques, and the cytotoxic C-terminal
CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC similarity).
CC -1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC (By similarity). Cleavage at Asp-739 by either caspase-3, 8 or -9
CC results in the production of the neurotoxic C31 peptide and the
CC increased production of beta-amyloid peptides (By similarity).
CC -1- PTM: N- and O-glycosylated (By similarity).
CC -1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific. Phosphorylation can affect APP
CC processing, neuronal differentiation and interaction with other
CC proteins (By similarity).
CC -1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates (By similarity).
CC Extracellular zinc-binding increases binding of heparin to APP and
CC inhibits collagen-binding (By similarity).
CC -1- SIMILARITY: Belongs to the APP family.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M58726; AAA36828.1; -; mRNA.
CC EMBL; M58727; AAA36829.1; -; mRNA.
CC EMBL; AB125150; BAD51938.1; -; mRNA.
CC HSSP; P08592; 1NMJ.
CC SMR; P53601; 28-123, 124-189, 287-342, 460-569.
CC InterPro; IPR008155; A4_APP.
CC InterPro; IPR008154; A4_extra.
CC InterPro; IPR001253; Beta-APP.
CC InterPro; IPR002223; Prot inh. Kunitz-m.
CC PANTHER; PTHR10083:SF6; Beta-APP; 6.
CC Pfam; PF02177; A4_EXTRA; 1.
CC Pfam; PF03494; Beta-APP; 1.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC PRINTS; PR00203; AMYLOIDA.
CC PRINTS; PR00759; BASICPTASE.

```

DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits;
KW Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron;
KW Metal-binding; Notch signaling pathway; Phosphorylation;
KW Protease inhibitor; Proteoglycan; Serine protease inhibitor; Signal;
KW Transmembrane; Zinc.
FT SIGNAL 1 17 By similarity.
FT CHAIN 18 770 Amyloid beta A4 protein.
FT CHAIN 18 687 Soluble APP-alpha (Potential).
FT CHAIN 18 671 Soluble APP-beta (Potential).
FT CHAIN 672 770 C39 (Potential).
FT CHAIN 672 713 Beta-amyloid protein 42 (Potential).
FT CHAIN 672 711 Beta-amyloid protein 40 (Potential).
FT CHAIN 688 770 C83 (Potential).
FT CHAIN 688 713 P3(42) (Potential).
FT CHAIN 712 770 Gamma-CTF(59) (Potential).
FT CHAIN 714 770 Gamma-CTF(57) (Potential).
FT CHAIN 721 770 Gamma-CTF(50) (Potential).
FT CHAIN 740 770 C31 (Potential).
FT TOPO_DOM 18 699 Extracellular (Potential).
FT TRANSMEM 700 723 Potential.
FT TOPO_DOM 724 770 Cytoplasmic (Potential).
FT DOMAIN 291 341 BPTI/Kunitz inhibitor.
FT REGION 96 110 Heparin-binding (By similarity).
FT REGION 181 188 Zinc-binding (By similarity).
FT REGION 391 423 Heparin-binding (By similarity).
FT REGION 491 522 Heparin-binding (By similarity).
FT REGION 523 540 Collagen-binding (By similarity).
FT REGION 732 751 Interaction with G(o)-alpha (By similarity).
FT MOTIF 724 734 Basolateral sorting signal (By similarity).
FT MOTIF 759 762 NPXY motif.
FT COMEBIAS 230 260 Asp/Glu-rich (acidic).
FT METAL 137 137 Poly-Thr.
FT METAL 147 147 Copper (By similarity).
FT METAL 149 149 Copper (By similarity).
FT METAL 151 151 Copper (By similarity).
FT METAL 677 677 Copper or zinc (By similarity).
FT METAL 681 681 Copper or zinc (By similarity).

Query Match 91.2%; Score 31; DB 1; Length 770;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
Db 687 KLVFFAE 693
|||||:

RESULT 58
A4 MOUSE STANDARD; PRT; 770 AA.
AC P12023; P97487; P97942; Q99K32;
DT 01-OCT-1989 (Rel. 12, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:
DE Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
DE (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
DE 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secreta
DE C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE (APP-C59); Gamma-CTF(57) (Gamma-secreta C-terminal fragment 57)

```

```

DE DE (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
DE DE (Gamma-secreta C-terminal fragment 50) (Amyloid intracellular domain
DE DE 50) (AID(50)); C31].
GN Name=App;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=88106489; PubMed=3322280;
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RL protein precursor.";
RN Biochem. Biophys. Res. Commun. 149:665-671(1987).
[2]
RP SEQUENCE REVISION.
RA Yamada T.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).
RC STRAIN-BALB/c; TISSUE=Brain;
RX MEDLINE=92098458; PubMed=1756177; DOI=10.1016/0167-4781(91)90231-A;
RA de Strooper B., van Leuven F., van den Bergh H.;
RT "The amyloid beta protein precursor or proteinase nexin II from mouse
RL is closer related to its human homolog than previously reported.";
RN Biochim. Biophys. Acta 1129:141-143(1991).
[4]
RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).
RC STRAIN=SAMP8; TISSUE=Hippocampus;
RX MEDLINE=21130647; PubMed=11235921; DOI=10.1139/bcb-79-1-57;
RA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
RA Alvarez J., Worley J.E.;
RT "Molecular cloning, expression, and regulation of hippocampal amyloid
RL precursor protein of senescence accelerated mouse (SAMP8).";
RN Biochem. Cell Biol. 79:57-67(2001).
[5]
RP NUCLEOTIDE SEQUENCE OF 1-19.
RX MEDLINE=92209998; PubMed=1555768; DOI=10.1016/0378-1119(92)90375-Y;
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M., Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RL Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RN Gene 112:189-195(1992).
[6]
RP PARTIAL NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM APP770).
RC TISSUE=Mammary tumor;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[7]
RP NUCLEOTIDE SEQUENCE OF 281-380, AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Kidney;
RX MEDLINE=89149813; PubMed=2493250;

```

RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 RN [8]
 RP NUCLEOTIDE SEQUENCE OF 289-364.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domesticus";
 RT precursor of Mus domesticus";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [9]
 RP NUCLEOTIDE SEQUENCE OF 656-737.
 RC STRAIN=129/Sv;
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecci M.,
 RA Loring J.P., Goate A.M.;
 RT "Introduction of six mutations into the mouse genome using 'Hit and
 RT Run' gene-targeting: introduction of familial Alzheimer's disease
 RT mutations into the mouse amyloid precursor protein gene and
 RT humanization of the A-beta fragment.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
 RX MEDLINE=93287808; PubMed=8510506; DOI=10.1016/0169-328X(93)90020-P;
 RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
 RT "Regional distribution of the alternatively spliced isoforms of beta
 RT APP RNA transcript in the brain of normal, heterozygous and homozygous
 RT weaver mutant mice as revealed by in situ hybridization
 RT histochemistry.";
 RL Brain Res. Mol. Brain Res. 17:340-346(1993).
 RN [11]
 RP INTERACTION WITH KNS2.
 RX MEDLINE=21010507; PubMed=11443355; DOI=10.1016/S0896-6273(00)00124-0;
 RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
 RT "Axonal transport of amyloid precursor protein is mediated by direct
 RT binding to the kinesin light chain subunit of kinesin-I.";
 RL Neuron 28:449-459(2000).
 RN [12]
 RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
 RC THR-743; TYR-757; ASN-759 AND TYR-762.
 RX MEDLINE=21408156; PubMed=1157249;
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,
 RA Kyriakis J.M., Nishimoto I.;
 RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/isolet-brain-1
 RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
 RL J. Neurosci. 21:6597-6607(2001).
 RN [13]
 RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
 RX MEDLINE=22028091; PubMed=11912189; DOI=10.1074/jbc.M108372200;
 RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
 RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
 RT with scaffold proteins of the JNK signaling cascade.";
 RL J. Biol. Chem. 277:20070-20078(2002).
 RN [14]
 RP INTERACTION OF CTF PEPTIDES WITH NUBS.
 RX MEDLINE=22008109; PubMed=12011466; DOI=10.1073/pnas.102192599;
 RA Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
 RA Meucci O., McGlade J.C., Rakic P., D'Adamio L.;
 RT "The gamma-secretase-generated intracellular domain of beta-amyloid
 RT precursor protein binds Numb and inhibits Notch signaling.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
 RN [15]
 RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
 RX MEDLINE=21437805; PubMed=1153691;
 RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
 RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
 RT gamma-secretase is rapidly degraded but distributes partially in a
 RT nuclear fraction of neurons in culture.";
 RL J. Neurochem. 78:1168-1178(2001).
 RN [1]
 RP FUNCTION: Functions as a cell surface receptor and performs

CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions. Can promote transcription activation through binding
 CC to APBB1/Tip60 and inhibit Notch signaling through interaction
 CC with Numb. Couples to apoptosis-inducing pathways such as those
 CC mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By
 CC similarity). Acts as a kinesin I membrane receptor, mediating the
 CC axonal transport of beta-secretase and presenilin 1. May be
 CC involved in copper homeostasis/oxidative stress through copper ion
 CC reduction. Can regulate neurite outgrowth through binding to
 CC components of the extracellular matrix such as heparin and
 CC collagen I and IV (By similarity). The splice isoforms that
 CC contain the BPTI domain possess protease inhibitor activity (By
 CC similarity).
 CC FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPX II-
 CC mediated phosphorylation (By similarity).
 CC FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis.
 CC SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
 CC its serine phosphorylation. Also interacts with GPCR-like protein
 CC BPP, PPRL1, APPBP1, IBI, KNS2 (via its TPR domains), APPBP2 (via
 CC BASS) and DDB1 (By similarity). In vitro, it binds MAPT via the
 CC MT-binding domains (By similarity). Associates with microtubules
 CC in the presence of APP and in a kinesin-dependent manner (By
 CC similarity). Interacts, through a C-terminal domain, with GNAO1
 CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
 CC neurons (By similarity). Beta-amyloid associates with HADH2 (By
 CC similarity).
 CC INTERACTION:
 CC P98084:Apba2; NbExp=1; IntAct=EBI-78814, EBI-81669;
 CC Q90XJ1:Apbb1; NbExp=1; IntAct=EBI-78814, EBI-81338;
 CC P97318:Dab1; NbExp=1; IntAct=EBI-78814, EBI-81680;
 CC
 CC Query Match 91.2%; Score 31; DB 1; Length 770;
 CC Best Local Similarity 85.7%; Pred. NO. 1.9e+02;
 CC Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 KLVFFAQ 7
 CC DB 687 KLVFFPAE 693
 CC
 CC RESULT 59
 CC A4_PANTR STANDARD; PRT; 770 AA.
 CC ID A4_PANTR
 CC AC Q5IS80;
 CC DT 10-MAY-2005 (Rel. 47, Created)
 CC DT 10-MAY-2005 (Rel. 47, Last sequence update)
 CC DT 13-SEP-2005 (Rel. 48, Last annotation update)
 CC DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 CC amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 CC Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
 CC APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
 CC Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 CC (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 CC secretase C-terminal fragment 50); C31].
 CC DE Name=APP;
 CC GN Name=APP;
 CC OS Pan troglodytes (Chimpanzee).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 CC OC Pan.
 CC OX NCBI_TaxID=9598;
 CC RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].
RX PubMed:15620360; DOI:10.1016/j.cell.2004.11.040;
RA Dorus S., Vallender E.J., Evans P.D., Andersen J.R., Gilbert S.L.,
RA Mahowald M., Wyckoff G.J., Malcom C.M., Lahn B.T.;
RT "Accelerated evolution of nervous system genes in the origin of Homo
RT sapiens";
RL Cell 119:1027-1040 (2004).

CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell motility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/rip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(o) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction. In vitro, copper-metallated APP induces neuronal
CC death directly or is potentiated through Cu(2+)-mediated low-
CC density lipoprotein oxidation (By similarity). Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPTI domain
CC possess protease inhibitor activity (By similarity).

CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).

CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).

CC -!- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
CC cytoplasmic proteins, and SHC1, Numb and Dab1 (By similarity). Binding
CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPP, FRLP1, IBL, KNS2
CC (via its TPR domains) (By similarity), APPBP2 (via Bass) and DDB1.
CC In vitro, it binds MAPT via the WT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC and nuclei of neurons (By similarity).

CC -!- DOMAIN: The basolateral sorting signal (Bass) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).

CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue. The NPXY site is also involved in clathrin-mediated
CC endocytosis (By similarity).

CC -!- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC C83 and C99. Subsequent processing of C83 by gamma-secretase
CC yields p3 peptides. This is the major secretory pathway and is
CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC gamma-secretase processing of C99 releases the amyloid beta

CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC major components of amyloid plaques, and the cytotoxic C-terminal
CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC similarity).

CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC results in the production of the neurotoxic C31 peptide and the
CC increased production of beta-amyloid peptides (By similarity).

CC -!- PTM: N- and O-glycosylated (By similarity).

CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific. Phosphorylation can affect APP
CC processing, neuronal differentiation and interaction with other
CC proteins (By similarity).

CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates (By similarity).
CC Extracellular zinc-binding increases binding of heparin to APP and
CC inhibits collagen-binding (By similarity).

CC -!- SIMILARITY: Belongs to the APP family.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
CC EMBL; AY655248; AAV74286.1; -; mRNA.
CC SMR; Q5IS80; 28-123, 124-189, 287-342, 460-569.
CC InterPro; IPR008155; A4_APP.
CC InterPro; IPR008154; A4_extra.
CC InterPro; IPR001255; Beta-APP.
CC InterPro; IPR012282; Cytochrome C R.
CC PANTHER; PTHR10093.SF6; Beta-APP; 6.
CC Pfam; PF02177; A4_EXTRA; 1.
CC Pfam; PF03494; Beta-APP; 1.
CC Pfam; PF00014; Kunitz BPTI; 1.
CC PRINTS; PR00203; AMYLOIDA4.
CC PRINTS; PR00759; BASICPTASE.
CC PRINTS; PR00204; BETAMYLOID.
CC ProDom; PD000222; Prot_inh_Kunz-m; 1.
CC SMART; SM00006; A4_EXTRA; 1.
CC SMART; SM00131; KU; 1.
CC PROSITE; PS00319; A4_EXTRA; 1.
CC PROSITE; PS00320; A4_INTRA; 1.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
CC PROSITE; PS02279; BPTI_KUNITZ_2; 1.

CC Amyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis;
CC Glycoprotein; Heparin-binding; Iron; Metal-binding;
CC Notch signaling pathway; Phosphorylation; Protease inhibitor;
CC Proteoglycan; Serine protease inhibitor; Signal; Transmembrane; Zinc.

FT SIGNAL 1 17 By similarity.
FT CHAIN 18 770 Amyloid beta A4 protein.
FT CHAIN 18 687 Soluble APP-alpha (Potential).
FT CHAIN 18 671 Soluble APP-beta (Potential).
FT CHAIN 672 770 C99 (Potential).
FT CHAIN 672 713 Beta-amyloid protein 42 (Potential).
FT CHAIN 672 711 Beta-amyloid protein 40 (Potential).
FT CHAIN 688 770 C83 (Potential).
FT PEPTIDE 688 713 P3(42) (Potential).
FT PEPTIDE 688 711 Gamma-CTF(59) (Potential).
FT CHAIN 712 770 Gamma-CTF(57) (Potential).
FT CHAIN 714 770 Gamma-CTF(50) (Potential).
FT CHAIN 721 770 C31 (Potential).
FT CHAIN 740 770 Extracellular (Potential).
FT TOPO_DOM 18 699 Potential.
FT TRANSMEM 700 723 Cytoplasmic (Potential).
FT TOPO_DOM 724 770 BPTI/Kunitz inhibitor.
FT DOMAIN 291 341 Heparin-binding (By similarity).
FT REGION 96 110 Zinc-binding (By similarity).
FT REGION 181 188 Heparin-binding (By similarity).
FT REGION 391 423

PT REGION 491 522 Heparin-binding (By similarity).
PT REGION 523 540 Collagen-binding (By similarity).
PT REGION 732 751 Interaction with G(o)-alpha (By similarity).
FT MOTIF 724 734 Basolateral sorting signal (By similarity).
FT MOTIF 759 762 NPXY motif.
FT COMPBIAS 230 260 Asp/Glu-rich (acidic).
FT COMPBIAS 274 280 Poly-Thr.
FT METAL 137 137 Copper (By similarity).
FT METAL 147 147 Copper (By similarity).
FT METAL 149 149 Copper (By similarity).
FT METAL 151 151 Copper (By similarity).
FT METAL 677 677 Copper or zinc (By similarity).
FT METAL 681 681 Copper or zinc (By similarity).
FT METAL 684 684 Copper or zinc (By similarity).
FT METAL 685 685 Copper or zinc (By similarity).
FT SITE 144 144 Required for Cu(2+) reduction (By similarity).
FT SITE 301 302 Reactive bond (By similarity).
FT SITE 671 672 Cleavage (by beta-secretase) (By similarity).
FT SITE 672 673 Cleavage (by caspase-6) (By similarity).
FT SITE 687 688 Cleavage (by alpha-secretase) (By similarity).
FT SITE 704 704 Implicated in free radical propagation (By similarity).
FT SITE 706 706 Susceptible to oxidation (By similarity).
FT SITE 711 712 Cleavage (by gamma-secretase; site 1) (By similarity).
FT SITE 713 714 Cleavage (by gamma-secretase; site 2) (By similarity).
FT SITE 720 721 Cleavage (by gamma-secretase; site 3) (By similarity).
FT SITE 739 740 Cleavage (by caspases-6, -8 or -9) (By similarity).
Query Match 91.28; Score 31; DB 1; Length 770;
Best Local Similarity 85.74; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFAQ 7
DB 687 KLVFFAE 693
RESULT 60
A4_PIG STANDARD; PRT; 770 AA.
AC PF5307; Q29023; Q9TU10;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease amyloid protein homolog) (Contains: Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C311).
GN Name=APP;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kimura A., Takahashi T.;
RT "Amyloid precursor protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1-136.
RC TISSUE=Small intestine;

RA Winteroe A.K., Fredholm M.;
RT "Evaluation and characterization of a porcine small intestine CDNA library.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE OF 667-723.
RX TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functions as a cell surface receptor and performs physiological functions on the surface of neurons relevant to neurite growth, neuronal adhesion and axonogenesis. Involved in cell mobility and transcription regulation through protein-protein interactions (By similarity). Can promote transcription activation through binding to APBB1/Tip60 and inhibit Notch signaling through interaction with Numb (By similarity). Couples to apoptosis-inducing pathways such as those mediated by G(O) and JIP (By similarity). Inhibits G(o) alpha APase activity (By similarity). Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin 1 (By similarity). May be involved in copper homeostasis/oxidative stress through copper ion reduction (By similarity). In vitro, copper-metalated APP induces neuronal death directly or is potentiated through Cu(2+)-mediated low-density lipoprotein oxidation (By similarity). Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminus, to the PID domain of several cytoplasmic proteins, including APBB family members, the APBA family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP, FPR1, APPB1, IB1, KNS2 (via its TPR domains) (By similarity), APPB2 (via BASS) and DDB1. In vitro, it binds MAPT via the MT-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).
CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).
CC -!- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the

retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Aβeta40) and amyloid-beta 42 (Aβeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF (50), gamma-CTF (57) and gamma-CTF (59) (By similarity).

-!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-!- PTM: N- and O-glycosylated (By similarity).

-!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-!- PTM: Extracellular binding and reduction of copper, results in a corresponding oxidation of Cys-144 and Cys-158, and the formation of a disulfide bond (By similarity).

-!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-!- SIMILARITY: Belongs to the APP family.

-!- SIMILARITY: Contains 1 BPTi/Kunitz inhibitor domain.

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

EMBL; AB032550; BAA84580.1; -; mRNA.
 EMBL; 284022; CAB06313.1; -; mRNA.
 EMBL; X56127; CAA39592.1; -; mRNA.
 HSSP; P08592; 1NMJ.
 SMR; P79307; 28-123, 124-189, 287-342, 460-569.
 InterPro; IPR008155; A4_APP.
 InterPro; IPR008154; A4_extra.
 InterPro; IPR001255; Beta_APP.
 InterPro; IPR002223; Prot_inh_Kunz-m.
 PANTHER; PTHR10083.SF6; Beta_APP; 6.
 Pfam; PF02177; A4_EXTRA; 1.
 Pfam; PF03494; Beta_APP; 1.
 Pfam; PF00014; Kunitz_BPTi; 1.
 PRINTS; PR00203; AMYLOID4.
 PRINTS; PR00759; BASICPTASE.
 PRINTS; PR00204; BETAAMYLOID.
 ProDom; PD000222; Prot_inh_Kunz-m; 1.
 SMART; SM00006; A4_EXTRA; 1.
 SMART; SM00131; KU; 1.
 PROSITE; PS00319; A4_EXTRA; 1.
 PROSITE; PS00320; A4_INTRA; 1.
 PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Amyloid; Apoptosis; Cell adhesion; Coated pits; Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron; Metal-binding; Notch signaling pathway; Phosphorylation; Protease inhibitor; Serine protease inhibitor; Signal; Transmembrane; Zinc.
 SIGNAL 1 17 By similarity.
 FT CHAIN 18 770 Amyloid beta A4 protein.
 FT CHAIN 18 687 Soluble APP-alpha (Potential).
 FT CHAIN 18 671 Soluble APP-beta (Potential).
 FT CHAIN 672 713 C99 (By similarity).
 FT CHAIN 672 711 Beta-amyloid protein 40 (By similarity).
 FT CHAIN 672 713 Beta-amyloid protein 42 (By similarity).
 FT CHAIN 688 713 C83 (By similarity).
 FT PEPTIDE 688 713 P3(42) (By similarity).
 FT PEPTIDE 688 711 P3(40) (By similarity).
 FT CHAIN 712 770 Gamma-CTF (59).

FT	CHAIN	714	770	Gamma-CTF (57).
FT	CHAIN	721	770	Gamma-CTF (50) (By similarity).
FT	CHAIN	740	770	C31 (By similarity).
FT	TOPO_DOM	18	699	Extracellular (Potential).
FT	TRANSMEM	700	723	Potential.
FT	TOPO_DOM	724	770	Cytoplasmic (Potential).
FT	DOMAIN	291	341	BPTi/Kunitz inhibitor.
FT	REGION	96	110	Heparin-binding (By similarity).
FT	REGION	135	155	Copper-binding (By similarity).
FT	REGION	181	188	Zinc-binding (By similarity).
FT	REGION	391	423	Heparin-binding (By similarity).
FT	REGION	491	522	Heparin-binding (By similarity).
FT	REGION	523	540	Collagen-binding (By similarity).
FT	REGION	732	751	Interaction with G(o)-alpha (By similarity).
FT	MOTIF	724	734	Basolateral sorting signal.
FT	MOTIF	759	762	NPKY motif.
FT	COMPBias	230	260	Asp/Glu-rich (acidic).
FT	COMPBias	274	280	Poly-Thr.
FT	METAL	137	137	Copper (By similarity).
FT	METAL	147	147	Copper (By similarity).
FT	METAL	149	149	Copper (By similarity).
FT	METAL	151	151	Copper (Probable).
FT	METAL	677	677	Copper or zinc (By similarity).
FT	METAL	681	681	Copper or zinc (Probable).
FT	METAL	684	684	Copper or zinc (By similarity).
FT	METAL	685	685	Copper or zinc (By similarity).
FT	SITE	144	144	Required for Cu(2+) reduction (By similarity).

Query Match 91.2%; Score 31; DB 1; Length 770;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
 |||||:
 Db 687 KLVFFAE 693

RESULT 61
 A4_RAT
 ID A4_RAT STANDARD; PRT; 770 AA.
 AC P08592;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF (59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF (57) (Gamma-secretase C-terminal fragment 57); Gamma-CTF (50) (Gamma-secretase C-terminal fragment 50); C31].
 GN Name=APP;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=88312583; PubMed=2900758;
 RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K., Seeburg P.H.;
 RA "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.";
 RL EMBO J. 7:1365-1370(1988).
 [2]
 RP PROTEIN SEQUENCE OF 18-44.
 RX MEDLINE=88264430; PubMed=2968652;
 RA Schubert D., Schroeder R., LaCorbiere M., Saitoh T., Cole G.;
 RT "Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core protein.";

RL Science 241:223-226 (1988).
 RN [3]
 RP PROTEIN SEQUENCE OF 18-32.
 RX MEDLINE=91217087; PubMed=1673681;
 RA Potempa A., Styles J., Mehta P., Kim K.S., Miller D.L.;
 RT "Purification and tissue level of the beta-amyloid peptide precursor
 of rat brain.";
 RL J. Biol. Chem. 266:8464-8469 (1991).
 RN [4]
 RP NUCLEOTIDE SEQUENCE OF 289-364.
 RC TISSUE=Liver;
 RX MEDLINE=89183625; PubMed=2648331;
 RA Kang J., Mueller-Hill B.;
 RT "The sequence of the two extra exons in rat preA4.";
 RL Nucleic Acids Res. 17:2130-2130 (1989).
 RN [5]
 RP PROTEIN SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
 RX MEDLINE=21443797; PubMed=11483588; DOI=10.1074/jbc.C100357200;
 RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
 RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
 family resembling gamma-secretase-like cleavage of Notch.";
 RL J. Biol. Chem. 276:35235-35238 (2001).
 RN [6]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=96187032; PubMed=8624099;
 RA Sandbrink R., Masters C.L., Beyreuther K.;
 RT "APP gene family. Alternative splicing generates functionally related
 isoforms.";
 RL Ann. N. Y. Acad. Sci. 777:281-287 (1996).
 RN [7]
 RP TISSUE SPECIFICITY OF APPICAN.
 RX MEDLINE=9526326; PubMed=7744833; DOI=10.1074/jbc.270.20.11839;
 RA Shioi J., Pangalos M.N., Ripellino J.A., Vassiliacopoulou D.,
 RA Mytilineou C., Margolis R.U., Robakis N.K.;
 RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
 brain and is produced by astrocytes but not by neurons in primary
 neural cultures.";
 RL J. Biol. Chem. 270:11839-11844 (1995).
 RN [8]
 RP TISSUE SPECIFICITY OF ISOFORMS.
 RX MEDLINE=97150061; PubMed=8995834;
 RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
 RT "Expression of the APP gene family in brain cells, brain development
 and aging.";
 RL Gerontology 43:119-131 (1997).
 RN [9]
 RP INTERACTION WITH DBP1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
 TYR-762.
 RX MEDLINE=99127916; PubMed=9930726;
 RA Watanabe T., Sukeyawa J., Tomita S., Iijima K.-I., Oguchi S.,
 RA Suzuki T., Nairn A.C., Greengard P.;
 RT "A 127-kDa protein (UV-DBP) binds to the cytoplasmic domain of the
 Alzheimer's amyloid precursor protein.";
 RL J. Neurochem. 72:549-556 (1999).
 RN [10]
 RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.
 RX MEDLINE=99162676; PubMed=10024359;
 RA Brouillet E., Tremblay A., Galanaud D., Volovitch M., Boulliot C.,
 RA Valenza C., Prochiantz A., Allinquant B.;
 RT "The amyloid precursor protein interacts with Go heterotrimeric
 protein within a cell compartment specialized in signal
 transduction.";
 RL J. Neurosci. 19:1717-1727 (1999).
 RN [11]
 RP COPPER-BINDING.
 RX MEDLINE=94320627; PubMed=7913895; DOI=10.1016/0014-5793(94)00658-X;
 RA Heese L., Behr D., Masters C.L., Multhaup G.;
 RT "The beta A4 amyloid precursor protein binding to copper.";
 RL FEBS Lett. 349:109-116 (1994).
 RN [12]
 RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
 RX MEDLINE=95256193; PubMed=7737970; DOI=10.1074/jbc.270.18.10388;
 RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
 RT "The chondroitin sulfate attachment site of appican is formed by
 splicing out exon 15 of the amyloid precursor gene.";
 RL J. Biol. Chem. 270:10388-10391 (1995).
 RN [13]
 RP BETA-AMYLOID METAL-BINDING.
 RX MEDLINE=99316162; PubMed=10386999; DOI=10.1021/bi990438f;
 RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
 RA Scarpa R.C., Cuaungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
 RA Bush A.I.;
 RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
 peroxide through metal ion reduction.";
 RL Biochemistry 38:7609-7616 (1999).
 RN [14]
 RP BETA-AMYLOID ZINC-BINDING.
 RX MEDLINE=99343552; PubMed=10413512; DOI=10.1021/bi990205o;
 RA Liu S.T., Howlett G., Barrow C.J.;
 RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
 of the A beta peptide of Alzheimer's disease.";
 RL Biochemistry 38:9373-9378 (1999).
 RN [15]
 RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
 GLY-704.
 RX MEDLINE=21959460; PubMed=11959460; DOI=10.1016/S0925-4439(01)00097-7;
 RA Kaneki J., Varadarajan S., Aksenova M., Butterfield D.A.;
 RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
 peptide 1-42-associated oxidative stress and neurotoxicity.";
 RL Biochim. Biophys. Acta 1586:190-198 (2001).
 RN [16]
 RP PHOSPHORYLATION.
 RX MEDLINE=97239592; PubMed=9085254;
 RA Olshi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
 RA Greengard P., Suzuki T.;
 RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
 phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
 cultured cells.";
 RL Mol. Med. 3:111-123 (1997).
 RN [17]
 RP PHOSPHORYLATION SITE SER-730.
 RX MEDLINE=99262094; PubMed=10329382; DOI=10.1006/bbrc.1999.0637;
 RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
 RA Greengard P., Nairn A.C., Suzuki T.;
 RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
 precursor protein at Ser655 by a novel protein kinase.";
 RL Biochem. Biophys. Res. Commun. 258:300-305 (1999).
 RN [18]
 RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
 THR-743.
 RX MEDLINE=99274744; PubMed=10341243;
 RA Ando K., Olshi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
 RA Kirino Y., Greengard P., Suzuki T.;
 RT "Role of phosphorylation of Alzheimer's amyloid precursor protein
 during neuronal differentiation.";
 RL J. Neurosci. 19:4421-4427 (1999).
 RN [19]
 RP PHOSPHORYLATION SITE THR-743.
 RX MEDLINE=20396183; PubMed=10936190;
 RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
 RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
 RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
 protein by cyclin-dependent kinase 5.";
 RL J. Neurochem. 75:1085-1091 (2000).
 RN [20]
 RP CARBOHYDRATE STRUCTURE OF APPICAN.
 RX MEDLINE=21463085; PubMed=11479316; DOI=10.1074/jbc.M105818200;
 RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
 RA Suganara K., Robakis N.K.;
 RT "Appican, the proteoglycan form of the amyloid precursor protein,
 contains chondroitin sulfate E in the repeating disaccharide region
 and 4-O-sulfated galactose in the linkage region.";
 RL J. Biol. Chem. 276:37155-37160 (2001).
 RN [21]
 RP FUNCTION. Functions as a cell surface receptor and performs
 physiological functions on the surface of neurons relevant to
 neurite growth, neuronal adhesion and axonogenesis. Involved in

cell mobility and transcription regulation through protein-protein interactions (By similarity). Can promote transcription activation through binding to APBB1/Tip60 and inhibit Notch signaling through interaction with Numb (By similarity). Couples to apoptosis-inducing pathways such as those mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin 1 (By similarity). May be involved in copper homeostasis/oxidative stress through copper ion reduction. Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity). The splice isoforms that contain the BPTI domain possess protease inhibitor activity (By similarity).

-!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron. Rat and mouse beta-amyloid peptides bind only weakly transient metals and have little reducing activity due to substitutions of transient metal chelating residues. Beta-APP42 may activate mononuclear phagocytes in the brain and elicit inflammatory responses. Promotes both tau aggregation and TPK II-mediated phosphorylation (By similarity).

Query Match 91.2%; Score 31; DB 1; Length 770;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFPAQ 7
 |||||:
 Db 687 KLVFPAE 693

RESULT 62

Q6RH30 CANFA
 ID Q6RH30 CANFA PRELIMINARY; PRT; 770 AA.

AC Q6RH30
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DE Beta amyloid protein isoform APP770.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.

OX NCBI_TaxID=9615;

RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Nakata M.;

RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

DR EMBL; AY498706; AAR9726.1; -; mRNA.

DR HSSP; Q16019; 1AAP.

DR SMR; Q6RH30; 28-123, 124-189, 287-342, 460-569.

DR Ensembl; ENSCARG0000008557; Canis familiaris.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

DR InterPro; IPR008155; A4_APP.

DR InterPro; IPR001255; Beta-APP.

DR InterPro; IPR002223; Prot_inh_Kunz-m.

DR Pfam; PF02177; A4_EXTRA; 1.

DR Pfam; PF03494; Beta-APP; 1.

DR Pfam; PF00014; Kunitz BPTI; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00759; BASICPTASE.

DR PRINTS; PR00204; BETAAMYLOID.

DR ProDom; PD000222; Prot_inh_Kunz-m; 1.

DR SMART; SM00006; A4_EXTRA; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
 SQ SEQUENCE 770 AA; 86929 MW; 4560E18BB405F588 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 770;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFPAQ 7
 |||||:
 Db 687 KLVFPAE 693

RESULT 63

Q56JK6 CANFA
 ID Q56JK6 CANFA PRELIMINARY; PRT; 770 AA.

AC Q56JK6

DT 10-MAY-2005 (TRENBLrel. 30, Created)

DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)

DE Beta-amyloid protein 770.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;

OC Canis.

OX NCBI_TaxID=9615;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;

RT "Relationship between canine dementia and Alzheimer's disease.";

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY926579; AAX81908.1; -; mRNA.

DR SMR; Q56JK6; 28-123, 124-189, 287-342, 460-569.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0020037; F:heme binding; IEA.

DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR008155; A4_APP.

DR InterPro; IPR008154; A4_extra.

DR InterPro; IPR01255; Beta-APP.

DR InterPro; IPR012282; Cytochrome_c_R.

DR Pfam; PF02177; A4_EXTRA; 1.

DR Pfam; PF03494; Beta-APP; 1.

DR Pfam; PF00014; Kunitz BPTI; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00759; BASICPTASE.

DR PRINTS; PR00204; BETAAMYLOID.

DR SMART; SM00006; A4_EXTRA; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00320; A4_INTRA; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.

SQ SEQUENCE 770 AA; 86998 MW; 81ADDE2D3FB8DC6D CRC64;

Query Match

Best Local Similarity 91.2%; Score 31; DB 2; Length 770;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFPAQ 7
 |||||:
 Db 687 KLVFPAE 693

RESULT 64

Q53ZT3 MOUSE
 ID Q53ZT3 MOUSE PRELIMINARY; PRT; 770 AA.

AC Q53ZT3

DT 13-SEP-2005 (TRENBLrel. 31, Created)

DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)

DE Amyloid-beta protein-like protein long isoform.

GN Name=App;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RA Szendro P.I., Cadenas C., Eichele G.;
 RT "Sequence of an alternative spliced amyloid-beta precursor protein
 RT homolog.";
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DE EMBL; AY267348; AAF23169.1; -; mRNA.
 DR MGI; MGI:88059; App.
 DR GO; GO:0016021; C: integral to membrane; IDA.
 DR GO; GO:0016020; C: membrane; TAS.
 DR GO; GO:0005515; P: protein binding; IPI.
 DR GO; GO:0030198; P: extracellular matrix organization and bioge. .; IGI.
 SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CA7A CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 770;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFPAQ 7
 |||||
 DB 687 KLVFFFAE 693
 RESULT 65
 Q547B7 RAT PRELIMINARY; PRT; 770 AA.
 AC Q547B7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE APP770.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN NUCLEOTIDE SEQUENCE.
 RP Feng J., Song S., Zheng J.;
 RT "A new beta amyloid precursor protein cDNA found in Rat6 embryo
 RT fibroblasts.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DE EMBL; AF513015; AAM90259.1; -; mRNA.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0005488; P: binding; IEA.
 DR GO; GO:0020037; P: heme binding; IEA.
 DR GO; GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
 DR GO; GO:0006118; P: electron transport; IEA.
 SQ SEQUENCE 770 AA; 86704 MW; C26C9D6B2929A7 CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 770;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFPAQ 7
 |||||
 DB 687 KLVFFFAE 693
 RESULT 66
 A4 TETFL
 ID A4_TETFL STANDARD; PRT; 780 AA.
 AC Q73683;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog precursor (Contains:
 DE Beta-amyloid protein (Beta-APP) (A-beta)).
 GN Name=APP;
 OS Tetraodon fluviatilis (Puffer fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OC NCBI_TaxID=47145;
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE; 98252138; PubMed=9599080; DOI=10.1016/S0378-1119(98)00032-8;
 RA Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
 RT "Analysis of pufferfish homologues of the A1-rich human APP gene.";
 RL Gene 210:17-24(1998).
 CC -1- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the APP family.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 DE EMBL; AF018165; AAC41275.1; -; mRNA.
 DR HSP; P10646; IIRH.
 DR SNR; O73683; 29-124, 478-586.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Prot inh Kunz-m.
 DR PANTHER; PTHR10083:SP6; Beta-APP; 5.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR ProDom; PD000222; Prot inh Kunz-m; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KW Amyloid; Glycoprotein; Protease inhibitor; Serine protease inhibitor;
 KW Signal; Transmembrane.
 FT SIGNAL 1 18 Potential.
 FT CHAIN 19 780 Alzheimer's disease amyloid A4 protein
 FT homolog.
 FT TOPO_DOM 682 724 Beta-amyloid protein (Potential).
 FT TRANSMEM 712 732 Extracellular (Potential).
 FT TOPO_DOM 733 780 Potential.
 FT DOMAIN 323 382 Cytoplasmic (Potential).
 FT SITE 769 772 BPTI/Kunitz inhibitor.
 FT CARBOHYD 560 560 Clathrin-binding (By similarity).
 FT DISULFID 327 378 N-linked (GLCNAC...) (Potential).
 FT DISULFID 336 361 By similarity.
 FT SEQUENCE 780 AA; 88238 MW; 60071BE94520191D CRC64;
 Query Match 91.2%; Score 31; DB 1; Length 780;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFPAQ 7
 |||||
 DB 697 KLVFFFAE 703

```

RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RT Hammon N., Iserani S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AALH01000042; EMB17351.1; -; Genomic DNA.
SQ SEQUENCE 364 AA; 40535 MW; 7A0B6786C6815E29 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 364;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 157 KLVFFVQ 163
|||||

RESULT 69
Q54L66.DICDI PRELIMINARY; PRT; 421 AA.
AC Q54L66;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DD0187166;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugchang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Turggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Filcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsey R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Lousaged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox B.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAF101000141; EAL63992.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 421 AA; 48326 MW; EA92A3934FE63F36 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 421;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;

```

```

RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RT Hammon N., Iserani S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AALH01000042; EMB17351.1; -; Genomic DNA.
SQ SEQUENCE 364 AA; 40535 MW; 7A0B6786C6815E29 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 364;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 157 KLVFFVQ 163
|||||

RESULT 69
Q54L66.DICDI PRELIMINARY; PRT; 421 AA.
AC Q54L66;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DD0187166;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugchang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Turggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Filcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsey R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Lousaged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox B.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAF101000141; EAL63992.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 421 AA; 48326 MW; EA92A3934FE63F36 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 421;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;

```

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7
||:|:
Db 75 KLIFPAQ 81

RESULT 70

Q4N8N8_THEPA
ID Q4N8N8_THEPA PRELIMINARY; PRT; 480 AA.
AC Q4N8N8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=TP01_0426;
OS Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxID=5875;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J.,
RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,
RA Silva J.C., Uterback T.R., Feldblyum T.V., Pertea M., Allen J.,
RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
RA Venter J.C., Fraser C.M., Nene V.;
RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RT "Genome sequence of Theileria parva, a bovine pathogen that transforms
RT lymphocytes."
RL Science 309:134-137(2005).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Uterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RC -1- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 042C35CDC02A7158 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 480;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7
||:|:
Db 108 KLIFPAE 114

RESULT 71

Q4UGZ4_THEAN
ID Q4UGZ4_THEAN PRELIMINARY; PRT; 557 AA.
AC Q4UGZ4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=TA20805;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;

OC Theileria.
OX NCBI_TaxID=5874;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrell B.G.;
RA "The chromosome 1 sequence of Theileria annulata."
RT Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR940347; CAI73645.1; -; Genomic_DNA.
DR Hypothetical protein.
KW SEQUENCE 557 AA; 64191 MW; 203AA30E5F22D073 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 557;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7
||:|:
Db 191 KLIFPAE 197

RESULT 72

Q728F0_DESVH
ID Q728F0_DESVH PRELIMINARY; PRT; 66 AA.
AC Q728F0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=DVU2653;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS 8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
[1]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15077118; DOI=10.1038/nbt959;
RX Heideberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.P., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Daviden T.M., Zafar N., Zhou L., Radune D.,
RA Dmitrov G., Hance M., Tran K., Khouri H.M., Gill J., Uterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough."
RL Nat. Biotechnol. 22:554-559(2004).
DR EMBL; AB017318; AAS97125.1; -; Genomic_DNA.
DR TIGR; DVU2653; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 66 AA; 7605 MW; 633FBB080C3962A6 CRC64;

Query Match 85.3%; Score 29; DB 2; Length 66;
Best Local Similarity 71.4%; Pred. No. 56;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7
||:|:
Db 35 KLIFPAK 41

RESULT 73

Q6D3D0_ERWCT
ID Q6D3D0_ERWCT PRELIMINARY; PRT; 81 AA.
AC Q6D3D0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Molybdopterin converting factor subunit 1.
GN Namesoad; Synonyms=chlA4, chlM; OrderedLocusNames=ECA2814;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).

```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holvea M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmon G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RA "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
DR EMBL; BX950851; CAG75714.1; -; Genomic DNA.
DR GO; GO:0006777; P:mo-molybdopterin cofactor biosynthesis; IEA.
DR GO; GO:0006790; P:sulfur metabolism; IEA.
DR InterPro; IPR010034; Moad.
DR InterPro; IPR003749; This.
DR Pfam; PF02597; This; 1.
DR TIGRFAMs; TIGR01682; moad; 1.
KW Complete proteome.
SQ SEQUENCE 81 AA; 8998 MW; 81EBB4AB90A96911 CRC64;

Query Match 85.3%; Score 29; DB 2; Length 81;
Best Local Similarity 71.4%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 3 KILFFAQ 9

RESULT 74
QBVR5 ECOLI
ID Q8VR5 ECOLI PRELIMINARY; PRT; 95 AA.
AC Q8VR5;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE CadC (Fragment).
GN Name=cadC;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=83/39;
RX MEDLINE=22063667; PubMed=12067342;
RA Tauschek M., Strugnell R.A., Robins-Browne R.M.;
RT "Characterization and evidence of mobilization of the LEE
RT pathogenicity island of rabbit-specific strains of enteropathogenic
RT Escherichia coli.";
RL Mol. Microbiol. 44:1533-1550(2002).
DR EMBL; AF453441; AAL57517.1; -; Genomic DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR001867; Trans_reg_C.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00486; Trans_reg_C; 1.
DR ProDom; PD000329; Trans_reg_C; 1.
FT NON_TER 95
SQ SEQUENCE 95 AA; 10865 MW; 1569318B458687D5 CRC64;

Query Match 85.3%; Score 29; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFAQ 7
DB 3 KILFFAQ 9

RESULT 75
Q6GZK0 ECOLI
ID Q6GZK0 ECOLI PRELIMINARY; PRT; 97 AA.
AC Q6GZK0;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Cad operon transcriptional activator (Fragment).
GN Name=cadC;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=4787;
RX PubMed=15358417; DOI=10.1016/j.femsle.2004.07.052;
RA Derfulian H., Tremblay D., Hazel J.;
RT "Molecular characterization of extraintestinal pathogenic Escherichia
RT coli (ExPEC) pathogenicity islands in F165-positive E. coli strain
RT from a diseased animal.";
RL FEMS Microbiol. Lett. 238:321-332(2004).
DR EMBL; AY560911; AAT48691.1; -; Genomic DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR001867; Trans_reg_C.
DR Pfam; PF00486; Trans_reg_C; 1.
DR ProDom; PD000329; Trans_reg_C; 1.
FT NON_TER 97
SQ SEQUENCE 97 AA; 11079 MW; B4DC0569318B4586 CRC64;

Query Match 85.3%; Score 29; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFAQ 7
DB 37 LVFFAQ 42

Search completed; December 29, 2005, 17:47:37
Job time : 99.2258 secs

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:57 ; Search time 15.129 Seconds
(without alignments)
44.518 Million cell updates/sec

Title: US-10-009-122-18
Perfect score: 34
Sequence: 1 KLVPFAO 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

```
Minimum DB seg length: 0
Maximum DB seg length: 20000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : PIR 80:★

```
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	31	91.2	43	2	S23094		beta-amyloid prote
2	31	91.2	42	2	PN0512		beta-amyloid prote
3	31	91.2	57	2	A60045		Alzheimer's diseas
4	31	91.2	57	2	F60045		Alzheimer's diseas
5	31	91.2	57	2	D60045		Alzheimer's diseas
6	31	91.2	57	2	E60045		Alzheimer's diseas
7	31	91.2	57	2	G60045		Alzheimer's diseas
8	31	91.2	57	2	B60045		Alzheimer's diseas
9	31	91.2	82	2	PQ0438		Alzheimer's diseas
10	31	91.2	695	1	A49795		Alzheimer's diseas
11	31	91.2	695	2	A27485		Alzheimer's diseas
12	31	91.2	695	2	S00550		Alzheimer's diseas
13	31	91.2	747	2	JH0773		Alzheimer's diseas
14	31	91.2	754	2	T06249		protoporphyrin IX
15	31	91.2	758	2	T02325		protoporphyrin IX
16	31	91.2	770	1	QRHUA4		Alzheimer's diseas
17	31	91.2	778	2	B86218		protein T27G7.20 [
18	29	85.3	115	2	AE0523		conserved hypothet
19	29	85.3	152	2	T06645		hypothetical prote
20	29	85.3	156	2	B64735		yacC protein - Esc
21	29	85.3	156	2	F85495		hypothetical prote
22	29	85.3	156	2	F90644		hypothetical prote
23	29	85.3	231	2	H85138		hypothetical prote
24	29	85.3	247	2	T32514		hypothetical prote
25	29	85.3	352	2	T48903		wax synthase [impo
26	29	85.3	428	2	T48008		hypothetical prote
27	29	85.3	512	2	C91368		transcription acti
28	29	85.3	512	2	A86109		transcription acti
29	29	85.3	512	2	C41968		transcription acti

103	25	73.5	166	2	A70024	conserved hypothe	176	25	73.5	500	2	S56489	hypothetical 54.3K
104	25	73.5	170	2	G81375	hypothetical prote	177	25	73.5	501	2	E89786	hypothetical prote
105	25	73.5	181	2	E69900	hypothetical prote	178	25	73.5	510	2	E71695	hypothetical prote
106	25	73.5	208	2	D71258	probable glpG prot	179	25	73.5	513	2	A80021	conserved hypothe
107	25	73.5	215	2	S74602	hypothetical prote	180	25	73.5	516	2	A87260	conserved hypothe
108	25	73.5	224	1	WMVZRL	26.3K late gene tr	181	25	73.5	533	2	F70551	hypothetical prote
109	25	73.5	224	2	C36848	A2L protein - vari	182	25	73.5	540	2	T48619	tRNA synthase-like
110	25	73.5	224	2	G72163	A2L protein - vari	183	25	73.5	545	2	F64579	site-specific DNA-
111	25	73.5	224	2	T28543	hypothetical prote	184	25	73.5	545	2	F71932	type II DNA modifi
112	25	73.5	228	2	T30706	probable transacti	185	25	73.5	546	2	S48932	hypothetical prote
113	25	73.5	233	2	T10198	hypothetical prote	186	25	73.5	557	2	F69481	probable acid-CoA
114	25	73.5	264	2	B71448	hypothetical prote	187	25	73.5	559	2	G71327	probable apolipop
115	25	73.5	268	2	AH2122	branched-chain ami	188	25	73.5	586	1	RNEGB1	DNA-directed RNA p
116	25	73.5	274	2	H83707	bacitracin resista	189	25	73.5	589	2	D70031	ABC transporter (A
117	25	73.5	278	2	A83840	undecaprenol kinas	190	25	73.5	592	2	T15413	hypothetical prote
118	25	73.5	280	2	A12704	conserved hypothe	191	25	73.5	594	2	T40808	probable DNA polym
119	25	73.5	285	2	A97487	probable iron-sulf	192	25	73.5	602	2	T37254	acetylcholinestera
120	25	73.5	296	2	B75426	hypothetical prote	193	25	73.5	609	2	T11774	NADH2 dehydrogenas
121	25	73.5	296	2	S53960	CTK3 protein - yea	194	25	73.5	610	2	T11544	NADH2 dehydrogenas
122	25	73.5	296	2	A36966	probable dTDP-rham	195	25	73.5	624	2	H90071	hypothetical prote
123	25	73.5	301	2	A81066	transcription regu	196	25	73.5	627	2	A82714	hypothetical prote
124	25	73.5	303	2	T23583	hypothetical prote	197	25	73.5	632	2	A25784	hypothetical 70K p
125	25	73.5	305	2	T33578	hypothetical prote	198	25	73.5	637	2	B97496	hypothetical ABC t
126	25	73.5	305	2	E69946	hypothetical prote	199	25	73.5	655	2	G96524	protein T1N15.9 li
127	25	73.5	308	2	D95321	NodB1 transcrip	200	25	73.5	675	2	S53831	NADH2 dehydrogenas
128	25	73.5	311	1	ZZRDM	nodulation protein	201	25	73.5	680	2	T27078	hypothetical prote
129	25	73.5	311	2	A83746	transposase (16) B	202	25	73.5	721	2	T08956	AIW1 protein - Ara
130	25	73.5	315	2	T09165	probable peroxidas	203	25	73.5	740	2	S61568	probable membrane
131	25	73.5	316	2	F71338	probable ribose/ga	204	25	73.5	758	2	T25751	hypothetical prote
132	25	73.5	318	2	G69596	cephalosporin-C de	205	25	73.5	783	1	JDE222	DNA-directed DNA p
133	25	73.5	318	2	E87637	hypothetical prote	206	25	73.5	783	2	AE0514	DNA polymerase II
134	25	73.5	331	2	T26871	hypothetical prote	207	25	73.5	783	2	H85487	DNA polymerase II
135	25	73.5	334	2	B72301	endoglucanase - Th	208	25	73.5	813	2	C97292	ATPases with chape
136	25	73.5	334	2	C84964	hypothetical prote	209	25	73.5	831	2	T49721	hypothetical prote
137	25	73.5	336	2	G84025	polysugar degradin	210	25	73.5	841	2	T48508	beta-adaptin-like
138	25	73.5	343	1	C70418	probable alcohol d	211	25	73.5	845	2	T07039	Hcr9-0 protein - t
139	25	73.5	345	2	T28026	hypothetical prote	212	25	73.5	853	2	T17461	disease resistance
140	25	73.5	346	2	D81288	probable fucose sy	213	25	73.5	855	2	T17460	disease resistance
141	25	73.5	347	2	A75537	hypothetical prote	214	25	73.5	860	2	T27084	hypothetical prote
142	25	73.5	347	2	T20618	hypothetical prote	215	25	73.5	946	2	D86503	protein F9C16.9 li
143	25	73.5	358	2	AE2425	hypothetical prote	216	25	73.5	987	2	S62752	probable DNA-direc
144	25	73.5	359	2	C84983	hypothetical prote	217	25	73.5	1058	2	T47525	kinesin-related pr
145	25	73.5	359	2	T21840	hypothetical prote	218	25	73.5	1078	2	T30879	glucan heavy chain
146	25	73.5	364	2	AB0418	probable membrane	219	25	73.5	1090	2	T30576	glucan synthase -
147	25	73.5	371	2	C83736	transposase (15) B	220	25	73.5	1253	2	F86436	hypothetical prote
148	25	73.5	372	2	A64176	hypothetical prote	221	25	73.5	1304	2	T19397	hypothetical prote
149	25	73.5	380	2	F70399	hydrogenase expres	222	25	73.5	1333	1	XOHUDH	xanthine dehydroge
150	25	73.5	384	2	AE1636	N-acetylornithine	223	25	73.5	1339	2	T38991	conserved hypothe
151	25	73.5	385	2	S54103	beta-lactamase (BC	224	25	73.5	1469	2	T24216	chromosome condens
152	25	73.5	386	2	G75079	hypothetical prote	225	25	73.5	1513	2	T23681	hypothetical prote
153	25	73.5	386	2	B71066	hypothetical prote	226	25	73.5	1520	2	B82274	conserved hypothe
154	25	73.5	388	2	B89777	capsular polysacch	227	25	73.5	1622	2	T45240	hypothetical prote
155	25	73.5	406	2	AC2267	hypothetical prote	228	25	73.5	1817	2	AD2165	two-component hybr
156	25	73.5	408	2	C96984	probable Mn transp	229	25	73.5	1821	2	AG2335	hypothetical prote
157	25	73.5	413	2	A86814	phosphoribosylamin	230	25	73.5	1867	2	T38348	probable 1,3-beta-
158	25	73.5	416	2	D47116	trifoliotoxin synth	231	25	73.5	1955	2	T41170	hypothetical prote
159	25	73.5	420	2	A96535	unknown protein, 1	232	25	73.5	2526	2	T20531	hypothetical prote
160	25	73.5	433	2	T17654	hypothetical prote	233	25	73.5	2722	2	T20532	hypothetical prote
161	25	73.5	443	2	T45574	anthranilate N-hyd	234	25	73.5	2738	2	E88320	protein F07A11.6 l
162	25	73.5	446	2	C64205	signal recognition	235	25	73.5	20	2	JU0330	hypothetical prote
163	25	73.5	449	2	A64053	glutamate dehydrog	236	24	70.6	20	2	A99091	hypothetical prote
164	25	73.5	453	2	F75206	maltose-binding pe	237	24	70.6	62	2	B34514	MHC class II histo
165	25	73.5	460	2	T43224	hypothetical prote	238	24	70.6	66	2	AE3608	hypothetical prote
166	25	73.5	466	2	T02324	hypothetical prote	239	24	70.6	74	2	E84214	hypothetical prote
167	25	73.5	470	2	A13442	glycolate oxidase	240	24	70.6	80	2	F96787	protein T4012.7 li
168	25	73.5	471	2	S21102	hypothetical prote	241	24	70.6	94	2	D71284	hypothetical prote
169	25	73.5	472	1	S55379	cytochrome P450 Cy	242	24	70.6	109	2	B72213	conserved hypothe
170	25	73.5	479	2	AE2117	hypothetical prote	243	24	70.6	112	2	A69268	hypothetical prote
171	25	73.5	479	2	F86285	F9L1.11 protein -	244	24	70.6	115	2	AD0414	probable exported
172	25	73.5	492	2	B83020	hypothetical prote	245	24	70.6	133	2	S78156	H+-transporting tw
173	25	73.5	497	2	T32090	hypothetical prote	246	24	70.6	142	2	T23519	hypothetical prote
174	25	73.5	500	2	H91283	hypothetical prote	247	24	70.6	145	2	AG1588	hypothetical prote
175	25	73.5	500	2	B86125	hypothetical prote	248	24	70.6				

249 24 70.6 145 2 AD1551
250 24 70.6 147 1 S75850
251 24 70.6 147 2 S65579
252 24 70.6 147 2 T24057
253 24 70.6 155 2 T04304
254 24 70.6 156 2 H95252
255 24 70.6 156 2 F98117
256 24 70.6 156 2 JQ1377
257 24 70.6 166 2 E71040
258 24 70.6 176 1 I64161
259 24 70.6 177 2 C83495
260 24 70.6 178 2 T16280
261 24 70.6 178 2 D81269
262 24 70.6 187 2 H96593
263 24 70.6 190 2 A95895
264 24 70.6 191 2 T22302
265 24 70.6 193 2 B90157
266 24 70.6 194 2 T24491
267 24 70.6 194 2 B97211
268 24 70.6 198 2 AF1569
269 24 70.6 200 2 C86528
270 24 70.6 201 2 C72094
271 24 70.6 201 2 JH0617
272 24 70.6 201 2 S76151
273 24 70.6 203 2 T30317
274 24 70.6 206 2 B81221
275 24 70.6 207 2 B81256
276 24 70.6 209 2 D95186
277 24 70.6 209 2 E98053
278 24 70.6 211 2 S14920
279 24 70.6 216 2 F69166
280 24 70.6 221 2 T43159
281 24 70.6 221 2 T17997
282 24 70.6 223 2 H83462
283 24 70.6 224 2 T03205
284 24 70.6 224 2 T32655
285 24 70.6 227 2 T37499
286 24 70.6 227 2 T50899
287 24 70.6 227 2 H90109
288 24 70.6 228 2 B81214
289 24 70.6 228 2 H81789
290 24 70.6 231 2 S76372
291 24 70.6 233 2 AF3222
292 24 70.6 234 2 D95021
293 24 70.6 234 2 A97893
294 24 70.6 236 2 D72355
295 24 70.6 238 2 S78263
296 24 70.6 238 2 D82405
297 24 70.6 257 2 C69862
298 24 70.6 258 2 AG0459
299 24 70.6 258 2 H81321
300 24 70.6 261 2 D64166

ALIGNMENTS

RESULT 1
S23094
beta-amyloid protein precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C:Accession: S23094
R:Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A>Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A:Reference number: S23094; MUID:92316198; PMID:1618299
A:Accession: S23094
A:Molecule type: protein
A:Residues: 1-33 <KOJ>
A:Cross-references: UNIPARC:UPI00001777FB
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 91.2%; Score 31; DB 2; Length 33;
Best Local Similarity 85.7%; Pred. No. 1.5; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1;
QY 1 KLVFFPAQ 7
|||||:
DB 21 KLVFFPAE 27
RESULT 2
PN0512
beta-amyloid protein - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: PN0512
R:Shinochigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, T.; Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A>Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment
A:Reference number: PN0512; MUID:93290653; PMID:7685598
A:Accession: PN0512
A:Molecule type: protein
A:Residues: 1-42 <SHI>
A:Cross-references: UNIPROT:Q7M088; UNIPARC:UPI0000031588
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid

Query Match 91.2%; Score 31; DB 2; Length 42;
Best Local Similarity 85.7%; Pred. No. 1.9; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1;
QY 1 KLVFFPAQ 7
|||||:
DB 16 KLVFFPAE 22
RESULT 3
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.2%; Score 31; DB 2; Length 57;
Best Local Similarity 85.7%; Pred. No. 2.5; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1;
QY 1 KLVFFPAQ 7
|||||:
DB 21 KLVFFPAE 27
RESULT 4
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: F60045
A:Molecule type: mRNA

A;Residues: 1-57 <JOH>
 A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.2%; Score 31; DB 2; Length 57;
 Best Local Similarity 85.7%; Pred. No. 2.5;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||:
 Db 21 KLVFFPAE 27

RESULT 5

D60045
 Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C;Accession: D60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: D60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>

A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56124
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.2%; Score 31; DB 2; Length 57;
 Best Local Similarity 85.7%; Pred. No. 2.5;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||:
 Db 21 KLVFFPAE 27

RESULT 6

E60045
 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
 C;Species: Ovis sp. (sheep)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C;Accession: E60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: E60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>

A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56130
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.2%; Score 31; DB 2; Length 57;
 Best Local Similarity 85.7%; Pred. No. 2.5;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||:
 Db 21 KLVFFPAE 27

RESULT 7

G60045
 Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
 C;Species: Cavia porcellus (guinea pig)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C;Accession: G60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: G60045
 A;Molecule type: mRNA

A;Residues: 1-57 <JOH>
 A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56126
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.2%; Score 31; DB 2; Length 57;
 Best Local Similarity 85.7%; Pred. No. 2.5;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||:
 Db 21 KLVFFPAE 27

RESULT 8

B60045
 Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
 C;Species: Ursus maritimus (polar bear)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
 C;Accession: B60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: B60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>

A;Cross-references: UNIPROT:Q29149; UNIPARC:UPI0000125049; EMBL:X56128; NID:g2165; PIDN:
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 91.2%; Score 31; DB 2; Length 57;
 Best Local Similarity 85.7%; Pred. No. 2.5;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||:
 Db 21 KLVFFPAE 27

RESULT 9

PQ0438
 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
 C;Accession: PQ0438; C60045

R;Davidson, J.S.; West, R.L.; Korikalapudi, P.; Maroun, L.B.
 Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
 A;Reference number: PQ0438; MUID:93075180; PMID:1445331

A;Accession: PQ0438
 A;Molecule type: DNA

A;Residues: 1-82 <DAV>
 A;Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: C60045
 A;Molecule type: mRNA
 A;Residues: 12-68 <JOH>

A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56129
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 91.2%; Score 31; DB 2; Length 82;
 Best Local Similarity 85.7%; Pred. No. 3.6;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||:
 Db 32 KLVFFPAE 38

RESULT 10

A49795
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
 C/Species: Macaca fascicularis (crab-eating macaque)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: A49795
 R/Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.
 Am. J. Pathol. 138, 1423-1435, 1991
 A/Title: Homology of the amyloid beta protein precursor in monkey and human supports a hypothesis of the amyloid beta protein precursor in Alzheimer's disease
 A/Reference number: A49795; MUID:91273117; PMID:1905108
 A/Accession: A49795
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-695 <POD>
 A/Cross-references: UNIPARC:UPI000002A2F2; GB:M58727; NID:G342062; PIDN:AAA36829.1; PID:A49795
 C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C/Keywords: alternative splicing

Query Match 91.2%; Score 31; DB 1; Length 695;
 Best Local Similarity 85.7%; Pred. No. 28;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||:
 Db 612 KLVFFPAE 618

RESULT 11

A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N/Alternate names: proteinase nexin II
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
 C/Accession: A27485; S19727; I49485
 R/Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987
 A/Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor
 A/Reference number: A27485; MUID:88106489; PMID:3322280
 A/Accession: A27485
 A/Molecule type: mRNA
 A/Residues: 1-695 <YAM>
 A/Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:G191568; PIDN:A27485
 R/de Strooper, B.; van Leeuwen, F.; van den Berghe, H.
 Biochim. Biophys. Acta 1129, 141-143, 1991
 A/Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer to the Alzheimer's disease amyloid beta protein precursor than to the mouse amyloid beta protein precursor

A/Reference number: S19727; MUID:92096458; PMID:1756177
 A/Accession: S19727
 A/Molecule type: mRNA
 A/Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
 A/Cross-references: UNIPARC:UPI000002A2F9; EMBL:X59379
 R/Izumi, R.; Yamada, T.; Yoshikawa, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
 Gene 112, 189-195, 1992
 A/Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid beta protein precursor
 A/Reference number: I49485; MUID:92203998; PMID:1555768
 A/Accession: I49485
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-19 <RES>
 A/Cross-references: UNIPARC:UPI00000003B7; GB:D10603; NID:G220328; PIDN:BA01456.1; PID:A27485
 C/Genetics:

A/Map position: 16C3
 C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C/Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 91.2%; Score 31; DB 2; Length 695;
 Best Local Similarity 85.7%; Pred. No. 28;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFPAQ 7
 |||||:
 Db 612 KLVFFPAE 618

RESULT 12

S00550
 Alzheimer's disease amyloid beta protein precursor - rat
 N/Alternate names: beta-A4 amyloid protein
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
 C/Accession: S00550; A41245; A39820; S46251
 R/Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
 EMBO J. 7, 1365-1370, 1988
 A/Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
 A/Reference number: S00550; MUID:88312583; PMID:2900758
 A/Accession: S00550
 A/Molecule type: mRNA
 A/Residues: 1-695 <SHI>
 A/Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2PB; EMBL:X07648; NID:G55616; PID:S00550
 R/Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
 Science 241, 223-226, 1988
 A/Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core protein
 A/Reference number: A41245; MUID:88264430; PMID:2968652
 A/Accession: A41245
 A/Molecule type: protein
 A/Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
 A/Cross-references: UNIPARC:UPI00001777PD
 A/Note: evidence for heparan sulfate attachment
 R/Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.
 FEBS Lett. 349, 109-116, 1994
 A/Title: The beta-A4 amyloid precursor protein binding to copper.
 A/Reference number: S46251; MUID:94320627; PMID:7913895
 A/Contents: annotation: copper binding sites
 A/Note: rat peptides were isolated but not sequenced
 R/Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
 J. Biol. Chem. 266, 8464-8469, 1991
 A/Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
 A/Reference number: A39820; MUID:91217087; PMID:1673681
 A/Accession: A39820
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 18-32 <POT>
 A/Cross-references: UNIPARC:UPI00001777FE
 A/Experimental source: brain
 C/Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C/Superfamily: Alzheimer's disease amyloid beta protein; amyloid; glycoprotein; transmembrane protein
 C/Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
 F/625-648/Domain: transmembrane #status predicted <TM>

Query Match 91.2%; Score 31; DB 2; Length 695;
 Best Local Similarity 85.7%; Pred. No. 28;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |||||:
 Db 612 KLVFFPAE 618

RESULT 13

JH0773
 Alzheimer's disease amyloid beta protein precursor - African clawed frog
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
 C/Accession: JH0773
 R/Okado, H.; Okamoto, H.
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
 A/Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental expression
 A/Reference number: JH0773; MUID:93129227; PMID:1282805
 A/Accession: JH0773
 A/Molecule type: mRNA

A;Residues: 1-747 <OKA>
A;Cross-references: UNIPARC:UPI00000FC980; GB:SS2417; NID:G263150; PIDN:AAB24853.1; PID:
A;Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; amyloid
P:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 91.2%; Score 31; DB 2; Length 747;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||:||||:
DB 664 KLVFFPAE 670

RESULT 14
T06249
protoporphyrin IX magnesium chelatase (EC 4.99.1.-) D chain - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06249
R:Luo, M.; Weinstein, J.D.
submitted to the EMBL Data Library, July 1997
A;Reference number: Z15566
A;Accession: T06249
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: mRNA
A;Residues: 1-754 <LUO>
A;Cross-references: UNIPROT:Q22437; UNIPARC:UPI0000035C61; EMBL:AF014399; NID:G2318116;
A;Experimental source: cv. Spring
C:Genetics:
A;Gene: Chld
C:Function:
A;Description: catalyzes the magnesium insertion step in chlorophyll biosynthesis
C:Superfamily: magnesium chelatase, subunit Chld
C:Keywords: lyase

Query Match 91.2%; Score 31; DB 2; Length 754;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||:||||:
DB 462 KLVFFPAQ 468

RESULT 15
T02925
protoporphyrin IX magnesium chelatase (EC 4.99.1.-) chain chld - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T02925
R:Papenbrock, J.; Kruse, E.; Graefe, S.; Haenel, F.; Grimm, B.
submitted to the EMBL Data Library, December 1996
A;Description: Identification of a plant Chld cDNA sequence homologous to a bacterial ge
A;Reference number: Z14773
A;Accession: T02925
A;Status: translated from GB/EMBL/DBBJ
A;Molecule type: mRNA
A;Residues: 1-758 <PAP>
A;Cross-references: UNIPROT:Q24133; UNIPARC:UPI0000127862; EMBL:Y10022; NID:e1013894; PI
C:Genetics:
A;Gene: chld
C:Superfamily: magnesium chelatase, subunit Chld
C:Keywords: lyase

Query Match 91.2%; Score 31; DB 2; Length 758;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|||:||||:

DB 467 KLVFFAQ 473

RESULT 16
Q8HUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibi
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C:Accession: S02260; S05194; A32277; A33260; A34866; I39452; I39451; I39453; I59562; A44
4668; A28583; A29302; A60805; J00038; S06121; A60355; A59011; A38384; S29076; S38252; S3
R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288,'V',365-770 <LEML>
A;Cross-references: UNIPARC:UPI000002A2F2; EMBL:X13466
A;Note: alternative splice form APP(695)
R:Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A;Cross-references: UNIPARC:UPI000016AEFC; EMBL:X13466; NID:G35598; PIDN:CAA31830.1; PID
A;Note: alternative splice form APP(695)
R:La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAP>
A;Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:G178863; PIDN:AAA51768.1; PID:
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Cross-references: UNIPARC:UPI0000148176
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: UNIPARC:UPI000002DB1C; GB:M33112; NID:G178613; PIDN:AAB59502.1; PID:
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A;Molecule type: DNA
A;Residues: 1-530,'QWLMPPVPAFWFAKVGR', <YOS2>
A;Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:G178608; PIDN:AAB59501.1; PID:
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum

A;Note: revised physical map for reference I39451
 R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.U.; Power, M.D.; Lieberburg, I.; van Duine
 Science 248, 1124-1126, 1990
 A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
 A;Reference number: I39453; MUID:90260663; PMID:2111584
 A;Accession: I39453
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 656-737 <LEV>
 A;Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:g178618; PIDN:AAAS1727.1; PID:
 A;Note: a mutation with 693-Gln is presented
 R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
 A;Reference number: I59562; MUID:92022553; PMID:1925564
 A;Accession: I59562
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 689-716, 'F', 718-737 <MUR>
 A;Cross-references: UNIPARC:UPI000011F7EA; GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:
 R;Kamino, K.; Ort, H.T.; Payami, H.; Wijeman, E.M.; Alonso, M.E.; Pulat, S.M.; Anderson,
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
 A;Reference number: A44017; MUID:93035397; PMID:1415269
 A;Accession: A44017
 A;Molecule type: DNA
 A;Residues: 687-692, 'G', 694-718 <KAMI>
 A;Cross-references: UNIPARC:UPI000011F7EB; GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:
 A;Experimental source: familial Alzheimer disease family SB
 A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
 A;Accession: B4017
 A;Molecule type: DNA
 A;Residues: 687-718 <KAM2>
 A;Cross-references: UNIPARC:UPI000016B394; GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:
 A;Experimental source: familial Alzheimer disease family LIT
 A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
 A;Note: this sequence has a silent mutation
 R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
 Nature 325, 733-736, 1987
 A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfad
 A;Reference number: A03134; MUID:87144572; PMID:2881207
 A;Accession: A03134
 A;Molecule type: mRNA
 A;Residues: 1-288, 'V', 365-770 <KAN>
 A;Cross-references: UNIPARC:UPI000002A2F2; GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g
 A;Note: alternative splice form APP(695)
 R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
 A;Reference number: A29030; MUID:87231971; PMID:3035574
 A;Accession: A29030
 A;Molecule type: mRNA
 A;Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A;Cross-references: UNIPARC:UPI000016A545; GB:M16765; NID:g178539; PIDN:AAAS1722.1; PID:
 A;Note: the authors translated the codon GAG for residue 647 as Asp
 R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
 A;Reference number: A47584; MUID:87120328; PMID:3810169
 A;Accession: A47584
 A;Molecule type: mRNA
 A;Residues: 674-756, 'S', 758-770 <GOL>
 A;Cross-references: UNIPARC:UPI00001420E5; GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:
 A;Experimental source: brain
 R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
 Science 235, 880-884, 1987
 A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
 A;Reference number: A47585; MUID:87120329; PMID:2949367
 A;Accession: A47585
 A;Molecule type: mRNA
 A;Residues: 674-703 <TANI>
 A;Cross-references: UNIPARC:UPI000016A46P; GB:M15532; NID:g177957; PIDN:AAAS1564.1; PID:

R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muell
 EMBO J. 7, 949-957, 1988
 A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pre
 A;Reference number: S02638; MUID:88296437; PMID:2900137
 A;Accession: S02638
 A;Molecule type: mRNA
 A;Residues: 672-678 <DYR>
 A;Cross-references: UNIPARC:UPI0000035AB0
 R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Nev
 Nature 331, 528-530, 1988
 A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associa
 A;Reference number: S00707; MUID:88122640; PMID:2893290
 A;Accession: S00707
 A;Molecule type: mRNA
 A;Residues: 286-344, 'I', 365-366 <TAN2>
 A;Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PI
 A;Experimental source: promyelocytic leukemia cell line HL60
 A;Note: alternative splice form APP(751)
 R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hau, D.; Greenberg, B.; D
 Nature 331, 525-527, 1988
 A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
 A;Reference number: S00925; MUID:88122639; PMID:2893289
 A;Accession: S00925
 A;Molecule type: mRNA
 A;Residues: 1-344, 'I', 365-770 <PO2>
 A;Cross-references: UNIPARC:UPI000002A2F6; GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA
 A;Note: alternative splice form APP(751)
 R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibito
 A;Reference number: A38949; MUID:88122641; PMID:2893291
 A;Accession: A38949
 A;Molecule type: mRNA
 A;Residues: 287-367 <KIT>
 A;Cross-references: UNIPARC:UPI000014553B; GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:
 A;Experimental source: glioblastoma cell line
 A;Note: alternative splice form APP(770)
 R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Asht
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three
 A;Reference number: A30320
 A;Accession: A30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 284-288, 'V', 365-770 <VIT1>
 A;Cross-references: UNIPARC:UPI0000174094
 A;Accession: B30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 122-288, 'V', 365-770 <VIT2>
 A;Cross-references: UNIPARC:UPI0000174094
 A;Accession: C30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 606-770 <VIT3>
 A;Cross-references: UNIPARC:UPI0000174094
 R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b
 A;Reference number: A31087; MUID:88124954; PMID:2893379
 A;Accession: A31087
 A;Molecule type: mRNA

Query Match 91.2%; Score 31; DB 1; Length 770;
 Best Local Similarity 85.7%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFPAQ 7
 |||||
 Db 687 KLVFPAE 693

RESULT 17

B86218
 protein T27G7.20 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-May-2004
 C:Accession: B86218
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Lin, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maifi, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: B86218
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-778 <STO>
 A:Cross-references: UNIPARC:UPI000016D8B1; GB:AE005172; NID:g6664313; PIDN:AAF22895.1; C
 C:Genetics:
 A:Gene: T27G7.20
 A:Map position: 1
 C:Superfamily: magnesium chelatase, subunit ChlD

Query Match 91.2%; Score 31; DB 2; Length 778;
 Best Local Similarity 85.7%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 ||:||||
 Db 485 KLVFFPAQ 491

RESULT 18
 AE0523
 conserved hypothetical protein STY0189 [imported] - Salmonella enterica subsp. enterica
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AE0523
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AE0523
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-115 <PAR>
 A:Cross-references: UNIPARC:UPI0000059A0B; GB:AL513382; PIDN:CAD01325.1; PID:g16501453;
 C:Genetics:
 A:Gene: STY0189

Query Match 85.3%; Score 29; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFPAQ 7
 |||||
 Db 59 LVFFPAQ 64

RESULT 19
 T06645
 hypothetical protein T20K18.220 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T06645
 R:Sevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew

submitted to the Protein Sequence Database, April 1999
 A:Reference number: Z15790
 A:Accession: T06645
 A:Molecule type: DNA
 A:Residues: 1-152 <BEV>
 A:Cross-references: UNIPROT:Q9STZ9; UNIPARC:UPI00000A0722; EMBL:AL049640; GSPDB:GNO00062;
 A:Experimental source: cultivar Columbia; BAC clone T20K18
 C:Genetics:
 A:Gene: ATSP:T20K18.220
 A:Map position: 4
 A:Introns: 87/3; 109/3
 C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match 85.3%; Score 29; DB 2; Length 152;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPA 6
 |||||
 Db 9 KLVFFPA 14

RESULT 20
 B84735
 yacc protein - Escherichia coli (strain K-12)
 C:Species: Escherichia coli
 C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
 C:Accession: B84735; A33863; S45199
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 .A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: B84735
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-156 <BLAT>
 A:Cross-references: UNIPROT:Q8X949; UNIPARC:UPI00000D0877; GB:AE000121; GB:U00096; NID:G
 A:Experimental source: strain K-12, substrain MG1655
 R:Xie, Q.W.; Tabor, C.W.; Tabor, H.
 J. Bacteriol. 171, 4457-4465, 1989
 A:Title: Spermidine biosynthesis in Escherichia coli: promoter and termination regions o
 A:Reference number: A33863; MUID:89327165; PMID:2666401
 A:Accession: A33863
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 42-156 <XIE>
 A:Cross-references: UNIPARC:UPI000013A023; GB:J02804; NID:gl47850; PIDN:AAA24642.1; PID:G
 R:Fujita, N.
 submitted to the EMBL Data Library, January 1994
 A:Reference number: S45181
 A:Accession: S45199
 A:Molecule type: DNA
 A:Residues: 42-156 <FUJ>
 A:Cross-references: UNIPARC:UPI000013A023; EMBL:D26562; NID:g473770; PIDN:BAA05578.1; PI
 A:Experimental source: strain K-12 substrain W3110
 C:Genetics:
 A:Gene: yacc

Query Match 85.3%; Score 29; DB 2; Length 156;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFPAQ 7
 |||||
 Db 100 LVFFPAQ 105

RESULT 21
 P85495
 hypothetical protein yacc [imported] - Escherichia coli (strain O157:H7, substrain EDL93
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: F85495
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: F85495
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <STO>
A;Cross-references: UNIPROT:Q8X949; UNIPARC:UPI000000D0877; GB:AE005174; NID:g12512834; E
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yacC

Query Match 85.3%; Score 29; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LVFFAQ 7
|||||
Db 100 LVFFAQ 105

RESULT 22
F90644
hypothetical protein ECs0126 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F90644
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90644
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <HAY>
A;Cross-references: UNIPROT:Q8X949; UNIPARC:UPI000000D0877; GB:BA000007; PIDN:BA033549.1;
A;Experimental source: strain O157:H7, substrain R1MD 050952
C;Genetics:
A;Gene: ECs0126

Query Match 85.3%; Score 29; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LVFFAQ 7
|||||
Db 100 LVFFAQ 105

RESULT 23
H85138
hypothetical protein AT4g12800 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85138
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: H85138
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-231 <STO>
A;Cross-references: UNIPROT:Q9SV79; UNIPARC:UPI000000A7E0E; GB:NC_001268; NID:g7267992; F
C;Genetics:
A;Gene: AT4g12900
A;Map position: 4
C;Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match 85.3%; Score 29; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFA 6
|||||
Db 12 KLVPFA 17

RESULT 24
T32514
hypothetical protein C44B12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
C;Accession: T32514
R;Tin-Wollam, A.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid C44B12.
A;Reference number: Z21183
A;Accession: T32514
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-247 <TIN>
A;Cross-references: UNIPROT:O44145; UNIPARC:UPI00001793B3; EMBL:AF036692; PIDN:AAB88324
A;Experimental source: strain Bristol N2; clone C44B12
C;Genetics:
A;Gene: CESP:C44B12.1
A;Map position: 4
A;Introns: 28/3; 82/1; 164/1; 192/1

Query Match 85.3%; Score 29; DB 2; Length 247;
Best Local Similarity 71.4%; Pred. No. 30;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFAQ 7
|:|:|:|
Db 224 KIVFFSQ 230

RESULT 25
T48903
wax synthase [imported] - Simmondsia chinensis
C;Species: Simmondsia chinensis
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T48903
R;Lardizabal, K.D.; Metz, J.G.; Sakamoto, T.; Hutton, W.C.; Pollard, M.R.; Lassner, M.W.
Plant Physiol. 122, 645-655, 2000
A;Title: Purification of a jojoba embryo wax synthase, cloning of its cDNA and producti
A;Reference number: Z25002
A;Accession: T48903
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-352 <LAR>
A;Cross-references: UNIPROT:Q9XGV6; UNIPARC:UPI000000A1C81; EMBL:AF149919; PIDN:AAD38041

Query Match 85.3%; Score 29; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFA 6
|||||
Db 135 KLVPFA 140

RESULT 26
T48008
hypothetical protein T17J13.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
C;Accession: T48008
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24482

A:Accession: T48008
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-428 <RIE>
A:Cross-references: UNIPROT:Q9MLQ8; UNIPARC:UPI00000488B7; EMBL:AL138651
A:Experimental source: cultivar Columbia; BAC clone T17013
C:Genetics:
A:Map position: 3
A:Introns: 137/3
A>Note: T17J13.120
C:Superfamily: N-hydroxycinnamoyl/benzoyl transferase

Query Match 85.3%; Score 29; DB 2; Length 428;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFFA 6
|||||
DB 271 KLVFFFA 276

RESULT 27

C91268
transcription activator of cad operon [imported] - Escherichia coli (strain O157:H7, sub
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
A:Accession: C91268
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C91268
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-512 <HAY>
A:Cross-references: UNIPROT:Q8XDS2; UNIPARC:UPI00000D031B; GB:BA000007; PIDN:BA838538.1;
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs5115

Query Match 85.3%; Score 29; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFFAQ 7
|||||
DB 37 LVFFFAQ 42

RESULT 28

A86109
transcription activator of cad operon [imported] - Escherichia coli (strain O157:H7, sub
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
A:Accession: A86109
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A86109
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-512 <STO>
A:Cross-references: UNIPROT:Q8XDS2; UNIPARC:UPI00000D031B; GB:AE005174; NID:gl2519113; F
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: cadC

Query Match 85.3%; Score 29; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFFAQ 7
|||||
DB 37 LVFFFAQ 42

RESULT 29

C41968
transcription activator cadC - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
A:Accession: C41968; S56362; D65223
R:Watson, N.; Dunyak, D.S.; Rosey, E.L.; Slonczewski, J.L.; Olson, E.R.
J. Bacteriol. 174, 530-540, 1992
A:Title: Identification of elements involved in transcriptional regulation of the Escher
A:Reference number: A41968; MUID:92105022; PMID:1370290
A:Accession: C41968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-512 <WAT>
A:Cross-references: UNIPROT:P23890; UNIPARC:UPI0000126DA9; GB:M67452; NID:gl45451; PIDN
A>Note: sequence extracted from NCBI backbone (NCBIN:75631, NCBIP:75632)
R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A:Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
A:Reference number: S56314; MUID:95334362; PMID:7610040
A:Accession: S56362
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-512 <BUR>
A:Cross-references: UNIPARC:UPI0000126DA9; EMBL:U14003; NID:gl263172; PIDN:AAA37033.1; P
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: D65223
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-512 <BLAT>
A:Cross-references: UNIPARC:UPI0000126DA9; GB:AE000486; GB:U000096; NID:gl790574; PIDN:AA
A:Experimental source: strain K-12, substrain MGI655
C:Genetics:
A:Gene: cadC
C:Keywords: DNA binding; transcription regulation; transmembrane protein

Query Match 85.3%; Score 29; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFFAQ 7
|||||
DB 37 LVFFFAQ 42

RESULT 30

B96666
protein P22C12.6 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
A:Accession: B96666
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: B96666
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-776 <STO>
A;Cross-references: UNIK
C;Genetics:
A;Gene: F22C12.6
A;Map position: 1

Query Match	85.3%	Score 29;	DB 2;	Length 776;
Best Local Similarity	71.4%	Pred. No. 91;		
Matches	5;	Conservative	2;	Mismatches
				0;
				Indels
				0;
				Gaps
				0;

QY 1 KLVFFAQ 7
:|:|
pb 129 QLIFFAQ 135

RESULT 31
S30236
genome polyprotein - zucchini yellow mosaic virus (strain Singapore) (fragment)
N:Contains: coat protein; nuclear inclusion protein a; RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: zucchini yellow mosaic virus, ZYMV
A:Variety: strain Singapore
C:Date: 19-Mar-1997 #sequence revision 29-Aug-1997 #text change 09-Jul-2004

C/Accession: S30236
R/Wu, M.; Yeong, C.Y.; Lee, S.C.; Wong, S.M.
Nucleic Acids Res. 21, 1317, 1993
A/Title: Nucleotide sequence of the 3' half of zucchini yellow mosaic virus (Singapore isolate)
A/Reference number: S30236; MUID:93219099; PMID:8464715
A/Accession: S30236
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-1016 <WUM>
A/Cross-references: UNIPROT:Q05912; UNIPARC:UPI00000ECC69; EMBL:X69509; NID:Q289233; PID:Q289233
A/Note: The nucleotide sequence was submitted to the EMBL Data Library, September 1992
C/Superfamily: tobacco etch virus genome polyprotein
C/Keywords: coat protein; genome-linked protein; nucleotidyltransferase; phosphoprotein;
F/9-61/Product: Vpg protein #status predicted <VPG>
F/62-494/Product: nuclear inclusion protein a #status predicted <NTA>
F/495-1010/Product: RNA-directed RNA polymerase #status predicted <POL>
F/1011-1016/Product: coat protein (fragment) #status predicted <COP>
F/125/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted
F/125/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

```

Query Match      85.3%; Score 29; DB 2; Length 1016;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatch 0; Indels 0; Gaps 0;

```

Qy 1 KLVFFA 6
|||
Db 837 KLVFFA 842

RESULT 32
F90736
molybdopterin biosynthesis protein D chain [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2004
C:Accession: F90736
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: F90736
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-81 <HAY>
A:Cross-references: UNIPROT:Q8X807; UNIPARC:UPI00000D09BP; GB:BA000007; PIDN:BA034285.1
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: EC0862
C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 82.4%; Score 28; DB 2; Length 81;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 0; Indels

Qy	1	KLVEFAQ	7
		::	
Dh	3	KVLFFAO	9

RESULT 33

molybdenum cofactor biosynthesis protein D VC1027 [imported] - *Vibrio cholerae* (strain: A82251)
 C:Species: *Vibrio cholerae*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 16-Aug-2004
 C:Accession: A82251
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 Richardson, D.; Ermlaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
 L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000
 Article: DNA Sequence of the cholera pathogen *Vibrio cholerae*.
 A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: A82251
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-81 <HEI>
A:Cross-references: UNIPROT:Q9K7F8; UNIPARC:UPI00000C2E58; GB:AE800
A:Experimental source: serogroup O1; strain Ni9661; biotype B1 Tor
C:Genetics:
A:Gene: VC1027

A;Map position: 1
C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein
F:81/Modified site: 1-thioglycine (Gly) #status predicted

Query Match	82.4%;	Score 28;	DB 2;	Length 81;
Best Local Similarity	71.4%;	Pred. No. 18;		
Matches	5;	Conservative	2;	Mismatches
			0;	Indels
			0;	Gaps

QY	1	KLVFFAQ	7
		:	
rh	3	KLVFFAQ	9

RESIT.T 34

G85596
molybdopterin biosynthesis [imported] - Escherichia coli (strain O157:H7, substrain EDL
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: G85596
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.T.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
a:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7

A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85586

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-81 <STO>

A,Cross-references: UNIPROT:Q8H807; UNIPARC:UPI00000D09BF; GB:AE005174; NID:gl25137733
A,Experimental source: strain O157:H7, substrain EDJ933
C,Genetics:
A,Gene: moad
C,Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match	82.4%	Score 28;	DB 2;	Length 81;
Best Local Similarity	71.4%	Pred. No. 18;		
Matches	5;	Conservative	2;	Mismatches
			0;	Indels
			0;	Gaps
			0;	

Qy 1 KLVEFAQ 7
|::|||
pb 3 KVLPEAQ 9

```

RESULT 35
H64814
molybdopterin biosynthesis protein D chain [validated] - Escherichia coli (strain K-12)
N:Alternate names: moad protein; molybdopterin-converting factor 10K chain; molybdopterin
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C:Accession: H64814; S35001; A46585; S31882
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen
A.: Rose, D.J.; Mau, B.; Shaq, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H64814
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-81 <BLAT>
A:Cross-references: UNIPROT:P30748; UNIPARC:UPI00001116DF; GB:AE0000181; GB:U00096; NID:9
R:Rivers, S.D.; McNaught, E.; Blasco, F.; Giordano, G.; Boxer, D.H.
Mol. Microbiol. 8, 1071-1081, 1993
A:Title: Molecular genetic analysis of the moa operon of Escherichia coli K-12 required
A:Reference number: S34998; MUID:93368423; PMID:8361352
A:Accession: S35001
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-44, 'R', 46-81 <RIV>
A:Cross-references: UNIPARC:UPI000016F2FD; EMBL:X70420; NID:G42007; PIDN:CMA49864.1; PID
A:Experimental source: strain K12
R:Pitterle, D.M.; Rajagopalan, K.V.
J. Biol. Chem. 268, 13499-13505, 1993
A:Title: The biosynthesis of molybdopterin in Escherichia coli. Purification and charact
A:Reference number: A46585; MUID:93293873; PMID:8514782
A:Accession: A46585
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8, 'E', 10-15 <PIT>
A:Cross-references: UNIPARC:UPI0000178EC3
A:Note: sequence extracted from NCBI backbone (NCBIP:134491)
C:Genetics:
A:Gene: moad
A:Map position: 17.7 min
A:Complex: heterodimer with D chain (PTR:S31883) [validated, MUID:93293873]
C:Function:
A:Description: required for the addition of the Mo-binding dithiolene group to a molybdo
C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein
C:Keywords: heterodimer; molybdopterin biosynthesis
F:81/Modified site: 1-thioglycine (gly) #status predicted

Query Match 82.4%; Score 28; DB 2; Length 81;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|:::|
Db 3 KVLFFPAQ 9

RESULT 36
D86866
prophage p83 protein 01 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86866
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: D86866
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-306 <STO>
A:Cross-references: UNIPROT:Q9CEB2; UNIPARC:UPI00000C6B67; GB:AE0005176; PID:g12724972; F
A:Experimental source: strain IL1403

```

C:Genetics:

A:Gene: ps301

Query Match 82.4%; Score 28; DB 2; Length 306;
 Best Local Similarity 71.4%; Pred. No. 64;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |:::|
 Db 182 KLVVYPAQ 188

RESULT 37

H71729

hypothetical protein Rp189 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii

C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004

C:Accession: H71729

R:Anderson, S.G.E.; Zomorodipour, A.; Anderson, J.O.; Sichert-Ponten, T.; Alsmark, U.

Nature 396, 133-140, 1998

A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499; PMID:9823893

A:Accession: H71729

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-321 <AND>

A:Cross-references: UNIPROT:Q9ZDX5; UNIPARC:UPI0000139421; GB:AJ235270; NID:

A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: Rp189

C:Superfamily: Rickettsia prowazekii hypothetical protein Rp189

Query Match 82.4%; Score 28; DB 2; Length 321;
 Best Local Similarity 83.3%; Pred. No. 67;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPA 6
 |:::|
 Db 178 KLIFFPA 183

RESULT 38

G96643

hypothetical protein T13M11.15 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: G96643

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Dwar, K.,

ansen, N.P.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: G96643

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-346 <STO>

A:Cross-references: UNIPROT:Q9SYB5; UNIPARC:UPI00000A936E; GB:AE0005173; NID:g4508079; P

C:Genetics:

A:Gene: T13M11.15

A:Map position: 1

Query Match 82.4%; Score 28; DB 2; Length 346;
 Best Local Similarity 85.7%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
 |:::|

Db 261 KLVPFFQ 267

RESULT 39

C84979
hypothetical protein cysG [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 18-Aug-2003
C;Accession: C84979
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: C84979
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-473 <STO>
A;Cross-references: UNIPARC:UPI000005E596; GB:AP0000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: cysG; BU425
C;Superfamily: siroheme synthase

Query Match 82.4%; Score 28; DB 2; Length 473;
Best Local Similarity 83.3%; Pred. No. 97; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 2 LVFFAQ 7
:|||||
Db 285 LVFFAQ 290

RESULT 40

S67962
valine-tRNA ligase (EC 6.1.1.9) - brine shrimp (fragments)
C;Species: Artemia sp. (brine shrimp)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 03-Jun-2002
C;Accession: S67962
R;Brandtsma, M.; Kerjan, P.; Dijk, J.; Janssen, G.M.C.; Moeller, W.
Eur. J. Biochem. 233, 277-282, 1995
A;Title: Valyl-tRNA synthetase from Artemia. Purification and association with elongation factor Tu
A;Reference number: S67962; MUID:96061959; PMID:7588756
A;Accession: S67962
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17,18-32 <BRA>
A;Cross-references: UNIPARC:UPI000007DF94; UNIPARC:UPI000007B488
C;Keywords: ligase

Query Match 79.4%; Score 27; DB 2; Length 32;
Best Local Similarity 83.3%; Pred. No. 13; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 2 LVFFAQ 7
:|||||
Db 18 MVFFAQ 23

RESULT 41

T35807
hypothetical protein SC8D9.03 SC8D9.03 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35807
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1999
A;Reference number: Z21589
A;Accession: T35807
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-182 <MUR>
A;Cross-references: UNIPROT:Q9Z588; UNIPARC:UPI00000DAEDF; EMBL:AL035569; PIDN: CAB37567.
A;Experimental source: strain A3 (2)

C;Genetics:

A;Gene: SC08DB:SC8D9.03
C;Superfamily: yeast conserved hypothetical protein YJL055w

Query Match 79.4%; Score 27; DB 2; Length 182;
Best Local Similarity 71.4%; Pred. No. 66;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7
:|||||
Db 160 ELVFFAE 166

RESULT 42

T47892
hypothetical protein T4C21.220 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47892
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.;
.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24479
A;Accession: T47892
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-214 <CHO>
A;Cross-references: UNIPROT:Q9LZY2; UNIPARC:UPI000009DAB0; EMBL:AL162295
A;Experimental source: cultivar Columbia; BAC clone T4C21
C;Genetics:
A;Map position: 3
A;Introns: 46/2; 65/2; 106/2; 128/3; 159/3; 197/3
A;Note: T4C21.220

Query Match 79.4%; Score 27; DB 2; Length 214;
Best Local Similarity 71.4%; Pred. No. 77;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFAQ 7
:|||||
Db 19 KLVPFYAR 25

RESULT 43

T26245
hypothetical protein W06G6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26245
R;McMurray, A.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z20180
A;Accession: T26245
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-300 <WIL>
A;Cross-references: UNIPROT:Q9XU61; UNIPARC:UPI0000061208; EMBL:Z83129; PIDN: CAB05641.1
A;Experimental source: clone W06G6
C;Genetics:
A;Gene: CESP.W06G6.6
A;Map position: 5
A;Introns: 171/2; 204/2

Query Match 79.4%; Score 27; DB 2; Length 300;
Best Local Similarity 83.3%; Pred. No. 11e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFA 6
:|||||
Db 281 KMVFFA 286

RESULT 44

B46678
endoglycosidase F3 (EC 3.2.-.-) precursor - Flavobacterium meningosepticum
C:Species: Flavobacterium meningosepticum
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: B46678
R:Tarentino, A.L.; Quinones, G.; Changchien, L.M.; Plummer Jr., T.H.
J. Biol. Chem. 268, 9702-9708, 1993
A:Title: Multiple endoglycosidase F activities expressed by Flavobacterium meningosepticum
A:Reference number: A46678; MUID:93252846; PMID:8486657
A:Accession: B46678
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-329 <FAR>
A:Cross-references: UNIPROT:P36913; UNIPARC:UPI0000129B37; GB:L06332; NID:gi48695; PIDN:
C:Keywords: glycosidase; hydrolase

Query Match 79.4%; Score 27; DB 2; Length 329;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|:|:|:
Db 2 KKIFFPAQ 8
|:|:|:

RESULT 45
H75505
tryptophanyl-tRNA synthetase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: H75505
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: H75505
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-330 <WHI>
A:Cross-references: UNIPROT:Q9RW7; UNIPARC:UPI0000136720; GB:AE001913; GB:AE000513; NID:
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0558
A:Map position: 1
C:Superfamily: tryptophan-tRNA ligase

Query Match 79.4%; Score 27; DB 2; Length 330;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|:|:|:
Db 78 KVVFFVQ 84
|:|:|:

RESULT 46
A64383
hypothetical protein MJO665 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 05-Oct-2004
C:Accession: A64383
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
raon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: A64383
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-341 <BUL>
A:Cross-references: UNIPROT:Q58079; UNIPARC:UPI0000139BA4; GB:U67513; GB:L77117; NID:gi38
C:Genetics:
A:Map position: REV591204-590179
A:Start codon: GTG
C:Superfamily: uncharacterized conserved protein

Query Match 79.4%; Score 27; DB 2; Length 341;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|:|:|:
Db 67 KLIFPAE 73
|:|:|:

RESULT 47
T26247
hypothetical protein W06G6.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26247
R:McMurray, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20180
A:Accession: T26247
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-349 <WII>
A:Cross-references: UNIPROT:Q9XU59; UNIPARC:UPI0000061209; EMBL:283129; PIDN:CAB05643.1,
A:Experimental source: clone W06G6
C:Genetics:
A:Gene: CESP:W06G6.8
A:Map position: 5
A:Introns: 172/2; 210/3; 247/2

Query Match 79.4%; Score 27; DB 2; Length 349;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPEA 6
|:|:|:
Db 324 KRVFFPA 329
|:|:|:

RESULT 48
H64251
replication initiation protein dnaA - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C>Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C:Accession: H64251
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: H64251
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-437 <TIGR>
A:Cross-references: UNIPROT:P35888; UNIPARC:UPI000012952C; GB:U39734; GB:L43967; NID:gi38
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: replication initiation protein dnaA
C:Keywords: ATP; nucleotide binding; P-loop
F:141-148/Region: nucleotide-binding motif A (P-loop)
F:202-206/Region: nucleotide-binding motif B

Query Match 79.4%; Score 27; DB 2; Length 437;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|:|:|:
Db 315 KLVFFPAK 321

RESULT 49

T04463
hypothetical protein F4D11.170 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04463
R;Bavan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Hoheisel, J.; Mewes, H.W.
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15360
A;Accession: T04463
A;Molecule type: DNA
A;Residues: 1-531 <BRV>
A;Cross-references: UNIPROT:O65536; UNIPARC:UPI000009EC78; EMBL:AL022537
A;Experimental source: cultivar Columbia; BAC clone F4D11
C;Genetics:
A;Map position: 4
A;Note: F4D11.170

Query Match 79.4%; Score 27; DB 2; Length 531;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|:|:|:|:
Db 79 KLVHFAQ 85

RESULT 50

G97000
diguanylate cyclase/phosphodiesterase domain (GGDEF) containing protein [imported] - Clo
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97000
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4836, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-571 <KUR>
A;Cross-references: UNIPROT:Q97KU8; UNIPARC:UPI00000C9FBF; GB:AE001437; PIDN:AAK78794.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0818

Query Match 79.4%; Score 27; DB 2; Length 571;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|:|:|:|:
Db 314 KVMFFPAQ 320

RESULT 51

AD3409
ABC transporter ATP-binding protein BMEI1258 [imported] - Brucella melitensis (strain 16
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 31-Dec-2004
C;Accession: AD3409
R;DeiVecchio, V.G.; Kapratli, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
M.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitend

A;Reference number: AD3252; PMID:11756688

A;Accession: AD3409

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-646 <KUR>

A;Cross-references: UNIPROT:Q8YG2; UNIPARC:UPI0000057FD3; GB:AE008917; PIDN:AAL52439.1

A;Experimental source: strain 16M

C;Genetics:

A;Gene: BMEI1258

A;Map position: 1

Query Match 79.4%; Score 27; DB 2; Length 646;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|:|:|:|:
Db 388 KVAFPAQ 394

RESULT 52

T31691
hypothetical protein F27E11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
C;Accession: T31691
R;Wamsley, P.; Keppler, D.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid F27E11.
A;Reference number: Z21069
A;Accession: T31691
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-655 <WAM>
A;Cross-references: UNIPROT:O16191; UNIPARC:UPI0000178DE0; EMBL:AF016413; PIDN:AA665255

A;Experimental source: strain Bristol N2; clone F27E11

C;Genetics:

A;Gene: CESP:F27E11.2

A;Map position: 5

A;Introns: 62/2; 78/3; 104/1; 144/1; 202/2; 249/3; 450/3; 540/2; 570/3; 631/1

Query Match 79.4%; Score 27; DB 2; Length 655;

Best Local Similarity 71.4%; Pred. No. 2.3e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVFFPAQ 7
|:|:|:|:
Db 39 KLVFFLQ 45

RESULT 53

D70425

conserved hypothetical protein aq_1442 - Aquifex aeolicus

C;Species: Aquifex aeolicus

C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 16-Aug-2004

C;Accession: D70425

R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;

V.

Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Accession: D70425

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-1054 <AQP>

A;Cross-references: UNIPROT:O67430; UNIPARC:UPI000005660F; GB:AE000740; NID:q2983826; P

A;Experimental source: strain VF5

C;Genetics:

A;Gene: aq_1442

C;Superfamily: Sensor diguanylate cyclase/c-di-GMP phosphodiesterase

Query Match 79.4%; Score 27; DB 2; Length 1054;

Best Local Similarity 83.3%; Pred. No. 3.6e+02;

```

Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      2  LVFFAQ 7
      :|||||
Db      997 IVFFAQ 1002

RESULT 54
T34558
hypotheical protein DKFPz434H2450.1 - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34558
R:Poutka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, October 1999
A:Reference number: Z21540
A:Accession: T34558
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-947;948-1273 <POU>
A:Cross-references: UNIPROT:Q9UFH2; UNIPARC:UPI00001775C3; UNIPARC:UPI00001775C4; EMBL:A
A:Experimental source: adult testis; clone DKFPz434H2450
A>Note: the cDNA sequence contains a +1 frameshift near codon 947
C:Genetics:
A>Note: DKFPz434H2450.1
C:Superfamily: dynein heavy chain, ciliary

Query Match      79.4%;  Score 27;  DB 2;  Length 1273;
Best Local Similarity 71.4%;  Pred. No. 4.3e+02;
Matches      5;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;

QY      1  KLVFPAQ 7
      :|:|:|
Db      538 KLIFLAQ 544

RESULT 55
T07200
hypotheical protein 49a - Chlorella vulgaris chloroplast
C:Species: chloroplast Chlorella vulgaris
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C:Accession: T07200
R:Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakae
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A>Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlo
A:Reference number: Z15985; MUID:97303241; PMID:9159184
A:Accession: T07200
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-49 <WAK>
A:Cross-references: UNIPARC:UPI000011E446; EMBL:AB001684; NID:g2224352; PIDN:BAA57847.1;
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match      76.5%;  Score 26;  DB 2;  Length 49;
Best Local Similarity 57.1%;  Pred. No. 32;
Matches      4;  Conservative      3;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1  KLVFPAQ 7
      :|:|:|:|
Db      19 KLIFFSQ 25

RESULT 56
AG3408
molybdopterin (mpt) converting factor, chain 1 [imported] - Brucella melitensis (strain
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 16-Aug-2004
C:Accession: AG3408
R:DelVecchio, V.G.; Kapratl, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

```

```

A>Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AB3252; PMID:11756688
A:Accession: AG3408
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-85 <KUR>
A:Cross-references: UNIPROT:Q8YGA7; UNIPROT:Q8G1L7; UNIPARC:UPI0000057FCE; GB:AE008917;
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11253
A:Map position: 1
C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match      76.5%;  Score 26;  DB 2;  Length 85;
Best Local Similarity 83.3%;  Pred. No. 55;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1  KLVFPA 6
      :|:|:|
Db      4  KLVYPA 9

RESULT 57
H82370
conserved hypothetical protein VC0057 [imported] - Vibrio cholerae (strain N16961 serogr
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: H82370
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chadson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P.
1, R.K.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: H82370
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <HEI>
A:Cross-references: UNIPROT:Q9KVT2; UNIPARC:UPI00000C2BAC; GB:AE004096; GB:AE003852; NID
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0057
A:Map position: 1

Query Match      76.5%;  Score 26;  DB 2;  Length 91;
Best Local Similarity 83.3%;  Pred. No. 58;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      2  LVFFAQ 7
      :|:|:|
Db      20 VVFFAQ 25

RESULT 58
B95049
hypotheical protein SP0424 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: B95049
R:Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A>Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: B95049
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <KUR>
A:Cross-references: UNIPROT:P59201; UNIPARC:UPI0000051423; GB:AE005672; PIDN:AAK74587.1;
A:Experimental source: strain TIGR4
C:Genetics:

```


QY	1	KLVFFA	6
			:
nb	84	KLVFFA	89

Qy 1 KLVFFA 6
| | | | |
: | | | |
Db 4 KLVFFA 9

RESULT 63
F64505
phosphoribosylformylglycinamide synthase (EC 6.3.5.3) I - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: F64505
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
erson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: F64505
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-230 <BUL>
A:Cross-references: UNIPROT:Q59042; UNIPARC:UPI0000132B59; GB:U67605; GB:L77117; MID:g15
C:Genetics:
A:Map position: FOR1629578-1630270
C:Superfamily: phosphoribosylformylglycinamide synthase component I
C:Keywords: ligase

Query Match 76.5%; Score 26; DB 2; Length 230;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVEPFAQ 7
|||
Db 29 ELVFFTQ 35
|||

RESULT 64
AD2307
hypothetical protein alr4011 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AD2307
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AD2307
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 <KUR>
A:Cross-references: UNIPROT:Q8YQ25; UNIPARC:UPI00000CE9AC; GB:BA000019; PIDN:BA075710.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr4011

Query Match 76.5%; Score 26; DB 2; Length 256;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVEPFAQ 7
|||
Db 235 KLLEFLQ 241
|||

A:Molecule type: DNA
A:Residues: 1-273 <BEV>
A:Cross-references: UNIPROT:Q9TOH9; UNIPARC:UPI00000AA99C; EMBL:AL049656; GSPDB:GN00062;
A:Experimental source: cultivar Columbia; BAC clone T6G15
C:Genetics:
A:Gene: ATSP:T6G15.140
A:Map position: 4
A:Introns: 48/1; 95/3; 111/3; 144/1; 220/3; 237/3
A:Superfamily: uncharacterized conserved protein

Query Match 76.5%; Score 26; DB 2; Length 273;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFPAQ 7
|||
Db 216 LVFFPAE 221
|||

RESULT 66
AC1342
ABC transporter (ATP-binding protein) homolog lmo21139 [imported] - Listeria monocytogene
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C:Accession: AC1342
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1342
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-300 <GLA>
A:Cross-references: UNIPROT:Q8Y5C6; UNIPARC:UPI00000CF1DD; GB:NC_003210; PIDN:CAD00217.1
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2139

Query Match 76.5%; Score 26; DB 2; Length 300;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVEPFAQ 7
|||
Db 92 QLIFPAE 98
|||

RESULT 67
A11712
ABC transporter (ATP-binding protein) homolog lin2244 [imported] - Listeria innocua (str
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C:Accession: A11712
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: A11712
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-300 <GLA>
A:Cross-references: UNIPROT:Q929N0; UNIPARC:UPI00000CC7D4; GB:AL592022; PIDN:CAC97473.1;
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin2244

A:Molecule type: DNA
A:Residues: 1-408 <DUZ>
A:Cross-references: UNIPROT:O02043; UNIPARC:UPI00000781F4; EMBL:AF000191; NID:g1946976;
A:Experimental source: strain Bristol N2; clone T23C6
C:Genetics:
A:Gene: CESP:T23C6.5
A:Map position: X
A:Introns: 30/1; 56/3; 107/3; 143/1; 214/3; 240/2; 295/3; 328/1; 377/3

Query Match 76.5%; Score 26; DB 2; Length 408;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFAQ 7
DB 36 LVFFSQ 41

RESULT 73
T39683
zootin-like protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T39683; T40195
R:Oliver, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z21869
A:Accession: T39683
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-124 <OLI>
A:Cross-references: UNIPROT:Q9Y7I8; UNIPARC:UPI00000697C4; EMBL:AL049489; PIDN:CAB39796.
A:Experimental source: strain 972h-1; cosmid c1778
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z21910
A:Accession: T40195
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 89-442 <WOO>
A:Cross-references: UNIPARC:UPI000006AD4A; EMBL:Z97992; PIDN:CAB10796.1; GSPDB:GN000067;
A:Experimental source: strain 972h-; cosmid c30D10
C:Genetics:
A:Gene: SPDB:SPBC1778.01c; SPDB:SPBC30D10.01
A:Map position: 2

Query Match 76.5%; Score 26; DB 2; Length 442;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVFFAQ 7
DB 437 VVFFAQ 442

RESULT 74
H81402
probable integral membrane protein Cj0560 [imported] - Campylobacter jejuni (strain NCTC)
C:Species: Campylobacter jejuni
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: H81402
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: H81402
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-442 <PAR>
A:Cross-references: UNIPROT:Q9PHV5; UNIPARC:UPI00000C217E; GB:AL139075; GB:AL1111168; NID
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:

A:Gene: Cj0560

Query Match 76.5%; Score 26; DB 2; Length 442;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
DB 313 KLVFFA 318

RESULT 75
F71039
hypothetical protein PH1606 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Oct-2004
C:Accession: F71039
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: F71039
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-447 <KAW>
A:Cross-references: UNIPROT:O59243; UNIPARC:UPI00000630DE; GB:AP000006; NID:g3236133; PI
A:Experimental source: strain OT3
A>Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1606
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH1142

Query Match 76.5%; Score 26; DB 2; Length 447;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
DB 207 KLVFFA 212

Search completed: December 29, 2005, 17:49:23
Job time : 18.129 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds
(without alignments)
37.818 Million cell updates/sec

Title: US-10-009-122-4
Perfect score: 31
Sequence: 1 KFPVFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : Published Applications AA.Main.*
1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	6	3	US-09-867-847-13
2	31	100.0	6	3	US-09-867-847-21
3	31	100.0	6	3	US-09-915-092-3
4	31	100.0	6	3	US-09-915-092-11
5	31	100.0	6	3	US-09-747-408-4
6	31	100.0	6	3	US-09-747-408-12
7	31	100.0	6	5	US-10-728-028-3
8	31	100.0	6	5	US-10-728-028-11
9	31	100.0	6	5	US-10-825-958-11
10	31	100.0	6	5	US-10-825-958-19
11	31	100.0	59	4	US-10-424-599-174685
12	31	100.0	64	4	US-10-424-599-164908
13	31	100.0	102	4	US-10-424-599-203722
14	31	100.0	175	4	US-10-437-963-118848
15	31	100.0	372	4	US-10-437-963-118846
16	31	100.0	373	4	US-10-437-963-118916
17	30	96.8	420	4	US-10-437-963-118773
18	28	90.3	54	4	US-10-424-599-266901
19	28	90.3	115	4	US-10-425-115-327241
20	28	90.3	126	4	US-10-425-115-280464
21	28	90.3	159	4	US-10-425-115-193086
22	28	90.3	240	4	US-10-767-701-37567
23	28	90.3	452	4	US-10-369-493-6279
24	28	90.3	490	5	US-10-994-726-438
25	28	90.3	506	3	US-09-877-476-2
26	28	90.3	506	3	US-09-877-476-28
27	28	90.3	506	3	US-09-877-476-30

28	90.3	506	3	US-09-877-476-36	Sequence 36, Appl
28	90.3	506	4	US-10-276-977-7	Sequence 7, Appli
28	90.3	506	4	US-10-758-524-2	Sequence 2, Appli
28	90.3	506	4	US-10-758-524-28	Sequence 28, Appl
28	90.3	506	4	US-10-758-524-30	Sequence 30, Appl
28	90.3	506	4	US-10-758-524-36	Sequence 36, Appl
28	90.3	508	4	US-10-282-122A-47052	Sequence 47052, A
28	90.3	508	5	US-10-994-726-437	Sequence 437, App
28	90.3	508	5	US-10-732-923-18725	Sequence 18725, A
28	90.3	509	5	US-10-732-923-18726	Sequence 18726, A
28	90.3	509	5	US-10-732-923-18737	Sequence 18737, A
28	90.3	509	5	US-10-732-923-18737	Sequence 18737, A
28	90.3	571	4	US-10-282-122A-51929	Sequence 51929, A
28	90.3	1089	4	US-10-369-493-2154	Sequence 2154, Ap
27	87.1	34	4	US-10-425-115-236339	Sequence 236339
27	87.1	46	4	US-10-425-115-200545	Sequence 200545,
27	87.1	47	4	US-10-424-599-232761	Sequence 232761,
27	87.1	48	4	US-10-425-115-206883	Sequence 206883,
27	87.1	56	4	US-10-437-963-176215	Sequence 176215,
27	87.1	57	4	US-10-425-114-38807	Sequence 38807, A
27	87.1	62	3	US-09-764-877-1136	Sequence 1136, Ap
27	87.1	62	4	US-10-242-515-1136	Sequence 1136, Ap
27	87.1	63	4	US-10-424-599-146372	Sequence 146372,
27	87.1	72	4	US-10-425-115-248149	Sequence 248149,
27	87.1	73	4	US-10-425-115-229605	Sequence 229605,
27	87.1	73	4	US-10-425-115-259222	Sequence 259222,
27	87.1	80	4	US-10-425-115-215979	Sequence 215979,
27	87.1	81	4	US-10-425-115-215979	Sequence 215979,
27	87.1	82	4	US-10-424-599-195261	Sequence 195261,
27	87.1	82	5	US-10-450-763-44156	Sequence 44156, A
27	87.1	83	4	US-10-425-115-275005	Sequence 275005,
27	87.1	88	4	US-10-424-599-259257	Sequence 259257,
27	87.1	92	4	US-10-424-599-246138	Sequence 246138,
27	87.1	96	4	US-10-424-599-207674	Sequence 207674,
27	87.1	99	4	US-10-425-115-221194	Sequence 221194,
27	87.1	103	4	US-10-424-599-182454	Sequence 182454,
27	87.1	103	4	US-10-437-963-201763	Sequence 201763,
27	87.1	104	4	US-09-823-153-4	Sequence 4, Appli
27	87.1	104	4	US-10-713-981-4	Sequence 4, Appli
27	87.1	106	4	US-10-425-115-215097	Sequence 215097,
27	87.1	107	4	US-10-424-599-207673	Sequence 207673,
27	87.1	107	4	US-10-437-963-146282	Sequence 146282,
27	87.1	125	4	US-10-425-115-289631	Sequence 289631,
27	87.1	131	4	US-10-424-599-208184	Sequence 208184,
27	87.1	131	4	US-10-424-599-221174	Sequence 221174,
27	87.1	144	5	US-10-450-763-56921	Sequence 56921, A
27	87.1	146	4	US-10-424-599-214877	Sequence 214877,
27	87.1	153	4	US-10-424-599-243854	Sequence 243854,
27	87.1	158	4	US-10-424-599-169140	Sequence 169140,
27	87.1	173	4	US-10-408-765A-1782	Sequence 1782, Ap
27	87.1	173	5	US-10-220-335-207	Sequence 207, App
27	87.1	189	4	US-10-432-198-4	Sequence 4, Appli
27	87.1	189	4	US-10-432-198-5	Sequence 5, Appli
27	87.1	189	4	US-10-432-198-6	Sequence 6, Appli
27	87.1	189	4	US-10-432-198-7	Sequence 7, Appli
27	87.1	206	4	US-10-238-075-489	Sequence 489, App
27	87.1	211	4	US-10-425-115-359320	Sequence 359320,
27	87.1	211	4	US-10-425-115-359323	Sequence 359323,
27	87.1	212	4	US-10-424-599-211252	Sequence 211252,
27	87.1	218	4	US-10-276-727A-7	Sequence 7, Appli
27	87.1	221	5	US-10-450-763-37353	Sequence 37353, A
27	87.1	221	5	US-10-450-763-53342	Sequence 53342, A
27	87.1	221	4	US-10-724-972A-7100	Sequence 7100, Ap
27	87.1	249	4	US-10-437-963-183912	Sequence 183912,
27	87.1	285	4	US-10-425-115-246512	Sequence 246512,
27	87.1	297	3	US-09-864-921-180	Sequence 180, App
27	87.1	297	5	US-10-766-682-180	Sequence 180, App
27	87.1	332	4	US-10-424-599-247557	Sequence 247557,
27	87.1	335	4	US-10-425-115-359332	Sequence 359332,
27	87.1	335	5	US-10-739-930-8473	Sequence 8473, Ap

101	27	87.1	347	4	US-10-425-114-47805	Sequence 47805, A	174	26	83.9	60	6	US-11-093-088-44	Sequence 44, Appl
102	27	87.1	351	4	US-10-275-595A-28	Sequence 28, Appl	175	26	83.9	61	4	US-10-424-599-279574	Sequence 279574, A
103	27	87.1	356	4	US-10-425-115-359329	Sequence 359329, A	176	26	83.9	61	4	US-10-767-701-48124	Sequence 48124, A
104	27	87.1	381	4	US-10-276-272A-10	Sequence 10, Appl	177	26	83.9	61	4	US-10-425-115-294863	Sequence 294863, A
105	27	87.1	388	4	US-10-437-963-102898	Sequence 102898, A	178	26	83.9	61	4	US-10-425-115-323415	Sequence 323415, A
106	27	87.1	389	4	US-10-276-272A-4	Sequence 4, Appl	179	26	83.9	62	4	US-10-424-599-148416	Sequence 148416, A
107	27	87.1	393	5	US-10-739-930-6015	Sequence 6015, Ap	180	26	83.9	65	4	US-10-125-258-43	Sequence 43, Appl
108	27	87.1	401	4	US-10-094-240-20	Sequence 20, Appl	181	26	83.9	65	6	US-11-092-429-43	Sequence 43, Appl
109	27	87.1	401	4	US-10-056-405-20	Sequence 20, Appl	182	26	83.9	65	6	US-11-092-430-43	Sequence 43, Appl
110	27	87.1	407	4	US-10-767-701-47158	Sequence 47158, A	183	26	83.9	65	6	US-11-093-225-43	Sequence 43, Appl
111	27	87.1	407	4	US-10-425-115-283373	Sequence 283373, A	184	26	83.9	65	6	US-11-092-027-43	Sequence 43, Appl
112	27	87.1	408	4	US-10-437-963-173765	Sequence 173765, A	185	26	83.9	65	6	US-11-092-427-43	Sequence 43, Appl
113	27	87.1	422	4	US-10-424-599-277445	Sequence 277445, A	186	26	83.9	65	6	US-11-093-088-43	Sequence 43, Appl
114	27	87.1	422	5	US-10-739-930-9013	Sequence 9013, Ap	187	26	83.9	68	4	US-10-424-599-130908	Sequence 130908, A
115	27	87.1	425	4	US-10-424-599-191171	Sequence 191171, A	188	26	83.9	71	4	US-10-424-599-218467	Sequence 218467, A
116	27	87.1	425	4	US-10-276-272A-6	Sequence 6, Appl	189	26	83.9	71	4	US-10-424-599-234678	Sequence 234678, A
117	27	87.1	428	4	US-10-425-115-295015	Sequence 295015, A	190	26	83.9	71	4	US-10-425-115-211132	Sequence 211132, A
118	27	87.1	444	4	US-10-437-963-102909	Sequence 102909, A	191	26	83.9	72	5	US-10-450-763-52260	Sequence 52260, A
119	27	87.1	454	5	US-10-501-282-2882	Sequence 2882, Ap	192	26	83.9	74	4	US-10-425-115-185420	Sequence 185420, A
120	27	87.1	471	6	US-11-021-951-185	Sequence 185, Ap	193	26	83.9	75	4	US-10-425-115-337684	Sequence 337684, A
121	27	87.1	478	5	US-10-486-781A-6	Sequence 6, Appl	194	26	83.9	76	4	US-10-425-115-259075	Sequence 259075, A
122	27	87.1	478	5	US-10-954-778-13	Sequence 13, Appl	195	26	83.9	82	4	US-10-425-115-350964	Sequence 350964, A
123	27	87.1	498	5	US-10-486-781A-11	Sequence 11, Appl	196	26	83.9	83	4	US-10-425-115-367965	Sequence 367965, A
124	27	87.1	581	4	US-10-282-122A-65905	Sequence 65905, A	197	26	83.9	93	4	US-10-424-599-266485	Sequence 266485, A
125	27	87.1	582	3	US-09-916-658-4	Sequence 4, Appl	198	26	83.9	93	4	US-10-437-963-178420	Sequence 178420, A
126	27	87.1	582	3	US-09-391-104-28	Sequence 28, Appl	199	26	83.9	96	4	US-10-425-115-349216	Sequence 349216, A
127	27	87.1	582	3	US-09-801-196-27	Sequence 27, Appl	200	26	83.9	97	4	US-10-424-599-182131	Sequence 182131, A
128	27	87.1	582	3	US-09-919-497-84	Sequence 84, Appl	201	26	83.9	98	4	US-10-437-963-109168	Sequence 109168, A
129	27	87.1	582	3	US-09-916-849A-2	Sequence 2, Appl	202	26	83.9	99	4	US-10-424-599-269978	Sequence 269978, A
130	27	87.1	582	4	US-10-133-797-6	Sequence 6, Appl	203	26	83.9	101	4	US-10-425-114-57111	Sequence 57111, A
131	27	87.1	582	4	US-10-131-985-43	Sequence 43, Appl	204	26	83.9	105	4	US-10-424-599-210257	Sequence 210257, A
132	27	87.1	582	4	US-10-411-010-26	Sequence 26, Appl	205	26	83.9	106	4	US-10-424-599-254314	Sequence 254314, A
133	27	87.1	582	4	US-10-447-315-9	Sequence 9, Appl	206	26	83.9	109	4	US-10-425-115-215142	Sequence 215142, A
134	27	87.1	582	4	US-10-276-272A-19	Sequence 19, Appl	207	26	83.9	111	3	US-09-933-767-303	Sequence 303, App
135	27	87.1	582	5	US-10-901-417-43	Sequence 43, Appl	208	26	83.9	111	4	US-10-004-860-303	Sequence 303, App
136	27	87.1	582	5	US-10-353-264-26	Sequence 26, Appl	209	26	83.9	111	4	US-10-023-282-303	Sequence 303, App
137	27	87.1	582	5	US-10-773-446-100	Sequence 100, App	210	26	83.9	114	4	US-10-424-599-235618	Sequence 235618, A
138	27	87.1	590	4	US-10-276-272A-2	Sequence 2, Appl	211	26	83.9	114	4	US-10-437-963-170598	Sequence 170598, A
139	27	87.1	592	4	US-10-282-122A-65055	Sequence 65055, A	212	26	83.9	117	4	US-10-424-599-280839	Sequence 280839, A
140	27	87.1	592	4	US-10-276-272A-12	Sequence 12, Appl	213	26	83.9	118	4	US-10-047-676A-17	Sequence 17, Appl
141	27	87.1	626	4	US-10-369-493-11939	Sequence 11939, A	214	26	83.9	118	4	US-10-424-599-212612	Sequence 212612, A
142	27	87.1	729	4	US-10-276-272A-15	Sequence 15, Appl	215	26	83.9	118	5	US-10-790-914-17	Sequence 17, Appl
143	27	87.1	738	4	US-10-221-097-48	Sequence 48, Appl	216	26	83.9	120	4	US-10-425-115-257063	Sequence 257063, A
144	27	87.1	814	4	US-10-425-115-214562	Sequence 214562, A	217	26	83.9	130	4	US-10-425-115-245327	Sequence 245327, A
145	27	87.1	833	4	US-10-041-018-255	Sequence 255, App	218	26	83.9	134	4	US-10-425-115-327283	Sequence 327283, A
146	27	87.1	856	4	US-10-041-018-204	Sequence 204, App	219	26	83.9	137	4	US-10-424-599-236305	Sequence 236305, A
147	27	87.1	856	4	US-10-041-018-240	Sequence 240, App	220	26	83.9	143	4	US-10-425-115-332247	Sequence 332247, A
148	27	87.1	856	4	US-10-041-018-340	Sequence 340, App	221	26	83.9	152	4	US-10-425-115-240443	Sequence 240443, A
149	27	87.1	930	4	US-10-276-272A-13	Sequence 13, Appl	222	26	83.9	159	4	US-10-437-963-106452	Sequence 106452, A
150	27	87.1	1024	3	US-09-841-739-2	Sequence 2, Appl	223	26	83.9	176	4	US-10-424-599-222299	Sequence 222299, A
151	27	87.1	1024	3	US-09-864-921-97	Sequence 97, Appl	224	26	83.9	190	4	US-10-424-599-144945	Sequence 144945, A
152	27	87.1	1024	4	US-10-156-733-2	Sequence 2, Appl	225	26	83.9	191	3	US-09-738-626-6093	Sequence 6093, Ap
153	27	87.1	1024	4	US-10-449-315-2	Sequence 2, Appl	226	26	83.9	225	4	US-10-425-115-208680	Sequence 208680, A
154	27	87.1	1024	5	US-10-766-682-97	Sequence 97, Appl	227	26	83.9	243	4	US-10-369-493-6935	Sequence 6935, Ap
155	27	87.1	1070	4	US-10-421-097-49	Sequence 49, Appl	228	26	83.9	293	4	US-10-652-857-4	Sequence 4, Appl
156	27	87.1	1204	3	US-09-841-739-5	Sequence 5, Appl	229	26	83.9	295	4	US-10-282-122A-65569	Sequence 65569, A
157	27	87.1	1204	4	US-10-449-315-5	Sequence 5, Appl	230	26	83.9	310	5	US-10-774-355A-1555	Sequence 1555, Ap
158	27	87.1	2697	3	US-09-961-527A-5	Sequence 5, Appl	231	26	83.9	314	5	US-10-774-355A-2197	Sequence 2197, Ap
159	26	83.9	28	4	US-10-767-701-48268	Sequence 48268, A	232	26	83.9	321	5	US-10-499-065A-564	Sequence 564, App
160	26	83.9	36	4	US-10-424-599-208993	Sequence 208993, A	233	26	83.9	343	4	US-10-156-761-9520	Sequence 9520, Ap
161	26	83.9	37	4	US-10-425-115-343187	Sequence 343187, A	234	26	83.9	344	4	US-10-210-172-42	Sequence 42, Appl
162	26	83.9	45	5	US-10-472-928-4052	Sequence 4052, Ap	235	26	83.9	363	4	US-10-437-963-176802	Sequence 176802, A
163	26	83.9	51	4	US-10-437-963-142406	Sequence 142406, A	236	26	83.9	373	4	US-10-437-963-125070	Sequence 125070, A
164	26	83.9	53	4	US-10-424-599-197895	Sequence 197895, A	237	26	83.9	384	5	US-10-501-282-6210	Sequence 6210, Ap
165	26	83.9	55	4	US-10-425-114-49675	Sequence 49675, A	238	26	83.9	390	4	US-10-369-493-6541	Sequence 6541, Ap
166	26	83.9	55	4	US-10-437-963-164041	Sequence 164041, A	239	26	83.9	390	5	US-10-732-923-7871	Sequence 7871, Ap
167	26	83.9	59	4	US-10-425-115-366583	Sequence 366583, A	240	26	83.9	393	4	US-10-369-493-13098	Sequence 13098, A
168	26	83.9	60	4	US-10-125-258-44	Sequence 44, Appl	241	26	83.9	397	4	US-10-017-161-2220	Sequence 2220, Ap
169	26	83.9	60	6	US-11-092-429-44	Sequence 44, Appl	242	26	83.9	397	4	US-10-292-798-1866	Sequence 1866, Ap
170	26	83.9	60	6	US-11-092-430-44	Sequence 44, Appl	243	26	83.9	400	5	US-10-739-930-8089	Sequence 8089, Ap
171	26	83.9	60	6	US-11-093-225-44	Sequence 44, Appl	244	26	83.9	404	4	US-10-369-493-15092	Sequence 15092, A
172	26	83.9	60	6	US-11-092-027-44	Sequence 44, Appl	245	26	83.9	414	4	US-10-369-493-11566	Sequence 11566, A
173	26	83.9	60	6	US-11-092-427-44	Sequence 44, Appl	246	26	83.9	414	4	US-10-282-122A-48315	Sequence 48315, A

247 26 83.9 426 3 US-09-738-626-6036
 248 26 83.9 426 4 US-10-627-476-424
 249 26 83.9 431 5 US-10-495-148-21
 250 26 83.9 431 5 US-10-732-923-11170
 251 26 83.9 437 5 US-10-501-282-5896
 252 26 83.9 442 4 US-10-437-963-145134
 253 26 83.9 444 4 US-10-369-493-9766
 254 26 83.9 446 4 US-10-732-923-23883
 255 26 83.9 459 4 US-10-369-493-18271
 256 26 83.9 459 5 US-10-732-923-23570
 257 26 83.9 465 4 US-10-424-599-254007
 258 26 83.9 466 5 US-10-732-923-11191
 259 26 83.9 470 4 US-10-437-963-155526
 260 26 83.9 483 4 US-10-369-493-5486
 261 26 83.9 483 4 US-10-369-493-5487
 262 26 83.9 504 6 US-11-097-143-21694
 263 26 83.9 518 4 US-10-032-585-7864
 264 26 83.9 526 4 US-10-369-493-3924
 265 26 83.9 536 4 US-10-424-599-212613
 266 26 83.9 548 4 US-10-282-122A-63246
 267 26 83.9 581 6 US-11-097-143-15831
 268 26 83.9 618 5 US-10-450-763-56476
 269 26 83.9 641 5 US-10-450-763-55856
 270 26 83.9 661 4 US-10-425-115-330488
 271 26 83.9 681 4 US-10-335-977-5995
 272 26 83.9 690 4 US-10-425-114-61393
 273 26 83.9 712 4 US-10-437-963-132561
 274 26 83.9 718 4 US-10-335-977-5996
 275 26 83.9 717 4 US-10-335-977-5997
 276 26 83.9 749 4 US-10-369-493-22359
 277 26 83.9 754 6 US-11-097-143-23787
 278 26 83.9 860 6 US-11-097-143-21294
 279 26 83.9 888 4 US-10-282-122A-63048
 280 26 83.9 891 6 US-11-097-143-26673
 281 26 83.9 919 5 US-10-200-545-95
 282 26 83.9 960 4 US-10-437-963-129061
 283 26 83.9 976 5 US-10-732-923-1219
 284 26 83.9 994 4 US-10-437-963-129064
 285 26 83.9 1082 3 US-10-282-122A-49664
 286 25 80.6 6 3 US-09-867-847-7
 287 25 80.6 6 3 US-09-867-847-11
 288 25 80.6 6 3 US-09-867-847-19
 289 25 80.6 6 3 US-09-867-847-20
 290 25 80.6 6 3 US-09-972-475-9
 291 25 80.6 6 3 US-09-915-092-1
 292 25 80.6 6 3 US-09-915-092-9
 293 25 80.6 6 3 US-09-915-092-10
 294 25 80.6 6 3 US-09-915-092-28
 295 25 80.6 6 3 US-09-956-625-25
 296 25 80.6 6 3 US-09-747-408-1
 297 25 80.6 6 3 US-09-747-408-3
 298 25 80.6 6 3 US-09-747-408-10
 299 25 80.6 6 3 US-09-747-408-11
 300 25 80.6 6 4 US-10-463-729-9

ALIGNMENTS

RESULT 1
 US-09-867-847-13
 ; Sequence 13, Application US/09867847
 ; Patent No. US20020094335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chalfour, Robert
 ; APPLICANT: Hebert, Lise
 ; APPLICANT: Kong, Xianqi
 ; APPLICANT: Gervais, Francine
 ; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
 ; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
 ; FILE REFERENCE: 14445-501 CIP
 ; CURRENT APPLICATION NUMBER: US/09/867,847
 ; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/168,594
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: 09/724,842
 ; PRIOR FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
 ; OTHER INFORMATION: or peptidomimetics
 ; US-09-867-847-13

Query Match 100.0%; Score 31; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
 Db 1 KPVFFA 6

RESULT 2

US-09-867-847-21
 ; Sequence 21, Application US/09867847
 ; Patent No. US20020094335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chalfour, Robert
 ; APPLICANT: Hebert, Lise
 ; APPLICANT: Kong, Xianqi
 ; APPLICANT: Gervais, Francine
 ; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
 ; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
 ; FILE REFERENCE: 14445-501 CIP
 ; CURRENT APPLICATION NUMBER: US/09/867,847
 ; CURRENT FILING DATE: 2001-09-20
 ; PRIOR APPLICATION NUMBER: 60/168,594
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: 09/724,842
 ; PRIOR FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 21
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
 ; OTHER INFORMATION: or peptidomimetics
 ; NAME/KEY: MOD RES
 ; LOCATION: (6)
 ; OTHER INFORMATION: AMIDATION
 ; US-09-867-847-21

Query Match 100.0%; Score 31; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
 Db 1 KPVFFA 6

RESULT 3

US-09-915-092-3
 ; Sequence 3, Application US/09915092
 ; Publication No. US20020115717A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gervais, Francine
 ; APPLICANT: Kong, Xianqi
 ; APPLICANT: Chalfour, Robert

```
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-3
```

```
Query Match 100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 1 KVFVFA 6
```

```
RESULT 4
US-09-915-092-11
; Sequence 11, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-11
```

```
Query Match 100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 1 KVFVFA 6
```

```
RESULT 5
US-09-747-408-4
; Sequence 4, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-4
```

```
Query Match 100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 1 KVFVFA 6
```

```
RESULT 6
US-09-747-408-12
; Sequence 12, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-12
```

```
Query Match 100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 1 KVFVFA 6
```

```
RESULT 7
US-10-728-028-3
; Sequence 3, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
```


; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-3

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
| | | | |
Db 1 KPVFFA 6

RESULT 8

US-10-728-028-11
; Sequence 11, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NEI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-11

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
| | | | |
Db 1 KPVFFA 6

RESULT 9

US-10-825-958-11
; Sequence 11, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-11

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
| | | | |
Db 1 KPVFFA 6

RESULT 10

US-10-825-958-19
; Sequence 19, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 6

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-19

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
| | | | |
Db 1 KPVFFA 6

RESULT 11

US-10-424-599-174685
; Sequence 174685, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 174685
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_12875C.1.pep
US-10-424-599-174685

Query Match 100.0%; Score 31; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db 11 KFVFFA 16

RESULT 12

US-10-424-599-164908
; Sequence 164908, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 164908
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_11992C.1.pep
US-10-424-599-164908

Query Match 100.0%; Score 31; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db 34 KFVFFA 39

RESULT 13

US-10-424-599-203722
; Sequence 203722, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 203722
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_25988C.1.pep
US-10-424-599-203722

Query Match 100.0%; Score 31; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db 5 KFVFFA 10

RESULT 14

US-10-437-963-118848
; Sequence 118848, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 118848
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_22120C.1.pep
US-10-437-963-118848

Query Match 100.0%; Score 31; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db 80 KFVFFA 85

RESULT 15

US-10-437-963-118846
; Sequence 118846, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 118846
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(372)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_22119C.1.pep
US-10-437-963-118846

Query Match 100.0%; Score 31; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 121 KVFVFA 126

RESULT 16

US-10-437-963-138916
; Sequence 138916, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 138916
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_4025C.1.pep
US-10-437-963-138916

Query Match 100.0%; Score 31; DB 4; Length 373;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 80 KVFVFA 85

RESULT 17

US-10-437-963-118773
; Sequence 118773, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 118773
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_22052C.1.pep

US-10-437-963-118773

Query Match 96.8%; Score 30; DB 4; Length 420;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 355 KVFVFA 360

RESULT 18

US-10-424-599-266901
; Sequence 266901, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 266901
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(54)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_83031C.1.pep
US-10-424-599-266901

Query Match 90.3%; Score 28; DB 4; Length 54;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 18 KVFVFA 23

RESULT 19

US-10-425-115-327241
; Sequence 327241, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 327241
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_61513C.1.pep
US-10-425-115-327241

Query Match 90.3%; Score 28; DB 4; Length 115;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||||:
72 KVFVFS 77

RESULT 20

US-10-425-115-290464
; Sequence 290464, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 290464
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRA4577_27992C.1.pep
US-10-425-115-290464

Query Match 90.3%; Score 28; DB 4; Length 126;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||||:
99 KFLFFA 104

RESULT 21

US-10-425-115-193086
; Sequence 193086, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 193086
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(159)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRA4577_10767C.1.pep
US-10-425-115-193086

Query Match 90.3%; Score 28; DB 4; Length 159;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||||:
89 RFVFFA 94

RESULT 22

US-10-767-701-37567
; Sequence 37567, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 37567
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C3123_1.pep
US-10-767-701-37567

Query Match 90.3%; Score 28; DB 4; Length 240;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||||:
155 KVFVFS 160

RESULT 23

US-10-369-493-6279
; Sequence 6279, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6279
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6279

Query Match 90.3%; Score 28; DB 4; Length 452;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||||:
291 RFVFFA 296

RESULT 24

US-10-994-726-438
; Sequence 438, Application US/10994726
; Publication No. US20050147999A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Lyme Disease Vaccines
; FILE REFERENCE: PB481DI

```

; CURRENT APPLICATION NUMBER: US/10/994,726
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: 09/830,230
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/US98/12718
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/057,483
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: 60/053,344
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,377
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/050,359
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 438
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-10-994-726-438

```

```

Query Match          90.3%; Score 28; DB 5; Length 490;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVFVFA 6
Db      23 RFLVFA 28

```

```

RESULT 25
US-09-877-476-2
; Sequence 2, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-877-476-2

```

```

Query Match          90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVFVFA 6
Db      356 KFLVFA 361

```

```

RESULT 26
US-09-877-476-28
; Sequence 28, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476

```

```

; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 176 amino acids from B. napus elongase KCS (SEQ
; OTHER INFORMATION: ID NO:4) and 3' 330 amino acids from A. thaliana
; OTHER INFORMATION: FAE1 (SEQ ID NO:2); designated Bn176
US-09-877-476-28

```

```

Query Match          90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVFVFA 6
Db      356 KFLVFA 361

```

```

RESULT 27
US-09-877-476-30
; Sequence 30, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 399 amino acids from A. thaliana FAE1 (SEQ ID
; OTHER INFORMATION: NO:2) and 3' 107 amino acids from B. napus
; OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At399
; NAME/KEY: VARIANT
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa = Pro or Gln
US-09-877-476-30

```

```

Query Match          90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVFVFA 6
Db      356 KFLVFA 361

```

```

RESULT 28
US-09-877-476-36
; Sequence 36, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476

```

```
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 506 amino acids from A. thaliana FAE1 (SEQ ID
; OTHER INFORMATION: NO:2) having a mutation at residue 92; designated
; OTHER INFORMATION: At K92R; hypothetical
US-09-877-476-36
```

```
Query Match          90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;
```

```
QY 1 KVFVFA 6
    ||:|||
Db 356 KFLFFA 361
```

```
RESULT 29
US-10-276-977-7
; Sequence 7, Application US/10276977
; Publication No. US20040049806A1
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
; APPLICANT: KUNST, LJERKA
; APPLICANT: SMITH, MARK A.
; APPLICANT: MOON, HANGSIK
; TITLE OF INVENTION: NUCLEIC ACID ENCODING A PLANT VERY LONG CHAIN
; FILE REFERENCE: 56120-5004US
; CURRENT APPLICATION NUMBER: US/10/276,977
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: PCT/IB01/01140
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,789
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-276-977-7
```

```
Query Match          90.3%; Score 28; DB 4; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;
```

```
QY 1 KVFVFA 6
    ||:|||
Db 356 KFLFFA 361
```

```
RESULT 30
US-10-758-524-2
; Sequence 2, Application US/10758524
; Publication No. US20040139498A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108002
; CURRENT APPLICATION NUMBER: US/10/758,524
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 09/877,476
; PRIOR FILING DATE: 2001-06-08
```

```
; PRIOR APPLICATION NUMBER: 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-758-524-2
```

```
Query Match          90.3%; Score 28; DB 4; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;
```

```
QY 1 KVFVFA 6
    ||:|||
Db 356 KFLFFA 361
```

```
RESULT 31
US-10-758-524-28
; Sequence 28, Application US/10758524
; Publication No. US20040139498A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108002
; CURRENT APPLICATION NUMBER: US/10/758,524
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 09/877,476
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 176 amino acids from B. napus elongase KCS (SEQ
; OTHER INFORMATION: ID NO:4) and 3' 330 amino acids from A. thaliana
; OTHER INFORMATION: FAE1 (SEQ ID NO:2); designated Bn176
US-10-758-524-28
```

```
Query Match          90.3%; Score 28; DB 4; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;
```

```
QY 1 KVFVFA 6
    ||:|||
Db 356 KFLFFA 361
```

```
RESULT 32
US-10-758-524-30
; Sequence 30, Application US/10758524
; Publication No. US20040139498A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108002
; CURRENT APPLICATION NUMBER: US/10/758,524
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 09/877,476
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 399 amino acids from A. thaliana PAE1 (SEQ ID
; OTHER INFORMATION: NO:2) and 3' 107 amino acids from B. napus
; OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At399
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa = Pro or Gln
US-10-758-524-30

Query Match          90.3%; Score 28; DB 4; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 356 KFLFFA 361

RESULT 33
US-10-758-524-36
; Sequence 36, Application US/10758524
; Publication No. US20040139498A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108002
; CURRENT APPLICATION NUMBER: US/10/758.524
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 05/877,476
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 506 amino acids from A. thaliana PAE1 (SEQ ID
; OTHER INFORMATION: NO:2) having a mutation at residue 92; designated
; OTHER INFORMATION: At K92R; hypothetical
US-10-758-524-36

Query Match          90.3%; Score 28; DB 4; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 356 KFLFFA 361

RESULT 34
US-10-282-122A-47052
; Sequence 47052, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
```

```
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47052
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-10-282-122A-47052

Query Match          90.3%; Score 28; DB 4; Length 508;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 41 RFVFFA 46

RESULT 35
US-10-994-726-437
; Sequence 437, Application US/10994726
; Publication No. US20050147999A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Lyme Disease Vaccines
; FILE REFERENCE: PB481D1
; CURRENT APPLICATION NUMBER: US/10/994,726
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: 09/830,230
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/US98/12718
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/057,483
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: 60/053,344
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,377
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/050,359
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 437
; LENGTH: 508
```

```
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-10-994-726-437

Query Match          90.3%; Score 28; DB 5; Length 508;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
    :|||||
Db 41 RVVFFA 46

RESULT 36
US-10-732-923-18725
; Sequence 18725, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18725
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Brassica juncea
US-10-732-923-18725

Query Match          90.3%; Score 28; DB 5; Length 509;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
    :|||||
Db 359 KFLFFA 364

RESULT 37
US-10-732-923-18726
; Sequence 18726, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18726
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Brassica juncea
US-10-732-923-18726

Query Match          90.3%; Score 28; DB 5; Length 509;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
    :|||||
Db 358 KFLFFA 363

RESULT 38
US-10-732-923-18737
; Sequence 18737, Application US/10732923
; Publication No. US20050108791A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18737
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Brassica rapa
US-10-732-923-18737

Query Match          90.3%; Score 28; DB 5; Length 509;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
    :|||||
Db 358 KFLFFA 363

RESULT 39
US-10-282-122A-51929
; Sequence 51929, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangou
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Hasselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51929
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51929
```


Query Match 90.3%; Score 28; DB 4; Length 571;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
||:||||
Db 314 KFMFFA 319

RESULT 40

US-10-369-493-2154
; Sequence 2154, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2154
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1089)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2154

Query Match 90.3%; Score 28; DB 4; Length 1089;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
||:||||
Db 13 KVFVFS 18

RESULT 41

US-10-425-115-236339
; Sequence 236339, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 236339
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_147123C.1.pep
US-10-425-115-236339

Query Match 87.1%; Score 27; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVP 5
|||||
Db 23 KVFVP 27

RESULT 42

US-10-425-115-200545
; Sequence 200545, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 200545
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_114485C.1.pep
US-10-425-115-200545

Query Match 87.1%; Score 27; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVP 5
|||||
Db 25 KVFVP 29

RESULT 43

US-10-424-599-232761
; Sequence 232761, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 232761
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52207C.1.pep
US-10-424-599-232761

Query Match 87.1%; Score 27; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVP 5
|||||
Db 11 KVFVP 15

RESULT 44

US-10-425-115-206883
; Sequence 206883, Application US/10425115

```
; Publication No. US200400214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 206883
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_120267C.1.pap
US-10-425-115-206883

Query Match      87.1%; Score 27; DB 4; Length 48;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 15 KFAFFA 20

RESULT 45
US-10-437-963-176215
; Publication 176215, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 176215
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73986C.1.pap
US-10-437-963-176215

Query Match      87.1%; Score 27; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
DB 13 KVFVFF 17

RESULT 46
US-10-425-114-38807
; Sequence 38807, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
```

```
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 38807
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700684806_FLI.pap
US-10-425-114-38807

Query Match      87.1%; Score 27; DB 4; Length 57;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
DB 29 KVFVFF 33

RESULT 47
US-09-764-877-1136
; Sequence 1136, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1136
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (55)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1136

Query Match      87.1%; Score 27; DB 3; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
DB 31 KVFVFF 35

RESULT 48
US-10-242-515-1136
; Sequence 1136, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
```

```
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1136
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (55)-
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (60)-
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-242-515-1136

Query Match      87.1%; Score 27; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KFVFF 5
      |||||
Db      31 KFVFF 35

RESULT 49
US-10-424-599-146372
; Sequence 146372, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 146372
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_103191C.1.pap
US-10-424-599-146372

Query Match      87.1%; Score 27; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KFVFF 5
      |||||

; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1136
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_157899C.1.pap
US-10-425-115-248149

Query Match      87.1%; Score 27; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KFVFF 5
      |||||
Db      67 KFVFF 71

RESULT 51
US-10-425-115-229605
; Sequence 229605, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 229605
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_140993C.1.pap
US-10-425-115-229605

Query Match      87.1%; Score 27; DB 4; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KFVFF 5
      |||||
Db      1 KFVFF 5

RESULT 52
US-10-425-115-259222
```

```
; Sequence 259222, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 259222
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_167996C.1.pep
US-10-425-115-259222

Query Match      87.1%; Score 27; DB 4; Length 80;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFF 6
      || |||
Db      66 KFTFFA 71

RESULT 53
US-10-425-115-215979
; Sequence 215979, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 215979
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_128569C.1.pep
US-10-425-115-215979

Query Match      87.1%; Score 27; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFF 5
      |||||
Db      30 KVFVFF 34

RESULT 54
US-10-424-599-195261
; Sequence 195261, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
```

```
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 195261
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_18348C.1.pep
US-10-424-599-195261

Query Match      87.1%; Score 27; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFF 5
      |||||
Db      66 KVFVFF 70

RESULT 55
US-10-450-763-44156
; Sequence 44156, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 44156
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-44156

Query Match      87.1%; Score 27; DB 5; Length 82;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFF 6
      :|||
Db      11 EFVFFA 16

RESULT 56
US-10-425-115-275005
; Sequence 275005, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 275005
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Zea mays
```

```
;
;
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_182395C.1.pep
US-10-425-115-275005

Query Match      87.1%; Score 27; DB 4; Length 83;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
Db      49 KVFVF 53

RESULT 57
US-10-424-599-259257
; Sequence 259257, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 259257
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_76133C.1.pep
US-10-424-599-259257

Query Match      87.1%; Score 27; DB 4; Length 88;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFA 6
Db     13 RFVFFA 18

RESULT 58
US-10-424-599-246138
; Sequence 246138, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 246138
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(92)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64294C.1.pep
US-10-424-599-246138

Query Match      87.1%; Score 27; DB 4; Length 92;

Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
Db      71 KVFVF 75

RESULT 59
US-10-424-599-207674
; Sequence 207674, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 207674
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_29556C.1.pep
US-10-424-599-207674

Query Match      87.1%; Score 27; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
Db      5 KVFVF 9

RESULT 60
US-10-425-115-221194
; Sequence 221194, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 221194
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_133318C.1.pep
US-10-425-115-221194

Query Match      87.1%; Score 27; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
Db     20 KVFVF 24

RESULT 61
```

US-10-424-599-182454
 ; Sequence 182454, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 182454
 ; LENGTH: 103
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_135769C.1.pep
 US-10-424-599-182454

Query Match 87.1%; Score 27; DB 4; Length 103;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 |||||
 DB 30 KVFVF 34

RESULT 62
 US-10-437-963-201763
 ; Sequence 201763, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 201763
 ; LENGTH: 103
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_97105C.1.pep
 US-10-437-963-201763

Query Match 87.1%; Score 27; DB 4; Length 103;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 |||||
 DB 43 KVFVF 47

RESULT 63
 US-09-823-153-4
 ; Sequence 4, Application US/09823153
 ; Patent No. US20020025540A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company

; APPLICANT: Roberts, Susan
 ; APPLICANT: Pak, Roger
 ; APPLICANT: Lewis, Martin
 ; APPLICANT: Smith, David
 ; APPLICANT: Hendrick, Joseph
 ; APPLICANT: Vinitsky, Alexander
 ; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX
 ; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
 ; FILE REFERENCE: D0004
 ; CURRENT APPLICATION NUMBER: US/09/823,153
 ; CURRENT FILING DATE: 2001-07-02
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 104
 ; TYPE: PRT
 ; ORGANISM: Human Beta App
 US-09-823-153-4

Query Match 87.1%; Score 27; DB 3; Length 104;
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 :|||||
 DB 21 EFVFFA 26

RESULT 64
 US-10-713-981-4
 ; Sequence 4, Application US/10713981
 ; Publication No. US20040121411A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; APPLICANT: Roberts, Susan
 ; APPLICANT: Pak, Roger
 ; APPLICANT: Lewis, Martin
 ; APPLICANT: Smith, David
 ; APPLICANT: Hendrick, Joseph
 ; APPLICANT: Vinitsky, Alexander
 ; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX
 ; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
 ; FILE REFERENCE: D0004 DIV
 ; CURRENT APPLICATION NUMBER: US/10/713,981
 ; CURRENT FILING DATE: 2003-11-14
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 104
 ; TYPE: PRT
 ; ORGANISM: Human Beta App
 US-10-713-981-4

Query Match 87.1%; Score 27; DB 4; Length 104;
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 :|||||
 DB 21 EFVFFA 26

RESULT 65
 US-10-425-115-215097
 ; Sequence 215097, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 215097
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_127767C.1.pep
US-10-425-115-215097

Query Match 87.1%; Score 27; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5
Db 97 KVFVF 101

RESULT 66

US-10-424-599-207673
; Sequence 207673, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 207673
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_29555C.1.pep
US-10-424-599-207673

Query Match 87.1%; Score 27; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5
Db 16 KVFVF 20

RESULT 67

US-10-437-963-146282
; Sequence 146282, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 146282

; LENGTH: 107
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_46920C.1.pep
US-10-437-963-146282

Query Match 87.1%; Score 27; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5
Db 18 KVFVF 22

RESULT 68

US-10-424-599-278159
; Sequence 278159, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278159
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93200C.1.pep
US-10-424-599-278159

Query Match 87.1%; Score 27; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5
Db 5 KVFVF 9

RESULT 69

US-10-425-115-208261
; Sequence 208261, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 208261
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_121527C.1.pep
US-10-425-115-208261

Query Match 87.1%; Score 27; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;

```
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KFVFF 5
Db 33 KFVFF 37

RESULT 70
US-10-425-115-286779
; Sequence 286779, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 286779
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(110)
; OTHER INFORMATION: unsure at all Xaa locations
;
; OTHER INFORMATION: Clone ID: MRT4577_24637C.1.pep
US-10-425-115-286779

Query Match 87.1%; Score 27; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KFVFF 5
Db 96 KFVFF 100

RESULT 71
US-09-864-408A-4214
; Sequence 4214, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 4214
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
US-09-864-408A-4214

Query Match 87.1%; Score 27; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 5.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KFVFF 5
```

```
Db 67 KFVFF 71

RESULT 72
US-10-425-115-256025
; Sequence 256025, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 256025
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_165087C.1.pep
US-10-425-115-256025

Query Match 87.1%; Score 27; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 6e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KFVFF 5
Db 47 KFVFF 51

RESULT 73
US-10-425-115-289631
; Sequence 289631, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 289631
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_27231C.1.pep
US-10-425-115-289631

Query Match 87.1%; Score 27; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 6.4e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KFVFF 5
Db 26 KFVFF 30

RESULT 74
US-10-424-599-208184
; Sequence 208184, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
```


; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 208184
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_30014C.1.pep
US-10-424-599-208184

Query Match 87.1%; Score 27; DB 4; Length 131;
Best Local Similarity 66.7%; Pred. No. 6.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
|||:
Db 118 KPIFFS 123

RESULT 75
US-10-424-599-221174
; Sequence 221174, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 221174
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41750C.1.pep
US-10-424-599-221174

Query Match 87.1%; Score 27; DB 4; Length 131;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
|||:
Db 83 KPAFFA 88

Search completed: December 29, 2005, 18:49:39
Job time : 70.2903 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds
(without alignments)
24.763 Million cell updates/sec

Title: US-10-009-122-4

Perfect score: 31

Sequence: 1 KVFVFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- 1: /cgm2_6/ptodata/1/iaa/5 COMB.pep.*
- 2: /cgm2_6/ptodata/1/iaa/6 COMB.pep.*
- 3: /cgm2_6/ptodata/1/iaa/H COMB.pep.*
- 4: /cgm2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 5: /cgm2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	6	2	US-09-747-408-4
2	31	100.0	6	2	US-09-747-408-12
3	30	96.8	1283	2	US-09-248-796A-18091
4	28	90.3	490	2	US-09-830-230A-438
5	28	90.3	506	2	US-08-888-998-2
6	28	90.3	506	2	US-09-362-633-2
7	28	90.3	506	2	US-09-877-476-2
8	28	90.3	506	2	US-09-877-476-28
9	28	90.3	506	2	US-09-877-476-30
10	28	90.3	506	2	US-09-877-476-36
11	28	90.3	508	2	US-09-830-230A-437
12	27	87.1	67	2	US-09-248-796A-26311
13	27	87.1	82	2	US-09-513-999C-4859
14	27	87.1	98	2	US-09-270-767-40694
15	27	87.1	98	2	US-09-270-767-55910
16	27	87.1	104	2	US-09-823-153-4
17	27	87.1	116	2	US-09-270-767-57813
18	27	87.1	238	2	US-09-902-540-10859
19	27	87.1	240	2	US-09-134-001C-5445
20	27	87.1	266	2	US-09-270-767-42516
21	27	87.1	320	2	US-09-248-796A-19539
22	27	87.1	340	2	US-09-270-767-40453
23	27	87.1	340	2	US-09-270-767-55669
24	27	87.1	475	2	US-09-270-767-45548
25	27	87.1	525	2	US-09-270-767-34763
26	27	87.1	525	2	US-09-270-767-49980
27	27	87.1	579	2	US-08-704-711A-1

28	87.1	579	2	US-09-521-220-1	Sequence 1, Appli
29	87.1	582	2	US-08-704-711A-2	Sequence 2, Appli
30	87.1	582	2	US-08-448-489-1	Sequence 1, Appli
31	87.1	582	2	US-09-211-704A-9	Sequence 9, Appli
32	87.1	582	2	US-09-521-220-2	Sequence 2, Appli
33	87.1	582	2	US-09-391-104-28	Sequence 28, Appli
34	87.1	582	2	US-09-919-497-84	Sequence 84, Appli
35	87.1	582	2	US-09-689-730-1	Sequence 1, Appli
36	87.1	1024	2	US-10-449-315-2	Sequence 2, Appli
37	87.1	1204	2	US-10-449-315-5	Sequence 5, Appli
38	83.9	45	2	US-09-270-767-37091	Sequence 37091, A
39	83.9	45	2	US-09-270-767-52308	Sequence 52308, A
40	83.9	46	2	US-09-798-635A-41	Sequence 41, Appli
41	83.9	60	2	US-10-125-258-44	Sequence 44, Appli
42	83.9	61	2	US-09-583-110-4895	Sequence 4895, Ap
43	83.9	65	2	US-10-125-258-43	Sequence 43, Appli
44	83.9	84	2	US-09-270-767-60733	Sequence 60733, A
45	83.9	104	2	US-09-621-976-6739	Sequence 6739, Ap
46	83.9	111	2	US-09-205-258-303	Sequence 303, App
47	83.9	111	2	US-10-004-860-303	Sequence 303, App
48	83.9	118	2	US-09-627-376-17	Sequence 17, Appli
49	83.9	118	2	US-10-047-676B-17	Sequence 17, Appli
50	83.9	156	2	US-09-270-767-45241	Sequence 45241, A
51	83.9	177	2	US-09-270-767-35390	Sequence 35390, A
52	83.9	177	2	US-09-270-767-50607	Sequence 50607, A
53	83.9	186	2	US-09-251-645-4	Sequence 4, Appli
54	83.9	201	2	US-09-270-767-33463	Sequence 33463, A
55	83.9	201	2	US-09-270-767-48680	Sequence 48680, A
56	83.9	249	2	US-09-270-767-38186	Sequence 38186, A
57	83.9	249	2	US-09-270-767-53403	Sequence 53403, A
58	83.9	249	2	US-09-248-796A-27128	Sequence 27128, A
59	83.9	328	2	US-09-830-910-2	Sequence 2, Appli
60	83.9	330	2	US-09-248-796A-15301	Sequence 15301, A
61	83.9	394	2	US-09-270-767-41366	Sequence 41366, A
62	83.9	394	2	US-09-270-767-56582	Sequence 56582, A
63	83.9	402	2	US-09-252-991A-25289	Sequence 25289, A
64	83.9	414	2	US-09-902-540-11308	Sequence 11308, A
65	83.9	426	2	US-09-602-787A-424	Sequence 424, App
66	83.9	437	2	US-09-489-039A-8958	Sequence 8958, Ap
67	83.9	446	2	US-09-252-991A-17185	Sequence 17185, A
68	83.9	453	2	US-09-489-039A-8303	Sequence 8303, Ap
69	83.9	493	2	US-09-252-991A-28992	Sequence 28992, A
70	83.9	557	2	US-09-540-236-2206	Sequence 2206, Ap
71	83.9	573	2	US-09-489-039A-11884	Sequence 11884, A
72	83.9	597	2	US-09-252-991A-22560	Sequence 22560, A
73	83.9	745	2	US-09-902-540-10275	Sequence 10275, A
74	83.9	892	2	US-09-540-236-2074	Sequence 2074, Ap
75	80.6	6	1	US-08-612-785B-9	Sequence 9, Appli
76	80.6	6	2	US-08-703-675C-32	Sequence 32, Appli
77	80.6	6	2	US-08-617-267C-9	Sequence 9, Appli
78	80.6	6	2	US-09-747-408-1	Sequence 1, Appli
79	80.6	6	2	US-09-747-408-3	Sequence 3, Appli
80	80.6	6	2	US-09-747-408-10	Sequence 10, Appli
81	80.6	6	2	US-09-747-408-11	Sequence 11, Appli
82	80.6	7	1	US-08-127-904-14	Sequence 14, Appli
83	80.6	7	1	US-08-612-785B-7	Sequence 7, Appli
84	80.6	7	2	US-08-703-675C-30	Sequence 30, Appli
85	80.6	7	2	US-08-617-267C-7	Sequence 7, Appli
86	80.6	7	2	US-09-264-709A-13	Sequence 13, Appli
87	80.6	7	2	US-09-747-408-2	Sequence 2, Appli
88	80.6	7	2	US-09-747-408-18	Sequence 18, Appli
89	80.6	7	2	US-09-747-408-19	Sequence 19, Appli
90	80.6	7	4	PCT-US94-10475-14	Sequence 14, Appli
91	80.6	8	1	US-08-612-785B-5	Sequence 5, Appli
92	80.6	8	1	US-08-630-645-1	Sequence 1, Appli
93	80.6	8	2	US-08-703-675C-28	Sequence 28, Appli
94	80.6	8	2	US-08-617-267C-5	Sequence 5, Appli
95	80.6	8	2	US-09-095-106A-44	Sequence 44, Appli
96	80.6	8	2	US-08-766-596A-1	Sequence 1, Appli
97	80.6	8	4	PCT-US96-314C-73	Sequence 73, Appli
98	80.6	8	4	PCT-US96-10220-1	Sequence 1, Appli
99	80.6	9	2	US-08-766-596A-64	Sequence 64, Appli
100	80.6	9	2	US-09-747-408-20	Sequence 20, Appli

101	25	80.6	10	2	US-08-970-833-3	Sequence 3, Appli	174	25	80.6	28	1	US-08-293-284A-4	Sequence 4, Appli
102	25	80.6	10	2	US-09-724-961-20	Sequence 20, Appli	175	25	80.6	28	1	US-08-461-216-2	Sequence 2, Appli
103	25	80.6	10	2	US-09-724-961-21	Sequence 21, Appli	176	25	80.6	28	2	US-09-388-890-2	Sequence 3, Appli
104	25	80.6	10	2	US-09-724-961-22	Sequence 22, Appli	177	25	80.6	28	2	US-09-388-890-3	Sequence 3, Appli
105	25	80.6	10	2	US-09-724-961-23	Sequence 23, Appli	178	25	80.6	28	2	US-09-388-890-4	Sequence 4, Appli
106	25	80.6	10	2	US-09-724-961-24	Sequence 24, Appli	179	25	80.6	28	2	US-09-388-890-5	Sequence 5, Appli
107	25	80.6	10	2	US-09-580-018-20	Sequence 20, Appli	180	25	80.6	28	2	US-09-388-890-6	Sequence 6, Appli
108	25	80.6	10	2	US-09-580-018-21	Sequence 21, Appli	181	25	80.6	28	2	US-09-388-890-7	Sequence 7, Appli
109	25	80.6	10	2	US-09-580-018-22	Sequence 22, Appli	182	25	80.6	28	2	US-09-388-890-8	Sequence 8, Appli
110	25	80.6	10	2	US-09-580-018-23	Sequence 23, Appli	183	25	80.6	28	2	US-09-388-890-9	Sequence 9, Appli
111	25	80.6	10	2	US-09-580-018-24	Sequence 24, Appli	184	25	80.6	28	2	US-09-388-890-10	Sequence 10, Appli
112	25	80.6	10	2	US-09-724-551-20	Sequence 20, Appli	185	25	80.6	28	2	US-09-388-890-11	Sequence 11, Appli
113	25	80.6	10	2	US-09-724-551-21	Sequence 21, Appli	186	25	80.6	28	2	US-09-388-890-12	Sequence 12, Appli
114	25	80.6	10	2	US-09-724-551-22	Sequence 22, Appli	187	25	80.6	28	2	US-09-388-890-13	Sequence 13, Appli
115	25	80.6	10	2	US-09-724-551-23	Sequence 23, Appli	188	25	80.6	28	2	US-09-388-890-14	Sequence 14, Appli
116	25	80.6	10	2	US-09-724-551-24	Sequence 24, Appli	189	25	80.6	28	2	US-08-723-661B-1	Sequence 1, Appli
117	25	80.6	10	2	US-09-724-940-20	Sequence 20, Appli	190	25	80.6	28	2	US-08-723-661B-2	Sequence 2, Appli
118	25	80.6	10	2	US-09-724-940-21	Sequence 21, Appli	191	25	80.6	28	2	US-09-660-954-2	Sequence 2, Appli
119	25	80.6	10	2	US-09-724-940-22	Sequence 22, Appli	192	25	80.6	28	2	US-09-660-954-3	Sequence 3, Appli
120	25	80.6	10	2	US-09-724-940-23	Sequence 23, Appli	193	25	80.6	28	2	US-09-660-954-4	Sequence 4, Appli
121	25	80.6	10	2	US-09-724-940-24	Sequence 24, Appli	194	25	80.6	28	2	US-09-660-954-5	Sequence 5, Appli
122	25	80.6	11	1	US-08-630-645-14	Sequence 14, Appli	195	25	80.6	28	2	US-09-660-954-6	Sequence 6, Appli
123	25	80.6	11	1	US-08-766-596A-14	Sequence 14, Appli	196	25	80.6	28	2	US-09-660-954-7	Sequence 7, Appli
124	25	80.6	11	2	US-09-988-842-9	Sequence 9, Appli	197	25	80.6	28	2	US-09-660-954-8	Sequence 8, Appli
125	25	80.6	11	2	US-09-988-842-25	Sequence 25, Appli	198	25	80.6	28	2	US-09-660-954-9	Sequence 9, Appli
126	25	80.6	11	4	FCT-US96-10220-14	Sequence 25, Appli	199	25	80.6	28	2	US-09-660-954-10	Sequence 10, Appli
127	25	80.6	14	2	US-09-594-366-5	Sequence 5, Appli	200	25	80.6	28	2	US-09-660-954-11	Sequence 11, Appli
128	25	80.6	14	2	US-09-992-800-5	Sequence 5, Appli	201	25	80.6	28	2	US-09-660-954-12	Sequence 12, Appli
129	25	80.6	15	1	US-08-612-785B-14	Sequence 14, Appli	202	25	80.6	28	2	US-09-660-954-13	Sequence 13, Appli
130	25	80.6	15	1	US-08-612-785B-37	Sequence 37, Appli	203	25	80.6	28	2	US-09-660-954-14	Sequence 14, Appli
131	25	80.6	15	2	US-08-612-785B-37	Sequence 37, Appli	204	25	80.6	28	2	US-08-898-300-4	Sequence 4, Appli
132	25	80.6	15	2	US-08-766-596A-56	Sequence 56, Appli	205	25	80.6	28	2	US-08-824-513-4	Sequence 4, Appli
133	25	80.6	15	2	US-08-766-596A-57	Sequence 57, Appli	206	25	80.6	28	2	US-09-623-548A-959	Sequence 959, App
134	25	80.6	15	2	US-08-766-596A-58	Sequence 58, Appli	207	25	80.6	28	2	US-09-623-548A-965	Sequence 965, App
135	25	80.6	15	2	US-08-766-596A-60	Sequence 60, Appli	208	25	80.6	28	2	US-09-623-548A-976	Sequence 976, App
136	25	80.6	15	2	US-08-766-596A-61	Sequence 61, Appli	209	25	80.6	28	2	US-09-623-548A-992	Sequence 992, App
137	25	80.6	15	2	US-08-766-596A-63	Sequence 63, Appli	210	25	80.6	28	2	US-09-623-548A-1003	Sequence 1003, App
138	25	80.6	15	2	US-08-766-596A-65	Sequence 65, Appli	211	25	80.6	28	2	US-09-657-276-959	Sequence 959, App
139	25	80.6	17	2	US-09-657-276-983	Sequence 65, Appli	212	25	80.6	28	2	US-09-657-276-965	Sequence 965, App
140	25	80.6	17	2	US-09-594-366-3	Sequence 3, Appli	213	25	80.6	28	2	US-09-657-276-976	Sequence 976, App
141	25	80.6	17	2	US-09-623-548A-950	Sequence 950, App	214	25	80.6	28	2	US-09-657-276-1003	Sequence 1003, App
142	25	80.6	17	2	US-09-623-548A-983	Sequence 983, App	215	25	80.6	28	2	US-09-865-294A-66	Sequence 66, Appli
143	25	80.6	17	2	US-09-992-800-3	Sequence 3, Appli	216	25	80.6	30	1	US-08-609-090-3	Sequence 3, Appli
144	25	80.6	17	2	US-09-657-276-950	Sequence 950, App	217	25	80.6	30	1	US-09-861-847A-1	Sequence 1, Appli
145	25	80.6	17	2	US-09-657-276-983	Sequence 983, App	218	25	80.6	33	1	US-08-609-090-4	Sequence 4, Appli
146	25	80.6	19	2	US-08-970-833-11	Sequence 11, Appli	219	25	80.6	34	1	US-08-475-579A-4	Sequence 4, Appli
147	25	80.6	19	2	US-09-723-384-5	Sequence 5, Appli	220	25	80.6	35	1	US-08-304-585-6	Sequence 6, Appli
148	25	80.6	19	2	US-09-724-961-75	Sequence 75, Appli	221	25	80.6	35	1	US-08-612-785B-16	Sequence 16, Appli
149	25	80.6	19	2	US-09-724-552-5	Sequence 5, Appli	222	25	80.6	35	1	US-08-612-785B-36	Sequence 36, Appli
150	25	80.6	19	2	US-09-580-018-75	Sequence 75, Appli	223	25	80.6	35	1	US-08-612-785B-38	Sequence 38, Appli
151	25	80.6	19	2	US-09-723-927-5	Sequence 5, Appli	224	25	80.6	35	1	US-08-612-785B-40	Sequence 40, Appli
152	25	80.6	19	2	US-09-724-489-5	Sequence 5, Appli	225	25	80.6	35	2	US-08-617-267C-16	Sequence 16, Appli
153	25	80.6	19	2	US-09-724-477-5	Sequence 5, Appli	226	25	80.6	35	2	US-09-623-548A-979	Sequence 979, App
154	25	80.6	19	2	US-09-723-762-5	Sequence 5, Appli	227	25	80.6	35	2	US-09-623-548A-1006	Sequence 1006, App
155	25	80.6	19	2	US-09-201-430-5	Sequence 5, Appli	228	25	80.6	35	2	US-09-657-276-979	Sequence 979, App
156	25	80.6	19	2	US-09-724-551-75	Sequence 75, Appli	229	25	80.6	36	1	US-08-609-090-6	Sequence 1006, App
157	25	80.6	19	2	US-10-815-353-5	Sequence 5, Appli	230	25	80.6	36	1	US-08-609-090-6	Sequence 6, Appli
158	25	80.6	19	2	US-10-816-529-5	Sequence 5, Appli	231	25	80.6	36	2	US-09-861-847A-6	Sequence 6, Appli
159	25	80.6	19	2	US-10-815-391-5	Sequence 5, Appli	232	25	80.6	38	1	US-09-861-847A-11	Sequence 11, Appli
160	25	80.6	19	2	US-10-816-022-5	Sequence 5, Appli	233	25	80.6	38	1	US-08-302-808-1	Sequence 1, Appli
161	25	80.6	19	2	US-09-724-940-75	Sequence 75, Appli	234	25	80.6	38	1	US-07-737-371E-68	Sequence 68, Appli
162	25	80.6	19	2	US-10-934-609-5	Sequence 5, Appli	235	25	80.6	38	1	US-08-986-948-1	Sequence 1, Appli
163	25	80.6	19	2	US-10-884-892-5	Sequence 5, Appli	236	25	80.6	38	2	US-09-623-548A-975	Sequence 975, App
164	25	80.6	20	2	US-08-970-833-10	Sequence 10, Appli	237	25	80.6	38	2	US-09-623-548A-1002	Sequence 1002, App
165	25	80.6	20	2	US-09-724-953-33	Sequence 33, Appli	238	25	80.6	38	2	US-09-657-276-975	Sequence 975, App
166	25	80.6	20	2	US-09-724-567-33	Sequence 33, Appli	239	25	80.6	39	1	US-09-657-276-1002	Sequence 1002, App
167	25	80.6	20	2	US-09-979-952-33	Sequence 33, Appli	240	25	80.6	39	1	US-08-304-585-5	Sequence 5, Appli
168	25	80.6	20	2	US-09-585-817-33	Sequence 33, Appli	241	25	80.6	39	1	US-08-302-808-2	Sequence 2, Appli
169	25	80.6	26	1	US-08-304-585-7	Sequence 7, Appli	242	25	80.6	39	1	US-08-609-090-7	Sequence 7, Appli
170	25	80.6	28	1	US-08-346-849-4	Sequence 4, Appli	243	25	80.6	39	1	US-08-682-245A-1	Sequence 1, Appli
171	25	80.6	28	1	US-08-302-808-7	Sequence 7, Appli	244	25	80.6	40	1	US-08-986-948-2	Sequence 2, Appli
172	25	80.6	28	1	US-08-609-090-2	Sequence 2, Appli	245	25	80.6	40	1	US-07-744-767A-1	Sequence 1, Appli
173	25	80.6	28	1	US-08-986-948-7	Sequence 7, Appli	246	25	80.6	40	1	US-08-235-400-2	Sequence 2, Appli
												US-08-476-464A-2	Sequence 2, Appli

```
247 25 80.6 40 1 US-08-304-585-1
248 25 80.6 40 1 US-08-304-585-8
249 25 80.6 40 1 US-08-302-808-3
250 25 80.6 40 1 US-08-433-734-1
251 25 80.6 40 1 US-08-609-090-8
252 25 80.6 40 1 US-07-737-3718-69
253 25 80.6 40 1 US-08-682-245A-2
254 25 80.6 40 1 US-08-986-948-3
255 25 80.6 40 1 US-08-461-216-1
256 25 80.6 40 2 US-08-959-148-1
257 25 80.6 40 2 US-09-242-724-22
258 25 80.6 40 2 US-08-723-661B-1
259 25 80.6 40 2 US-09-082-365-3
260 25 80.6 40 2 US-09-133-866-1
261 25 80.6 40 2 US-09-861-847A-7
262 25 80.6 40 2 US-09-861-847A-8
263 25 80.6 40 2 US-09-988-842-3
264 25 80.6 40 2 US-10-455-218-1
265 25 80.6 40 2 US-10-151-614-1
266 25 80.6 40 2 US-09-623-548A-956
267 25 80.6 40 2 US-09-623-548A-962
268 25 80.6 40 2 US-09-623-548A-968
269 25 80.6 40 2 US-09-623-548A-978
270 25 80.6 40 2 US-09-623-548A-989
271 25 80.6 40 2 US-09-623-548A-995
272 25 80.6 40 2 US-09-623-548A-1005
273 25 80.6 40 2 US-09-657-276-956
274 25 80.6 40 2 US-09-657-276-962
275 25 80.6 40 2 US-09-657-276-968
276 25 80.6 40 2 US-09-657-276-978
277 25 80.6 40 2 US-09-657-276-989
278 25 80.6 40 2 US-09-657-276-995
279 25 80.6 40 2 US-09-657-276-1005
280 25 80.6 40 2 US-09-962-955D-36
281 25 80.6 40 4 PCT-US92-06700-1
282 25 80.6 41 1 US-07-819-361-1
283 25 80.6 41 1 US-08-302-808-4
284 25 80.6 41 1 US-08-682-245A-3
285 25 80.6 41 1 US-08-986-948-4
286 25 80.6 42 1 US-07-744-767A-2
287 25 80.6 42 1 US-08-179-574-1
288 25 80.6 42 1 US-08-271-162-5
289 25 80.6 42 1 US-08-347-144-1
290 25 80.6 42 1 US-08-462-859A-19
291 25 80.6 42 1 US-08-123-659A-19
292 25 80.6 42 1 US-08-464-247A-19
293 25 80.6 42 1 US-08-464-248A-19
294 25 80.6 42 1 US-08-476-464A-1
295 25 80.6 42 1 US-08-304-585-2
296 25 80.6 42 1 US-08-302-808-5
297 25 80.6 42 1 US-08-268-348A-1
298 25 80.6 42 1 US-08-268-348A-2
299 25 80.6 42 1 US-08-268-348A-3
300 25 80.6 42 1 US-08-268-348A-4
```

ALIGNMENTS

```
RESULT 1
US-09-747-408-4
; Sequence 4, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
```

```
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-4
```

```
Query Match 100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KVFVFA 6
Db 1 KVFVFA 6
```

RESULT 2

```
US-09-747-408-12
```

```
; Sequence 12, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-12
```

```
Query Match 100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KVFVFA 6
Db 1 KVFVFA 6
```

RESULT 3

```
US-09-248-796A-18091
; Sequence 18091, Application US/09248796A
; Patent No. 6747137
```

```
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
```

```
; CURRENT APPLICATION NUMBER: US/09/248,796A
```

```
; CURRENT FILING DATE: 1999-02-12
```

```
; PRIOR APPLICATION NUMBER: US 60/074,725
```

```
; PRIOR FILING DATE: 1998-02-13
```

```
; PRIOR APPLICATION NUMBER: US 60/096,409
```

```
; PRIOR FILING DATE: 1998-08-13
```

```
; NUMBER OF SEQ ID NOS: 28208
```

```
; SEQ ID NO 18091
```

```
; LENGTH: 1283
```

```
; TYPE: PRT
```

```
; ORGANISM: Candida albicans
```

```
US-09-248-796A-18091
```

```
Query Match 96.8%; Score 30; DB 2; Length 1283;
Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVFVFA 6
Db      259 KTFVFA 264

RESULT 4
US-09-830-230A-438
; Sequence 438, Application US/09830230A
; Patent No. 6902893
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; FILE REFERENCE: PB481US
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: PCT/US98/12718
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/057,483
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: 60/053,344
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,377
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/050,359
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 438
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-230A-438

Query Match      90.3%; Score 28; DB 2; Length 490;
Best Local Similarity 83.3%; Pred. No. 5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      23 RFVFFA 28

RESULT 5
US-08-888-998-2
; Sequence 2, Application US/08888998
; Patent No. 6124524
; GENERAL INFORMATION:
; APPLICANT: JAMES, Douglas W.
; APPLICANT: LIM, Eda
; APPLICANT: KELLER, Janis
; APPLICANT: DOONER, Hugo K.
; TITLE OF INVENTION: FAEL GENES AND THEIR USES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION NUMBER: US/08/888,998
; FILING DATE: 26-OCT-1994

QY      1 KVFVFA 6
Db      356 KFLFFA 361

Query Match      90.3%; Score 28; DB 2; Length 506;
Best Local Similarity 83.3%; Pred. No. 5.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      356 KFLFFA 361

RESULT 6
US-09-362-633-2
; Sequence 2, Application US/09362633
; Patent No. 6184355
; GENERAL INFORMATION:
; APPLICANT: JAMES, Douglas W.
; APPLICANT: LIM, Eda
; APPLICANT: KELLER, Janis
; APPLICANT: DOONER, Hugo K.
; TITLE OF INVENTION: FAEL GENES AND THEIR USES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/09/362,633
; FILING DATE:
; APPLICATION DATA:
; APPLICATION NUMBER: 08/888,998
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REFERENCE/DOCKET NUMBER: 34,774
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 506 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
```

MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..506
 OTHER INFORMATION: /note= "Amino acid sequence of PAE1
 OTHER INFORMATION: protein."
 US-09-362-633-2

Query Match 90.3%; Score 28; DB 2; Length 506;
 Best Local Similarity 83.3%; Pred. No. 5.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
 ||:||||
 Db 356 KFLFFA 361

RESULT 7
 US-09-877-476-2

Sequence 2, Application US/09877476
 Patent No. 6713664
 GENERAL INFORMATION:
 APPLICANT: Jaworski, Jan G.
 APPLICANT: Blacklock, Brenda J.
 TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
 TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
 FILE REFERENCE: 07148-108001
 CURRENT APPLICATION NUMBER: US/09/877,476
 CURRENT FILING DATE: 2001-06-08
 PRIOR FILING DATE: 2000-06-08
 PRIOR APPLICATION NUMBER: US 60/210,326
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 506
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 US-09-877-476-2

Query Match 90.3%; Score 28; DB 2; Length 506;
 Best Local Similarity 83.3%; Pred. No. 5.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
 ||:||||
 Db 356 KFLFFA 361

RESULT 8

US-09-877-476-28
 Sequence 28, Application US/09877476
 Patent No. 6713664
 GENERAL INFORMATION:
 APPLICANT: Jaworski, Jan G.
 APPLICANT: Blacklock, Brenda J.
 TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
 TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
 FILE REFERENCE: 07148-108001
 CURRENT APPLICATION NUMBER: US/09/877,476
 CURRENT FILING DATE: 2001-06-08
 PRIOR FILING DATE: 2000-06-08
 PRIOR APPLICATION NUMBER: US 60/210,326
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 28
 LENGTH: 506
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: 5' 176 amino acids from B. napus elongase KCS (SEQ
 OTHER INFORMATION: ID NO:4) and 3' 330 amino acids from A. thaliana
 OTHER INFORMATION: PAE1 (SEQ ID NO:2); designated Bn176
 US-09-877-476-28

Query Match 90.3%; Score 28; DB 2; Length 506;
 Best Local Similarity 83.3%; Pred. No. 5.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
 ||:||||
 Db 356 KFLFFA 361

RESULT 9

US-09-877-476-30
 Sequence 30, Application US/09877476
 Patent No. 6713664
 GENERAL INFORMATION:
 APPLICANT: Jaworski, Jan G.
 APPLICANT: Blacklock, Brenda J.
 TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
 TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
 FILE REFERENCE: 07148-108001
 CURRENT APPLICATION NUMBER: US/09/877,476
 CURRENT FILING DATE: 2001-06-08
 PRIOR FILING DATE: 2000-06-08
 PRIOR APPLICATION NUMBER: US 60/210,326
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 30
 LENGTH: 506
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: 5' 399 amino acids from A. thaliana PAE1 (SEQ ID
 OTHER INFORMATION: NO:2) and 3' 107 amino acids from B. napus
 OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At399
 NAME/KEY: VARIANT
 LOCATION: (0)..(0)
 OTHER INFORMATION: Xaa = Pro or Gln
 US-09-877-476-30

Query Match 90.3%; Score 28; DB 2; Length 506;
 Best Local Similarity 83.3%; Pred. No. 5.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
 ||:||||
 Db 356 KFLFFA 361

RESULT 10

US-09-877-476-36
 Sequence 36, Application US/09877476
 Patent No. 6713664
 GENERAL INFORMATION:
 APPLICANT: Jaworski, Jan G.
 APPLICANT: Blacklock, Brenda J.
 TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
 TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
 FILE REFERENCE: 07148-108001
 CURRENT APPLICATION NUMBER: US/09/877,476
 CURRENT FILING DATE: 2001-06-08
 PRIOR FILING DATE: 2000-06-08
 PRIOR APPLICATION NUMBER: US 60/210,326
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 36
 LENGTH: 506
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: 506 amino acids from A. thaliana PAE1 (SEQ ID
 OTHER INFORMATION: NO:2) having a mutation at residue 92; designated
 OTHER INFORMATION: At K92R; hypothetical
 US-09-877-476-36

```
Query Match          90.3%; Score 28; DB 2; Length 506;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
DB      356 KLFVFA 361

RESULT 11
US-09-830-230A-437
; Sequence 437, Application US/09830230A
; Patent No. 6902893
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Lyme Disease Vaccines
; FILE REFERENCE: PB481US
; CURRENT APPLICATION NUMBER: US/09/830,230A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: PCT/US98/12718
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/057,483
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: 60/053,344
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,377
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/050,359
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 437
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-230A-437

Query Match          90.3%; Score 28; DB 2; Length 508;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
DB      41 RFVFFA 46

RESULT 12
US-09-248-796A-26311
; Sequence 26311, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26311
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26311

Query Match          87.1%; Score 27; DB 2; Length 67;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
DB      84 KVFVFF 88

RESULT 13
US-09-513-999C-4859
; Sequence 4859, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4859
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-4859

Query Match          87.1%; Score 27; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFF 5
DB      32 KVFVFF 36

RESULT 14
US-09-270-767-40694
; Sequence 40694, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40694
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-40694

Query Match          87.1%; Score 27; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFF 5
DB      84 KVFVFF 88

RESULT 15
US-09-270-767-55910
; Sequence 55910, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
```


; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55910
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55910

Query Match 87.1%; Score 27; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5
Db 84 KPVFF 88

RESULT 16
US-09-823-153-4
; Sequence 4, Application US/09823153
; Patent No. 6713248
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Roberts, Susan
; APPLICANT: Pak, Roger
; APPLICANT: Lewis, Martin
; APPLICANT: Smith, David
; APPLICANT: Hendrick, Joseph
; APPLICANT: Vinitzky, Alexander
; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX
; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
; FILE REFERENCE: D0004
; CURRENT APPLICATION NUMBER: US/09/823,153
; CURRENT FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Human Beta App
US-09-823-153-4

Query Match 87.1%; Score 27; DB 2; Length 104;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
Db 21 EFVFFA 26

RESULT 17
US-09-270-767-57813
; Sequence 57813, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57813
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57813

Query Match 87.1%; Score 27; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5
Db 62 KPVFF 66

RESULT 18
US-09-902-540-10859
; Sequence 10859, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10859
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10859

Query Match 87.1%; Score 27; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5
Db 132 KPVFF 136

RESULT 19
US-09-134-001C-5445
; Sequence 5445, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5445
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5445

Query Match 87.1%; Score 27; DB 2; Length 240;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
Db 168 QVFFFA 173

```
RESULT 20
US-09-270-767-42516
; Sequence 42516, Application US/09270767
; Patent No. 6703491
; ORGANISM: Drosophila melanogaster
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42516
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42516
Query Match      87.1%; Score 27; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 KVFVF 5
Db      62 KVFVF 66

RESULT 21
US-09-248-796A-19539
; Sequence 19539, Application US/09248796A
; Patent No. 6747137
; ORGANISM: Candida albicans
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19539
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19539
Query Match      87.1%; Score 27; DB 2; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 KVFVF 5
Db      23 KVFVF 27

RESULT 22
US-09-270-767-40453
; Sequence 40453, Application US/09270767
; Patent No. 6703491
; ORGANISM: Drosophila melanogaster
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40453
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-40453
Query Match      87.1%; Score 27; DB 2; Length 340;
Best Local Similarity 66.7%; Pred. No. 5.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY      1 KVFVFA 6
Db      310 KVFVFA 315

RESULT 23
US-09-270-767-55669
; Sequence 55669, Application US/09270767
; Patent No. 6703491
; ORGANISM: Drosophila melanogaster
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55669
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55669
Query Match      87.1%; Score 27; DB 2; Length 340;
Best Local Similarity 66.7%; Pred. No. 5.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY      1 KVFVFA 6
Db      310 KVFVFA 315

RESULT 24
US-09-270-767-45548
; Sequence 45548, Application US/09270767
; Patent No. 6703491
; ORGANISM: Drosophila melanogaster
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45548
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45548
Query Match      87.1%; Score 27; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 KVFVF 5
Db      49 KVFVF 53
```

```

RESULT 25
US-09-270-767-34763
; Sequence 34763, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 34763
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-34763

Query Match      87.1%; Score 27; DB 2; Length 525;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KPVFFA 6
Db      446 KYIFFA 451

RESULT 26
US-09-270-767-49980
; Sequence 49980, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 49980
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-49980

Query Match      87.1%; Score 27; DB 2; Length 525;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KPVFFA 6
Db      446 KYIFFA 451

RESULT 27
US-08-704-711A-1
; Sequence 1, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>

```

```

; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-1

Query Match      87.1%; Score 27; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KPVFF 5
Db      375 KPVFF 379

RESULT 28
US-09-521-220-1
; Sequence 1, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>

```

```
/
/ 21-OCT-1994
/ 17-MAR-1994
/ PRIOR APPLICATION DATA:
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: 08/704,711
/ FILING DATE: 21-OCT-1994
/ APPLICATION NUMBER: DE 4438838.1
/ FILING DATE: 21-OCT-1994
/ APPLICATION NUMBER: DE 4409663.1
/ FILING DATE: 17-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: GRANADOS, Patricia D.
/ REGISTRATION NUMBER: 33,683
/ REFERENCE/DOCKET NUMBER: 26083/124
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 579 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-521-220-1

Query Match      87.1%; Score 27; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
DB      375 KVFVF 379

RESULT 29
US-08-704-711A-2
; Sequence 2, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horet
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA: DE 4438838.1
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
/
/ REFERENCE/DOCKET NUMBER: 26083/124
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 582 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-704-711A-2

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
DB      378 KVFVF 382

RESULT 30
US-08-448-489-1
; Sequence 1, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-448-489-1

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
DB      378 KVFVF 382

RESULT 31
US-09-211-704A-9
; Sequence 9, Application US/09211704A
; Patent No. 6271014
; GENERAL INFORMATION:
; APPLICANT: de Saint-Vis, Blandine Marie
; APPLICANT: Fossiez, Francois
; APPLICANT: Caux, Christophe
; APPLICANT: Lebecque, Serge J.E.
; TITLE OF INVENTION: Mammalian Proteases; Related Reagents
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
/
```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/211,704A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/005,263
; FILING DATE: 09-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: SP0781K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 582 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-211-704A-9

Query Match 87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5
Db 378 KVFVF 382

RESULT 32
US-09-521-220-2
; Sequence 2, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 582 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-521-220-2

Query Match 87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5
Db 378 KVFVF 382

RESULT 33
US-09-391-104-28
; Sequence 28, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073 US P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-28

Query Match 87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5
Db 378 KVFVF 382

RESULT 34
US-09-919-497-84
; Sequence 84, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 582
; TYPE: PRT

```
; ORGANISM: Homo sapiens
US-09-919-497-84

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
      |||||
Db      378 KVVFF 382

RESULT 35
US-09-689-730-1
; Sequence 1, Application US/09689730
; Patent No. 6825024
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/09/689,730
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US/08/448,489
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-689-730-1

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
      |||||
Db      378 KVVFF 382

RESULT 36
US-10-449-315-2
; Sequence 2, Application US/10449315
; Patent No. 6942984
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/10/449,315
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US /09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1024
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-315-2

Query Match      87.1%; Score 27; DB 2; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
      |||||

; ORGANISM: Homo sapiens
US-10-449-315-5

Query Match      87.1%; Score 27; DB 2; Length 1204;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
      |||||
Db      355 KVVFF 359

RESULT 37
US-10-449-315-5
; Sequence 5, Application US/10449315
; Patent No. 6942984
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/10/449,315
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US /09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1204
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-315-5

Query Match      87.1%; Score 27; DB 2; Length 1204;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFF 5
      |||||
Db      355 KVVFF 359

RESULT 38
US-09-270-767-37091
; Sequence 37091, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37091
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-37091

Query Match      83.9%; Score 26; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |||||
Db      16 FVFFA 20

RESULT 39
US-09-270-767-52308
; Sequence 52308, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
```

; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52308
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-52308

Query Match 83.9%; Score 26; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
| | | | |
Db 16 FVFFA 20

RESULT 40

US-09-798-635A-41
; Sequence 41, Application US/09798635A
; Patent No. 6936432
; GENERAL INFORMATION:
; APPLICANT: Gopalan, Venkat
; APPLICANT: Jovanovic, Milan
; APPLICANT: Eder, Paul S.
; APPLICANT: Giordano, Tony
; APPLICANT: Powers, Gordon D.
; APPLICANT: Xavier, K. Ashish
; TITLE OF INVENTION: No. 6936432el Bacterial RNase P Proteins and
; FILE REFERENCE: 50093/016002
; CURRENT APPLICATION NUMBER: US/09/798,635A
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/516,061
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-798-635A-41

Query Match 83.9%; Score 26; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
| | | | |
Db 39 FVFFA 43

RESULT 41

US-10-125-258-44
; Sequence 44, Application US/10125258
; Patent No. 6891085
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Presnail, James K.
; APPLICANT: Weaver, Janine L.
; APPLICANT: Wong, James F. H.
; TITLE OF INVENTION: Antimicrobial Polypeptides and Their
; FILE REFERENCE: 35718/246215
; CURRENT APPLICATION NUMBER: US/10/125,258
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/285,355
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 44
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Ostrinia nubilalis
US-10-125-258-44

Query Match 83.9%; Score 26; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
| | | | |
Db 8 FVFFA 12

RESULT 42

US-09-583-110-4885
; Sequence 4885, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4885
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4885

Query Match 83.9%; Score 26; DB 2; Length 61;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5
| | | | |
Db 44 KFVF 48

RESULT 43

US-10-125-258-43
; Sequence 43, Application US/10125258
; Patent No. 6891085
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Presnail, James K.
; APPLICANT: Weaver, Janine L.
; APPLICANT: Wong, James F. H.
; TITLE OF INVENTION: Antimicrobial Polypeptides and Their
; FILE REFERENCE: 35718/246215
; CURRENT APPLICATION NUMBER: US/10/125,258
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/285,355
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Ostrinia nubilalis

US-10-125-258-43

Query Match 83.9%; Score 26; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||||
Db 8 FVFFA 12

RESULT 44

US-09-270-767-60733
; Sequence 60733, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60733
; LENGTH: 84
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-60733

Query Match 83.9%; Score 26; DB 2; Length 84;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
|||:
Db 48 KFIFF 52

RESULT 45

US-09-621-976-6739
; Sequence 6739, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6739
; LENGTH: 104
; TYPE: PRT
; ORGANISM: *Homo sapiens*
US-09-621-976-6739

Query Match 83.9%; Score 26; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||||
Db 31 FVFFA 35

RESULT 46

US-09-205-258-303
; Sequence 303, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.

; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963


```
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 303
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-303

Query Match      83.9%; Score 26; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFPA 6
DB      79 FVFPA 83

RESULT 47
US-10-004-860-303
; Sequence 303, Application US/10004860
; Patent No. 6914047
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 303
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-004-860-303

Query Match      83.9%; Score 26; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFPA 6
DB      79 FVFPA 83

RESULT 48
US-09-627-376-17
; Sequence 17, Application US/09627376
; Patent No. 6342385
; GENERAL INFORMATION:
; APPLICANT: Qi, Fengxia
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
; FILE REFERENCE: UAB-17402/22
; CURRENT APPLICATION NUMBER: US/09/627,376
```

```
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-627-376-17

Query Match      83.9%; Score 26; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFPA 6
DB      39 FVFPA 43

RESULT 49
US-10-047-676B-17
; Sequence 17, Application US/10047676B
; Patent No. 6699970
; GENERAL INFORMATION:
; APPLICANT: Qi, Fengxia
; APPLICANT: Caufield, Page W.
; APPLICANT: Chen, Ping
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
; FILE REFERENCE: UAB-17403/22
; CURRENT APPLICATION NUMBER: US/10/047,676B
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 09/627,376
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-047-676B-17

Query Match      83.9%; Score 26; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFPA 6
DB      39 FVFPA 43

RESULT 50
US-09-270-767-45241
; Sequence 45241, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45241
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45241

Query Match      83.9%; Score 26; DB 2; Length 156;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KFVFP 5
DB      11
```

```

Db      120 KPIFF 124

RESULT 51
US-09-270-767-35390
; Sequence 35390, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35390
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35390

Query Match      83.9%; Score 26; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFFA 6
      |||||
Db      122 FVFFFA 126

RESULT 52
US-09-270-767-50607
; Sequence 50607, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50607
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50607

Query Match      83.9%; Score 26; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFFA 6
      |||||
Db      122 FVFFFA 126

RESULT 53
US-09-251-645-4
; Sequence 4, Application US/09251645
; Patent No. 6281413
; GENERAL INFORMATION:
; APPLICANT: Kramer, Vance C.
; APPLICANT: Morgan, Michael K.
; APPLICANT: Anderson, Arne R.
; APPLICANT: Hart, Hope
; APPLICANT: Warren, Gregory W.
; APPLICANT: Dunn, Martha
; APPLICANT: Chen, Jeng S.

; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; TITLE OF INVENTION: AND NUCLEIC ACID SEQUENCES CODING THEREFOR
; FILE REFERENCE: CGC1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
US-09-251-645-4

Query Match      83.9%; Score 26; DB 2; Length 186;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFFA 6
      :|||
Db      134 QFIFFA 139

RESULT 54
US-09-270-767-33463
; Sequence 33463, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33463
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33463

Query Match      83.9%; Score 26; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFFA 6
      |||||
Db      80 FVFFFA 84

RESULT 55
US-09-270-767-48680
; Sequence 48680, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48680
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48680

Query Match      83.9%; Score 26; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFFA 6
      |||||
Db      80 FVFFFA 84

RESULT 56
US-09-270-767-48680
; Sequence 48680, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48680
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48680

Query Match      83.9%; Score 26; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFFA 6
      |||||

```

Db 80 FVFFA 84

RESULT 56

US-09-270-767-38186
; Sequence 38186, Application US/09270767
; Patent No. 6703491

GENERAL INFORMATION:

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 38186
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Drosophila melanogaster

FEATURE:

; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-38186

Query Match 83.9%; Score 26; DB 2; Length 249;

Best Local Similarity 80.0%; Pred. No. 6.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

Qy 1 KVFVF 5

Db 196 KFIFF 200

RESULT 57

US-09-270-767-53403
; Sequence 53403, Application US/09270767
; Patent No. 6703491

GENERAL INFORMATION:

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 53403
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Drosophila melanogaster

FEATURE:

; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-53403

Query Match 83.9%; Score 26; DB 2; Length 249;

Best Local Similarity 80.0%; Pred. No. 6.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

Qy 1 KVFVF 5

Db 196 KFIFF 200

RESULT 58

US-09-248-796A-27128
; Sequence 27128, Application US/09248796A
; Patent No. 6747137

GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 27128
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Candida albicans

US-09-248-796A-27128

Query Match 83.9%; Score 26; DB 2; Length 249;
Best Local Similarity 80.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5

Db 108 KFIFF 112

RESULT 59

US-09-830-910-2
; Sequence 2, Application US/09830910
; Patent No. 6482807

GENERAL INFORMATION:

; APPLICANT: Van Der Ley, Peter Andre
; APPLICANT: Hamstra, Hendrik Jan
; APPLICANT: Steeghs, Liana Juliana Josephine Margriet
; TITLE OF INVENTION: LPS with reduced toxicity from genetically modified
; FILE REFERENCE: Gram-negative bacteria
; FILE REFERENCE: LPS with reduced toxicity
; CURRENT APPLICATION NUMBER: US/09/830,910
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: PCT/NL98/00633
; PRIOR FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Neisseria meningitidis

US-09-830-910-2

Query Match 83.9%; Score 26; DB 2; Length 310;
Best Local Similarity 80.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5

Db 6 KFIFF 10

RESULT 60

US-09-248-796A-15301
; Sequence 15301, Application US/09248796A
; Patent No. 6747137

GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15301
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Candida albicans

FEATURE:

; NAME/KEY: UNSURE

```
; LOCATION: (4),(5)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-15301

Query Match      83.9%; Score 26; DB 2; Length 328;
Best Local Similarity 66.7%; Pred. No. 8.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|:|
Db 6 QFIFFA 11

RESULT 61
US-09-270-767-41366
; Sequence 41366, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41366
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41366

Query Match      83.9%; Score 26; DB 2; Length 394;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|:|
Db 267 KFWVFA 272

RESULT 62
US-09-270-767-56582
; Sequence 56582, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56582
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56582

Query Match      83.9%; Score 26; DB 2; Length 394;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|:|
Db 267 KFWVFA 272

RESULT 63
US-09-252-991A-25289
; Sequence 25289, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25289
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25289

Query Match      83.9%; Score 26; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFFA 6
   :|:|
Db 309 FVFFFA 313

RESULT 64
US-09-902-540-11308
; Sequence 11308, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11308
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11308

Query Match      83.9%; Score 26; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFFA 6
   :|:|
Db 185 FVFFFA 189

RESULT 65
US-09-602-787A-424
; Sequence 424, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kruger, Burkhard
; APPLICANT: Schuder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
```

```

; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03

```

```

; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 424
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-787A-424

Query Match      83.9%; Score 26; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVEFFA 6
      |||||
Db      120 FVEFFA 124

RESULT 66
US-09-489-039A-8958
; Sequence 8958, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8958
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8958

Query Match      83.9%; Score 26; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVEFFA 6
      |||||
Db      36 FVEFFA 40

RESULT 67
US-09-252-991A-17185
; Sequence 17185, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196,136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17185
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17185

Query Match      83.9%; Score 26; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVEFFA 6
      |||||

```

```
Db          48 FVFFA 52

RESULT 68
US-09-489-039A-8303
; Sequence 8303, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8303
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; NAME/KEY: UNSURE
; LOCATION: (133)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-489-039A-8303

Query Match      83.9%; Score 26; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |||||
Db      266 FVFFA 270

RESULT 69
US-09-252-991A-28992
; Sequence 28992, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28992
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28992

Query Match      83.9%; Score 26; DB 2; Length 493;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
      ||:|
Db      2 KRIFF 6

RESULT 70
US-09-540-236-2206
; Sequence 2206, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2206
; LENGTH: 557
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-2206

Query Match      83.9%; Score 26; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |||||
Db      355 FVFFA 359

RESULT 71
US-09-489-039A-11884
; Sequence 11884, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11884
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11884

Query Match      83.9%; Score 26; DB 2; Length 573;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |||||
Db      511 FVFFA 515

RESULT 72
US-09-252-991A-22560
; Sequence 22560, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22560
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22560

Query Match      83.9%; Score 26; DB 2; Length 597;
```

Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 2 FVFFA 6
|
|
|
|
Db 90 FVFFA 94

RESULT 73

US-09-540-540-10275
; Sequence 10275, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10275
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10275

Query Match 83.9%; Score 26; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
|
|
|
|
Db 185 FVFFA 189

RESULT 74

US-09-540-236-2074
; Sequence 2074, Application US/09540236
; Patent No. 6673310
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2074
; LENGTH: 892
; TYPE: PRT
; ORGANISM: M.catarthalis
US-09-540-236-2074

Query Match 83.9%; Score 26; DB 2; Length 892;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
|
|
|
|
Db 658 FVFFA 662

RESULT 75

US-08-612-785B-9
; Sequence 9, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid

; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-9

Query Match 80.6%; Score 25; DB 1; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFFA 6
|
|
|
|
Db 1 KLVFFA 6

Search completed: December 29, 2005, 17:52:34
Job time : 22.1323 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds
(without alignments)
32.238 Million cell updates/sec

Title: US-10-009-122-4

Perfect score: 31

Sequence: 1 KVFVFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	6	4	AB48477 Antifibri
2	31	100.0	6	4	AB48485 Antifibri
3	31	100.0	6	4	AB82625 All-D pep
4	31	100.0	6	4	AB82633 All-D pep
5	31	100.0	6	5	AU96813 Amyloid t
6	31	100.0	6	5	AU96821 Amyloid t
7	31	100.0	6	5	AAU11659 Peptide #
8	31	100.0	6	5	AAU11651 Peptide #
9	31	100.0	6	6	AAE35447 Abeta pep
10	31	100.0	6	6	AAE35440 Abeta pep
11	31	100.0	6	8	ADQ37264 Vaccine a
12	31	100.0	6	8	ADQ37316 Antifibri
13	31	100.0	6	8	ADQ37324 Antifibri
14	31	100.0	6	8	ADQ37272 Vaccine a
15	31	100.0	6	9	ADY37931 Amyloid-t
16	31	100.0	6	9	ADY37923 Amyloid-t
17	31	100.0	336	7	ABM89186 Rice abio
18	30	96.8	202	5	ADK35620 Novel hum
19	28	90.3	75	4	ABM17989 Human ner
20	28	90.3	452	8	ADN23626 Bacterial
21	28	90.3	485	8	ADN46740 Thermococ
22	28	90.3	490	2	AA119993 B. burgdo
23	28	90.3	506	2	AAE95594 Arabidops
24	28	90.3	506	5	AAE17850 Alternati

25	28	90.3	506	5	AAE17622	Aae17622 A. thalia
26	28	90.3	506	5	AAE17625	Aae17625 Arabidops
27	28	90.3	506	5	AAE17621	Aae17621 Brassica
28	28	90.3	506	5	AAE17608	Aae17608 Arabidops
29	28	90.3	506	2	AEA37517	Aea37517 Arabidops
30	28	90.3	508	2	AAV19992	Aay19992 B. burgdo
31	28	90.3	508	6	ABU19128	Abu19128 Protein e
32	28	90.3	571	6	ABU24005	Abu24005 Protein e
33	28	90.3	1089	8	ADN19501	Adn19501 Bacterial
34	27	87.1	52	3	AAG61668	Agg61668 Arabidops
35	27	87.1	57	8	ADX67964	Adx67964 Plant ful
36	27	87.1	62	4	ABB03189	Abb03189 Human mus
37	27	87.1	62	6	ABU12483	Abu12483 Novel hum
38	27	87.1	62	8	ADJ28509	Adj28509 Human mus
39	27	87.1	82	3	AAG00778	Agg00778 Human sec
40	27	87.1	82	4	ABG13797	Abg13797 Novel hum
41	27	87.1	91	4	AAO12276	Aao12276 Human pol
42	27	87.1	99	4	AAO10108	Aao10108 Human pol
43	27	87.1	104	4	AAE12897	Aae12897 Human rec
44	27	87.1	114	4	ABP33728	Abp33728 Human pro
45	27	87.1	115	5	ABP33134	Abp33134 Human iso
46	27	87.1	126	4	AAO02898	Aao02898 Human pol
47	27	87.1	132	4	AAO00490	Aao00490 Human pol
48	27	87.1	144	4	ABG26562	Abg26562 Novel hum
49	27	87.1	146	4	AAO07503	Aao07503 Human pol
50	27	87.1	148	8	ADQ66558	Adq66558 Novel hum
51	27	87.1	173	4	AAU27710	Aau27710 Human ful
52	27	87.1	173	5	AAU77842	Aau77842 Oestrogen
53	27	87.1	173	3	ADJ69976	Adj69976 Human hea
54	27	87.1	184	3	AAG47987	Aag47987 Arabidops
55	27	87.1	186	9	ABP38594	Abp38594 L. pneumo
56	27	87.1	189	5	AAU79255	Aau79255 Human mem
57	27	87.1	189	5	AAU79257	Aau79257 Rat membr
58	27	87.1	189	5	AAU79258	Aau79258 Rabbit me
59	27	87.1	189	5	AAU79256	Aau79256 Murine me
60	27	87.1	197	7	ABM73888	Abm73888 DNA clone
61	27	87.1	206	4	ABP52559	Abp52559 Escherich
62	27	87.1	221	4	ABG22983	Abg22983 Novel hum
63	27	87.1	221	4	ABG06994	Abg06994 Novel hum
64	27	87.1	227	8	ADH45453	Adh45453 Human mol
65	27	87.1	238	9	ABM91660	Abm91660 M. xanthu
66	27	87.1	240	5	ABP40600	Abp40600 Staphyloc
67	27	87.1	240	8	ADSO7805	Adso7805 Staphyloc
68	27	87.1	248	3	AAO10914	Aao10914 Arabidops
69	27	87.1	252	3	AAO10913	Aao10913 Arabidops
70	27	87.1	270	3	AAO10912	Aao10912 Arabidops
71	27	87.1	297	5	AAU80872	Aau80872 Human CLA
72	27	87.1	297	5	ABU81731	Abu81731 Human cas
73	27	87.1	312	8	ADP47907	Adp47907 Human CAT
74	27	87.1	313	3	AAO33404	Aao33404 Zea may
75	27	87.1	335	8	ADT58396	Adt58396 Plant pol
76	27	87.1	344	3	AAO28863	Aao28863 Arabidops
77	27	87.1	347	8	ADX78439	Adx78439 Plant ful
78	27	87.1	350	9	ADY15182	Ady15182 PRO polyp
79	27	87.1	350	9	ADY15180	Ady15180 PRO polyp
80	27	87.1	351	5	AAU74357	Aau74357 Human cyt
81	27	87.1	351	8	ABM80293	Abm80293 Tumour-as
82	27	87.1	393	8	ADT55938	Adt55938 Plant pol
83	27	87.1	401	5	ABP52840	Abp52840 Anopheles
84	27	87.1	401	7	ABR84483	AbR84483 Mosquito
85	27	87.1	409	8	ADN74449	Adn74449 Thale cre
86	27	87.1	422	8	ADT58936	Adt58936 Plant pol
87	27	87.1	436	5	ABP91404	Abp91404 Herbicida
88	27	87.1	454	6	ADB08942	AdB08942 Alloiooc
89	27	87.1	478	6	ABP73100	Abp73100 Amino aci
90	27	87.1	478	7	ADDI5262	AdDI5262 African m
91	27	87.1	498	6	ABP73103	Abp73103 Amino aci
92	27	87.1	504	7	ADC60748	Adc60748 Termitom
93	27	87.1	549	8	ADP29329	Adp29329 Human sec
94	27	87.1	579	2	AAE86406	Aae86406 Human mat
95	27	87.1	581	6	ABU37981	Abu37981 Protein e
96	27	87.1	581	9	ABP94410	Abp94410 Human MTL
97	27	87.1	582	2	AAE86407	Aae86407 Human mat

98	27	87.1	582	2	AAR75648	Aar75648 Human pla	171	26	83.9	223	8	AD75401	Ade75401 Goat alph
99	27	87.1	582	2	AAM52134	Aaw52134 Rabbit me	172	26	83.9	243	8	ADN24282	Adn24282 Bacterial
100	27	87.1	582	4	AAB84616	Aab84616 Amino aci	173	26	83.9	289	3	AAy74724	Aay74724 Neisseria
101	27	87.1	582	4	AAE10423	Aae10423 Human mat	174	26	83.9	289	3	AAy74722	Aay74722 Neisseria
102	27	87.1	582	5	AAU84294	Aau84294 Human end	175	26	83.9	289	3	AAy74723	Aay74723 Neisseria
103	27	87.1	582	5	AAE21037	Aae21037 Human mem	176	26	83.9	291	4	AAAB60656	Aab60656 N. mening
104	27	87.1	582	5	AAM50865	Aam50865 Matrix me	177	26	83.9	291	5	AAU85401	Aau85401 Neisseria
105	27	87.1	582	7	ADC15498	Adc15498 Human bas	178	26	83.9	293	3	AAy75633	Aay75633 Neisseria
106	27	87.1	582	7	AD641179	Ad641179 Human Pro	179	26	83.9	293	3	AAy75633	Aay75633 Neisseria
107	27	87.1	582	7	AD641177	Ad641177 Rat Prote	180	26	83.9	293	3	AAy75337	Aay75337 Neisseria
108	27	87.1	582	7	ADF13708	Adf13708 Tumour-As	181	26	83.9	293	3	AAy75338	Aay75338 Neisseria
109	27	87.1	582	7	ADN95889	Adn95889 Human BEC	182	26	83.9	293	8	ADR31670	Adr31670 N. mening
110	27	87.1	582	8	ADN07703	Adn07703 Human mat	183	26	83.9	295	6	ABU37645	Abu37645 Protein e
111	27	87.1	582	8	ABM81541	Abm81541 Tumour-as	184	26	83.9	299	6	ABP77830	Abp77830 N. gonorr
112	27	87.1	582	8	ADP23426	Adp23426 PRO polyP	185	26	83.9	317	7	ABP78259	Abp78259 N. gonorr
113	27	87.1	582	9	AE943378	Aeb943378 Human MTL	186	26	83.9	321	7	ADG90764	Adg90764 Hepatic s
114	27	87.1	582	6	ABP79179	Abp79179 N. gonorr	187	26	83.9	321	8	ADP04189	Adp04189 Human col
115	27	87.1	582	6	ABU37131	Abu37131 Protein e	188	26	83.9	322	4	AAU30371	Aau30371 Novel hum
116	27	87.1	582	8	AD322906	Ad322906 Bacterial	189	26	83.9	330	4	AAU49675	Aau49675 Propionib
117	27	87.1	738	4	AAAG67526	Aag67526 Amino aci	190	26	83.9	330	6	ABM46194	Abm46194 Propionib
118	27	87.1	833	8	ADM98835	Adm98835 HMG-CoA r	191	26	83.9	339	4	AAAG72670	Aag72670 Murine OR
119	27	87.1	841	4	AAW23595	Aam23595 Murine BS	192	26	83.9	344	7	ADE40136	Ade40136 Human NOV
120	27	87.1	856	8	ADM98920	Adm98920 HMG-CoA r	193	26	83.9	346	7	ADE62833	Ade62833 Rat Prote
121	27	87.1	856	8	ADM98784	Adm98784 HMG-CoA r	194	26	83.9	369	3	AAy75249	Aay75249 Neisseria
122	27	87.1	856	8	ADM98820	Adm98820 HMG-CoA r	195	26	83.9	371	3	AAy75248	Aay75248 Neisseria
123	27	87.1	1024	4	AAU02880	Aau02880 Human cas	196	26	83.9	371	3	AAy75247	Aay75247 Neisseria
124	27	87.1	1024	5	ABU810861	Abu810861 Human CLA	197	26	83.9	380	8	ADB12503	Adb12503 Allolococ
125	27	87.1	1024	5	ABU81720	Abu81720 Human cas	198	26	83.9	390	8	ADN23888	Adn23888 Bacterial
126	27	87.1	1024	6	ABG72211	Abg72211 Human cas	199	26	83.9	393	8	AUS24065	Aus24065 Bacterial
127	27	87.1	1024	6	ABG99643	Abg99643 Amino aci	200	26	83.9	395	6	ABP77710	Abp77710 N. gonorr
128	27	87.1	1070	4	AAAG67527	Aag67527 Amino aci	201	26	83.9	397	5	ABB49314	Abb49314 Listeria
129	27	87.1	1204	4	AAU02881	Aau02881 Human cas	202	26	83.9	400	8	ADT58012	Adt58012 Plant pol
130	27	87.1	1204	6	ABG72212	Abg72212 Protein e	203	26	83.9	407	7	ADC87413	Adc87413 Human GPC
131	27	87.1	2697	6	AAO26550	Aao26550 Cochliobo	204	26	83.9	402	7	ABO76543	Abp76543 Pseudomon
132	26	83.9	45	6	ABU02448	Abu02448 S. pneumo	205	26	83.9	404	8	AUS26059	Aus26059 Bacterial
133	26	83.9	53	8	ADX80309	Adx80309 Plant ful	206	26	83.9	405	6	ABM67471	Abm67471 Photorhab
134	26	83.9	60	8	ABP55940	Abp55940 Oestrinia	207	26	83.9	414	8	ABU20391	Abu20391 Protein e
135	26	83.9	61	8	ADK48370	Adk48370 Streptoco	208	26	83.9	414	8	ADS22533	Ads22533 Bacterial
136	26	83.9	62	1	AAAP94262	Aap94262 Antibacte	209	26	83.9	414	3	ABM92109	Abm92109 M. xanthu
137	26	83.9	63	1	AAO13635	Aao13635 Human pol	210	26	83.9	416	3	AAAG41542	Aag41542 Arabidops
138	26	83.9	65	6	ABP55939	Abp55939 Oestrinia	211	26	83.9	418	6	ABP79629	Abp79629 N. gonorr
139	26	83.9	65	6	ABP55939	Abp55939 Oestrinia	212	26	83.9	426	4	AAAB76721	Aab76721 Corynebac
140	26	83.9	69	9	ABE41581	Aeb41581 L. pneumo	213	26	83.9	426	4	AAAG92282	Aag92282 C. glutam
141	26	83.9	72	4	ABG21901	Abg21901 Novel hum	214	26	83.9	426	7	ADL65521	Adl65521 C. glutam
142	26	83.9	72	5	ADK36142	Adk36142 Novel hum	215	26	83.9	431	7	ADD69592	Add69592 Human REM
143	26	83.9	72	9	AEA20997	Aea20997 Novel hum	216	26	83.9	437	6	ADB11164	Adb11164 Allolococ
144	26	83.9	74	3	AAAG10726	Aag10726 Arabidops	217	26	83.9	437	7	ABO62441	Abp62441 Klebsiell
145	26	83.9	84	3	AAAG61260	Aag61260 Arabidops	218	26	83.9	438	6	ADA48730	Ada48730 Rice prot
146	26	83.9	84	3	AAAG57207	Aag57207 Arabidops	219	26	83.9	444	8	ADN27113	Adn27113 Bacterial
147	26	83.9	87	9	ABE38299	Aeb38299 L. pneumo	220	26	83.9	446	7	ABO68439	Abp68439 Pseudomon
148	26	83.9	90	4	AAU31916	Aau31916 Novel hum	221	26	83.9	448	8	ADG25774	Adg25774 Mycobacte
149	26	83.9	91	3	AAAG57206	Aag57206 Arabidops	222	26	83.9	453	7	ABO61786	Abp61786 Klebsiell
150	26	83.9	93	4	AAW92337	Aam92337 Human dfg	223	26	83.9	459	8	AUS29238	Aus29238 Bacterial
151	26	83.9	96	3	AAAG57205	Aag57205 Arabidops	224	26	83.9	479	3	AAAG41541	Aag41541 Arabidops
152	26	83.9	96	3	AAAG61259	Aag61259 Arabidops	225	26	83.9	483	8	ADN22834	Adn22834 Bacterial
153	26	83.9	101	8	ADX94447	Adx94447 Plant ful	226	26	83.9	483	8	ADN22833	Adn22833 Bacterial
154	26	83.9	111	4	ABBS0355	Abbs0355 Human sec	227	26	83.9	493	7	ABO80246	Abp80246 Pseudomon
155	26	83.9	111	7	ABO44612	Abp44612 Novel hum	228	26	83.9	504	4	ABE64964	Abp64964 Drosophill
156	26	83.9	111	7	ABO26692	Abp26692 Human pro	229	26	83.9	510	8	ADM67214	Adm67214 Murine ad
157	26	83.9	115	8	ADP84584	Adp84584 Human bre	230	26	83.9	511	6	ABM68291	Abm68291 Photorhab
158	26	83.9	116	6	ABP71848	Abp71848 Human Pur	231	26	83.9	512	3	AAAG41540	Aag41540 Arabidops
159	26	83.9	118	5	ABB09650	Abb09650 Amino aci	232	26	83.9	518	5	ABP74027	Abp74027 Candida a
160	26	83.9	118	6	ABG72548	Abg72548 Streptoco	233	26	83.9	526	8	ADN21271	Adn21271 Bacterial
161	26	83.9	118	8	ADU80825	Adu80825 Orfz, SEQ	234	26	83.9	540	7	ABM86731	Abm86731 Rice abio
162	26	83.9	137	4	AAO05457	Aao05457 Human pol	235	26	83.9	548	6	ABU35322	Abu35322 Protein e
163	26	83.9	138	4	AAO08691	Aao08691 Human pol	236	26	83.9	557	7	ADL04520	Adl04520 M. catarr
164	26	83.9	186	2	AAAY33725	Aay33725 Photorhab	237	26	83.9	573	8	ABO65367	Abp65367 Klebsiell
165	26	83.9	187	6	ABM69853	Abm69853 Photorhab	238	26	83.9	581	4	ABB63013	Abb63013 Drosophill
166	26	83.9	188	5	ABBS4792	Abbs4792 Lactococc	239	26	83.9	597	7	ABO73814	Abp73814 Pseudomon
167	26	83.9	191	4	AAAG92339	Aag92339 C. glutam	240	26	83.9	618	4	ABG226117	Abg226117 Novel hum
168	26	83.9	218	5	ABBS5107	Abbs5107 Lactococc	241	26	83.9	641	4	ABG225497	Abg225497 Propionib
169	26	83.9	220	6	ABP78312	Abp78312 N. gonorr	242	26	83.9	673	6	ABM65701	Abm65701 Propionib
170	26	83.9	223	5	AAE17475	Aae17475 Alpha-S2	243	26	83.9	690	8	ADY05578	Ady05578 Plant ful

244	26	83.9	717	2	AAW20827	Aaw20827 H. pylori
245	26	83.9	745	9	ABM91076	ABm91076 M. xanthu
246	26	83.9	749	8	ADS43929	AdS43929 Bacterial
247	26	83.9	754	4	ABB65665	AbB65665 Drosophil
248	26	83.9	854	7	ABM86804	ABm86804 Rice abio
249	26	83.9	860	4	ABB64834	AbB64834 Drosophil
250	26	83.9	888	7	ABU35124	ABu35124 Protein e
251	26	83.9	890	8	ABM88494	ABm88494 Rice abio
252	26	83.9	891	4	ABB66627	AbB66627 Drosophil
253	26	83.9	892	8	ADL04388	ADl04388 M. catarr
254	26	83.9	919	9	ADZ75752	AdZ75752 Xanthomon
255	26	83.9	931	8	ADS34925	AdS34925 Human aut
256	26	83.9	931	8	ADS34926	AdS34926 Human aut
257	26	83.9	931	8	ADS34924	AdS34924 Human aut
258	26	83.9	936	8	ADR66427	AdR66427 Human pro
259	26	83.9	936	8	ADR66427	AdR66427 Human pro
260	26	83.9	936	8	ADR66085	AdR66085 Human pro
261	26	83.9	1082	6	ABU21740	ABu21740 Protein e
262	26	83.9	1772	8	ADR12606	AdR12606 Gene vacc
263	25	80.6	6	2	AAW02314	AAw02314 Beta-amyl
264	25	80.6	6	2	AAW89378	AAw89378 Beta-amyl
265	25	80.6	6	4	AAW82631	AAw82631 All-D pep
266	25	80.6	6	4	AAW82632	AAw82632 All-D pep
267	25	80.6	6	4	AAW82633	AAw82633 All-D pep
268	25	80.6	6	4	AAW82634	AAw82634 All-D pep
269	25	80.6	6	4	AAW82635	AAw82635 All-D pep
270	25	80.6	6	4	AAW82636	AAw82636 All-D pep
271	25	80.6	6	4	AAW82637	AAw82637 All-D pep
272	25	80.6	6	5	ABG71009	ABg71009 Long form
273	25	80.6	6	5	ABM05157	ABm05157 Beta amyl
274	25	80.6	6	5	AAU96819	AAu96819 Amyloid t
275	25	80.6	6	5	AAU96820	AAu96820 Amyloid t
276	25	80.6	6	5	AAU96811	AAu96811 Amyloid t
277	25	80.6	6	5	ABM83305	ABm83305 Amyloid-b
278	25	80.6	6	5	AAU11657	AAu11657 Peptide #
279	25	80.6	6	5	AAU11658	AAu11658 Peptide #
280	25	80.6	6	5	AAU11648	AAu11648 Peptide #
281	25	80.6	6	5	AAU11650	AAu11650 Peptide #
282	25	80.6	6	6	AAE35446	AAe35446 Abeta pep
283	25	80.6	6	6	AAE35438	AAe35438 Abeta pep
284	25	80.6	6	6	AAE35445	AAe35445 Abeta pep
285	25	80.6	6	6	AAE35434	AAe35434 Abeta pep
286	25	80.6	6	8	ADJ64060	ADj64060 Human bet
287	25	80.6	6	8	ADQ37271	ADq37271 Vaccine a
288	25	80.6	6	8	ADQ37322	ADq37322 Antifibri
289	25	80.6	6	8	ADQ37315	ADq37315 Antifibri
290	25	80.6	6	8	ADQ37368	ADq37368 Beta-amyl
291	25	80.6	6	8	ADQ37270	ADq37270 Vaccine a
292	25	80.6	6	8	ADQ37313	ADq37313 Antifibri
293	25	80.6	6	8	ADQ37269	ADq37269 Vaccine a
294	25	80.6	6	8	ADQ37292	ADq37292 Vaccine a
295	25	80.6	6	8	ADQ37258	ADq37258 Vaccine a
296	25	80.6	6	8	ADQ37262	ADq37262 Vaccine a
297	25	80.6	6	8	ADQ37353	ADq37353 Beta-amyl
298	25	80.6	6	8	ADQ37323	ADq37323 Antifibri
299	25	80.6	6	9	ADY37930	ADy37930 Amyloid-t
300	25	80.6	6	9	ADY37921	ADy37921 Amyloid-t

ALIGNMENTS

RESULT 1
 ID AAB48477 standard; peptide; 6 AA.
 XX
 AC AAB48477;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Antifibrillogenic peptide #4.
 XX
 KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;

KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX Homo sapiens.
 XX WO200068263-A2.
 XX 16-NOV-2000.
 PD 04-MAY-2000; 2000WO-CA000515.
 XX 05-MAY-1999; 99US-0132592P.
 PR (NEUR-) NEUROCHEM INC.
 PA Chalifour R, Gervais F, Gupta A;
 PI WPI; 2001-031852/04.
 DR Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 PS Claim 7; Page 25; 46pp; English.
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 CC
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVFVFFA 6
 Db 1 KVFVFFA 6
 RESULT 2
 ID AAB48485 standard; peptide; 6 AA.
 XX
 AC AAB48485;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Antifibrillogenic peptide #12.
 XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 6 /note= "C-terminal amide"
 FT
 XX WO200068263-A2.
 XX 16-NOV-2000.
 PD 04-MAY-2000; 2000WO-CA000515.
 XX 05-MAY-1999; 99US-0132592P.
 PR (NEUR-) NEUROCHEM INC.
 PA

XX PI Chalifour R, Gervais F, Gupta A;
 XX DR WPI; 2001-031852/04.
 XX PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 XX PS Claim 7; Page 25; 46pp; English.
 XX CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 Db 1 KVFVFA 6
 RESULT 3
 AAB82625
 ID AAB82625 standard; peptide; 6 AA.
 AC AAB82625;
 XX DT 02-OCT-2001 (first entry)
 XX DE All-D peptide used in Alzheimer's disease vaccine.
 XX KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "all D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT WO200139796-A2.
 XX PN 07-JUN-2001.
 XX PD 29-NOV-2000; 2000WO-CA001413.
 XX PF 29-NOV-1999; 99US-0168594P.
 XX PR 28-NOV-2000; 2000US-00724842.
 XX PA (NEUR-) NEUROCHEM INC.
 XX PI Chalifour R, Hebert L, Kong X, Gervais F;
 XX DR WPI; 2001-441458/47.
 XX PT Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.
 XX PS Disclosure; Page 11; 31pp; English.
 XX CC The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and

CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 Db 1 KVFVFA 6
 RESULT 4
 AAB82633
 ID AAB82633 standard; peptide; 6 AA.
 AC AAB82633;
 XX DT 02-OCT-2001 (first entry)
 XX DE All-D peptide used in Alzheimer's disease vaccine.
 XX KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "all D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT WO200139796-A2.
 XX PN 07-JUN-2001.
 XX PD 29-NOV-2000; 2000WO-CA001413.
 XX PF 29-NOV-1999; 99US-0168594P.
 XX PR 28-NOV-2000; 2000US-00724842.
 XX PA (NEUR-) NEUROCHEM INC.
 XX PI Chalifour R, Hebert L, Kong X, Gervais F;
 XX DR WPI; 2001-441458/47.
 XX PT Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,

PT which elicits production of antibodies to prevent fibrillogenesis and
 FT associated cellular toxicity.

XX Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use in
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 31; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
 |||||
 Db 1 KPVFFA 6

RESULT 5
 AAU96813
 ID AAU96813 standard; peptide; 6 AA.

XX

AC AAU96813;

XX

DT 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #3.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..6 /note= "Preferably D-form residue"

XX WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX

PR 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais P, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 PT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A t-(A 1 n k) z-A 1 a b (I) where z = 0 - 1;
 CC A t = an amyloid targeting moiety; A 1 n k = a linker moiety; and A 1 a b
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (I) to the patient, and ultrasound imaging (I) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (1), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 31; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
 |||||
 Db 1 KPVFFA 6

RESULT 6

AAU96821
 ID AAU96821 standard; peptide; 6 AA.

XX

AC AAU96821;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #11.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..6

FT Modified-site 6 /note= "Preferably D-form residue"
 FT 6 /note= "Ala is amidated"
 XX WO200207781-A2.
 PN 31-JAN-2002.
 XX 25-JUL-2001; 2001WO-CA001071.
 XX 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.
 XX (NEUR-) NEUROCHEM INC.
 XX Gervais P, Kong X, Chalifour R, Migneault D;
 XX WPI; 2002-371447/40.
 XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 FT plaques and/or for the treatment of amyloidosis disorders.
 XX Claim 49; Page 21; 57pp; English.
 XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A-t-(A-l)n-k-z-A-l-a-b (1) where z = 0 - 1;
 CC A-t = an amyloid targeting moiety; A-l-n-k = a linker moiety; and A-l-a-b
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (1) to the patient, and ultrasound imaging (1) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (1), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementias), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 31; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 DB 1 KVFVFA 6
 RESULT 7
 AAU11659
 ID AAU11659 standard; peptide; 6 AA.
 XX AC AAU11659;
 XX 09-APR-2002 (first entry)
 DE Peptide #12, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
 XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX Synthetic.
 OS Key Location/Qualifiers
 XX Modified-site 6 /note= "C-terminal amide"
 FT FT
 XX WO200185093-A2.
 XX 15-NOV-2001.
 XX 22-DEC-2000; 2000WO-IB002078.
 XX 23-DEC-1999; 99US-0171877P.
 XX (NEUR-) NEUROCHEM INC.
 XX Green AM, Gervais P;
 XX WPI; 2002-075222/10.
 XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 FT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 FT inhibitor.
 XX Disclosure; Page 10; 68pp; English.
 PS The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 DB 1 KVFVFA 6
 RESULT 8
 AAU11651
 ID AAU11651 standard; peptide; 6 AA.
 XX AC AAU11651;
 XX 09-APR-2002 (first entry)
 DE Peptide #4, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
 XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
 XX Synthetic.
 OS WO200185093-A2.
 XX 15-NOV-2001.
 XX 22-DEC-2000; 2000WO-IB002078.
 XX 23-DEC-1999; 99US-0171877P.

XX PA (NEUR-) NEUROCHEM INC.
 XX PI Green AM, Gervais F;
 XX DR WPI; 2002-075222/10.
 XX PT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 XX FT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 XX PT inhibitor.
 XX PS Disclosure; Page 10; 68pp; English.
 XX CC The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFFA 6
 |||||
 Db 1 KVFVFFA 6

RESULT 9
 AAE35447
 ID AAE35447 standard; peptide; 6 AA.
 AC AAE35447;

DT 17-JUN-2003 (first entry)

DE Abeta peptide #18.

KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.

XX Unidentified.

XX Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"

XX WO200296937-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-CA000763.

XX 29-MAY-2001; 2001US-00867847.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX Claim 1; Page 59; 44pp; English.
 XX CC The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFFA 6
 |||||
 Db 1 KVFVFFA 6

RESULT 10

AAE35440

ID AAE35440 standard; peptide; 6 AA.

AC AAE35440;

DT 17-JUN-2003 (first entry)

DE Abeta peptide #11.

KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.

XX Unidentified.

XX Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "D-form residues"

XX WO200296937-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-CA000763.

XX 29-MAY-2001; 2001US-00867847.

XX (NEUR-) NEUROCHEM INC.

PI Gervais F, Hebert L, Chalifour RJ, Kong X;
 XX WPI; 2003-201269/19.
 XX
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX
 XX Claim 1; Page 59; 44pp; English.
 XX
 XX The invention relates to a method for prevention and/or treatment of an
 XX amyloid-related disease which comprises administration of an all-D-
 XX amyloid-beta peptide. The method is used for preventing and/or treating
 XX Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 XX angiopathy; for altering serum levels of amyloid-beta in a mammal and
 XX favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 XX the mammal; and reducing or inhibiting the formation of plaques. It is
 XX also used for treating AA (reactive) amyloid diseases including
 XX inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 XX arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 XX Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 XX disease. AA deposits are also produced as a result of chronic microbial
 XX infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 XX ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 XX Certain malignant neoplasms can also result in AA fibril amyloid deposits
 XX including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 XX and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 XX present sequence is an Abeta peptide used to illustrate the method of the
 XX invention
 XX
 XX Sequence 6 AA;
 XX
 XX Query Match 100.0%; Score 31; DB 6; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 KVFVFA 6
 XX Db |||||
 XX 1 KVFVFA 6
 XX
 XX RESULT 11
 XX ADQ37264
 XX ID ADQ37264 standard; peptide; 6 AA.
 XX AC ADQ37264;
 XX DT 07-OCT-2004 (first entry)
 XX DE Vaccine antigen amyloid-beta related amino acid sequence.
 XX
 XX amyloid-beta; amyloid-beta related disease;
 XX amyloid-beta fibril formation; immune response; neurotropic;
 XX neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 XX antihypertensive; vasotropic; cardiovascular; tranquiliser; uterine;
 XX anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 XX cardiac; antidepressant; endocrine; hypnotic;
 XX amyloid-beta fibril formation modulator; immune system modulator;
 XX Alzheimer's disease; mild cognitive impairment;
 XX mild-to-moderate cognitive impairment; vascular dementia;
 XX cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 XX senile dementia; Down's syndrome; inclusion body myositis;
 XX age-related macular degeneration; hypothyroidism;
 XX cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 XX behavioural dysfunction; neurological condition; psychological condition;
 XX vaccine antigen.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX FT Misc-difference 1..6
 XX FT /note= "D-form residues"
 XX
 XX WO2004058239-A1.

XX 15-JUL-2004.
 XX 24-DEC-2003; 2003WO-CA002021.
 XX 24-DEC-2002; 2002US-0436379P.
 XX 23-JUN-2003; 2003US-0482214P.
 XX (NEUK-) NEUROCHEM INT LTD.
 XX Gervais F, Bellini P;
 XX WPI; 2004-543342/52.
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 XX that prevents or treats amyloid-beta related disease and second agent
 XX that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 XX Disclosure; Page 67; 143pp; English.
 XX
 XX The present invention describes compositions (C) comprising: (a) a first
 XX agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 XX a second agent (a2) that is: (i) a peptide or peptidomimetic that
 XX modulates amyloid-beta fibril formation or induces a prophylactic or
 XX therapeutic immune response against amyloid-beta fibril formation; or
 XX (ii) an immune system modulator that prevents or inhibits amyloid-beta
 XX fibril formation. Also described is a kit comprising (C). (C) have
 XX neurotropic, neuroprotective, cerebroprotective, haemostatic,
 XX ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,
 XX uterine, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 XX neuroleptic, cardiac, antidepressant, endocrine and hypnotic activities,
 XX and can be used as amyloid-beta fibril formation modulators, and as
 XX immune system modulators. (C) can be used for preventing or treating an
 XX amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 XX (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 XX mild-to-moderate cognitive impairment, vascular dementia, cerebral
 XX amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 XX Down's syndrome, inclusion body myositis, age-related macular
 XX degeneration, or a condition associated with Alzheimer's disease
 XX (including hypothyroidism, cerebrovascular disease, cardiovascular
 XX disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 XX aggression, or incontinence), a neurological condition (e.g. Huntington's
 XX disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 XX Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 XX with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 XX field deficits, incoordination, gait disturbance, transient ischaemic
 XX attack or stroke, transient alertness, attention deficit, frequent falls,
 XX syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 XX haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 XX damage), or a psychological condition (e.g. depression, delusions,
 XX illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 XX disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 XX ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 XX excessive guilt) in a subject e.g. human having a genomic mutation in an
 XX amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 XX having amyloid-beta deposits. The present sequence represents a peptide
 XX that can be used as a vaccine antigen in the exemplification of the
 XX present invention.
 XX
 XX Sequence 6 AA;
 XX
 XX Query Match 100.0%; Score 31; DB 8; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 KVFVFA 6
 XX Db |||||
 XX 1 KVFVFA 6
 XX
 XX RESULT 12
 XX ADQ37316
 XX ID ADQ37316 standard; peptide; 6 AA.

XX AC ADQ37316;
XX DT 07-OCT-2004 (first entry)
XX DE Antifibrillogenic amyloidosis inhibiting peptide.
XX KW amyloid-beta; amyloid-beta related disease;
KW amyloid-beta fibril formation; immune response; neurotropic;
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
KW cardiant; antidepressant; endocrine; hypnotic;
KW amyloid-beta fibril formation modulator; immune system modulator;
KW Alzheimer's disease; mild cognitive impairment; dementia;
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
KW senile dementia; Down's syndrome; inclusion body myositis;
KW age-related macular degeneration; hypothyroidism;
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
KW behavioural dysfunction; neurological condition; psychological condition;
KW vaccine antigen.
XX OS Synthetic.
XX PN WO2004058239-A1.
XX PD 15-JUL-2004.
XX PF 24-DEC-2003; 2003WO-CA002021.
XX PR 24-DEC-2002; 2002US-0436379P.
XX PR 23-JUN-2003; 2003US-0482214P.
XX PA (NEUR-) NEUROCHEM INT LTD.
XX PI Gervais F, Bellini F;
XX DR WPI; 2004-543342/52.
XX KW Composition for treating e.g. Alzheimer's disease comprises first agent that prevents or treats amyloid-beta related disease and second agent that is either a peptide or peptidomimetic or an immune system modulator.
XX PS Disclosure; Page 69; 143pp; English.
XX CC The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have neurotropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser, uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls,

CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic damage), or a psychological condition (e.g. depression, delusions, illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep disturbance, insomnia, behavioural disinhibition, poor insight, suicidal ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt)) in a subject e.g. human having a genomic mutation in an amyloid precursor protein gene, an ApoE gene, or a presenilin gene; CC having amyloid-beta deposits. The present sequence represents a peptide that can be used as an antifibrillogenic amyloidosis inhibiting peptide CC in the exemplification of the present invention.
XX SQ Sequence 6 AA;
Query Match 100.0%; Score 31; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 26+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVFA 6
Db 1 KVFVFA 6
RESULT 13
ADQ37324
ID ADQ37324 standard; peptide; 6 AA.
XX AC ADQ37324;
XX DT 07-OCT-2004 (first entry)
XX DE Antifibrillogenic amyloidosis inhibiting peptide.
XX KW amyloid-beta; amyloid-beta related disease;
KW amyloid-beta fibril formation; immune response; neurotropic;
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
KW cardiant; antidepressant; endocrine; hypnotic;
KW amyloid-beta fibril formation modulator; immune system modulator;
KW Alzheimer's disease; mild cognitive impairment; vascular dementia;
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
KW senile dementia; Down's syndrome; inclusion body myositis;
KW age-related macular degeneration; hypothyroidism;
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
KW behavioural dysfunction; neurological condition; psychological condition;
KW vaccine antigen.
XX OS Synthetic.
XX PN WO2004058239-A1.
XX PD 15-JUL-2004.
XX PF 24-DEC-2003; 2003WO-CA002021.
XX PR 24-DEC-2002; 2002US-0436379P.
XX PR 23-JUN-2003; 2003US-0482214P.
XX PA (NEUR-) NEUROCHEM INT LTD.
XX PI Gervais F, Bellini F;
XX DR WPI; 2004-543342/52.
XX KW Composition for treating e.g. Alzheimer's disease comprises first agent that prevents or treats amyloid-beta related disease and second agent that is either a peptide or peptidomimetic or an immune system modulator.

XX PS Disclosure; Page 70; 143pp; English.

XX CC The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have

XX CC nootropic, neuroprotective, cerebroprotective, haemostatic, tranquiliser, ophthalmological, antithyroid, vasotropic, cardiovascular, muscular, uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic damage), or a psychological condition (e.g. depression, delusions, disturbance, insomnia, sexual disorder, weight loss, psychosis, a sleep ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt)) in a subject e.g. human having a presenilin gene; having amyloid-beta deposits. The present sequence represents a peptide that can be used as an antifibrillogenic amyloidosis inhibiting peptide in the exemplification of the present invention.

XX CC Sequence 6 AA;

Query Match 100.0%; Score 31; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||||
Db 1 KVFVFA 6

RESULT 14
ADQ37272
ID ADQ37272 standard; peptide; 6 AA.

XX AC ADQ37272;

XX DT 07-OCT-2004 (first entry)

XX DE Vaccine antigen amyloid-beta related amino acid sequence.

XX KW amyloid-beta; amyloid-beta related disease;

XX KW amyloid-beta fibril formation; immune response; nootropic;

XX KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;

XX KW antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;

XX KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;

XX KW cardiant; antidepressant; endocrine; hypnotic;

XX KW amyloid-beta fibril formation modulator; immune system modulator;

XX KW Alzheimer's disease; mild cognitive impairment;

XX KW mild-to-moderate cognitive impairment; vascular dementia;

XX KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;

KW senile dementia; Down's syndrome; inclusion body myositis;
KW age-related macular degeneration; hypothyroidism;
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
KW behavioural dysfunction; neurological condition; psychological condition;
KW vaccine antigen.
XX Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 1..6 /note= "D-form residues"
FT Modified-site 6 /note= "amidated"
WO2004058239-A1.
15-JUL-2004.
24-DEC-2003; 2003WO-CA002021.
24-DEC-2002; 2002US-0436379P.
23-JUN-2003; 2003US-0482214P.
(NEUR-) NEUROCHEM INT LTD.
Gervais F, Bellini F;
WPI; 2004-543342/52.
Composition for treating e.g. Alzheimer's disease comprises first agent that prevents or treats amyloid-beta related disease and second agent that is either a peptide or peptidomimetic or an immune system modulator.
Disclosure; Page 67; 143pp; English.
The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have nootropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, muscular, uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic damage), or a psychological condition (e.g. depression, delusions, disturbance, insomnia, sexual disorder, weight loss, psychosis, a sleep ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt)) in a subject e.g. human having a presenilin gene; having amyloid-beta deposits. The present sequence represents a peptide that can be used as an antifibrillogenic amyloidosis inhibiting peptide in the exemplification of the present invention.

XX SQ Sequence 6 AA;
Query Match 100.0%; Score 31; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KPVFFA 6
Db 1 KPVFFA 6
RESULT 15
ADY37931
ID ADY37931 standard; peptide; 6 AA.
XX AC ADY37931;
XX DT 19-MAY-2005 (first entry)
XX DE Amyloid-targeting peptide, SEQ ID NO:11, for use in imaging agent.
XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
XX KW transmissible spongiform encephalopathy; scrapie; BSE;
XX KW Alzheimers disease; neurological disease; amyloidosis;
XX KW non-insulin dependent diabetes; metabolic disorder.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 6 /note= "C-terminal amide"
XX FN US2005048000-A1.
XX PD 03-MAR-2005.
XX PF 03-DEC-2003; 2003US-00728028.
XX PR 25-JUL-2000; 2000US-0220808P.
XX PR 24-JUL-2001; 2001US-00915092.
XX PR 29-JAN-2003; 2003US-0443291P.
XX PA (NEUR-) NEUROCHEM INT LTD.
XX PI Gervais F, Kong X, Chalifour R, Migneault D;
XX WPI; 2005-212201/22.
XX PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform encephalopathy, primary amyloidosis or Alzheimer's disease.
XX PS Disclosure; SEQ ID NO 11; 34pp; English.
XX CC The invention relates to an amyloid-targeting imaging agent. The imaging agent comprises an amyloid targeting moiety (such as a peptide) joined to a labeling moiety via a linking moiety, and is preferably able to cross the blood-brain barrier. The invention also relates to a kit for preparing a radiopharmaceutical preparation from the imaging agent of the invention, a method for imaging amyloid deposition in a patient and a method for diagnosing an amyloid-related condition in a patient. The amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-related conditions such as Creutzfeld-Jakob disease (CJD), Kuru, transmissible cerebral amyloidoses (also known as transmissible virus dementias), familial CJD, scrapie, transmissible mink encephalopathy, bovine spongiform encephalopathy (BSE), inflammation-associated amyloid, type II diabetes, primary amyloidosis, feline spongiform encephalopathy, non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-mediated diseases, dialysis-related amyloidosis, light chain-related amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a patient. The agent does not exhibit excessive toxicity or irritation, does not induce an allergic response, and permits an earlier diagnosis of

CC amyloid-related conditions, thereby allowing earlier treatment and hence prevention of the undesirable effects of such disorders. Sequences ADY37921-ADY3947 and ADY37949 represent peptides which may be used as the amyloid-targeting moiety in an imaging agent of the invention.
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 31; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KPVFFA 6
Db 1 KPVFFA 6
RESULT 16
ADY37923
ID ADY37923 standard; peptide; 6 AA.
XX AC ADY37923;
XX DT 19-MAY-2005 (first entry)
XX DE Amyloid-targeting peptide, SEQ ID NO:3, for use in imaging agent.
XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
XX KW transmissible spongiform encephalopathy; scrapie; BSE;
XX KW Alzheimers disease; neurological disease; amyloidosis;
XX KW non-insulin dependent diabetes; metabolic disorder.
XX OS Synthetic.
XX FN US2005048000-A1.
XX PD 03-MAR-2005.
XX PF 03-DEC-2003; 2003US-00728028.
XX PR 25-JUL-2000; 2000US-0220808P.
XX PR 24-JUL-2001; 2001US-00915092.
XX PR 29-JAN-2003; 2003US-0443291P.
XX PA (NEUR-) NEUROCHEM INT LTD.
XX PI Gervais F, Kong X, Chalifour R, Migneault D;
XX WPI; 2005-212201/22.
XX PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform encephalopathy, primary amyloidosis or Alzheimer's disease.
XX PS Disclosure; SEQ ID NO 3; 34pp; English.
XX CC The invention relates to an amyloid-targeting imaging agent. The imaging agent comprises an amyloid targeting moiety (such as a peptide) joined to a labeling moiety via a linking moiety, and is preferably able to cross the blood-brain barrier. The invention also relates to a kit for preparing a radiopharmaceutical preparation from the imaging agent of the invention, a method for imaging amyloid deposition in a patient and a method for diagnosing an amyloid-related condition in a patient. The amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-related conditions such as Creutzfeld-Jakob disease (CJD), Kuru, transmissible cerebral amyloidoses (also known as transmissible virus dementias), familial CJD, scrapie, transmissible mink encephalopathy, bovine spongiform encephalopathy (BSE), inflammation-associated amyloid, type II diabetes, primary amyloidosis, feline spongiform encephalopathy, non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-mediated diseases, dialysis-related amyloidosis, light chain-related amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a patient. The agent does not exhibit excessive toxicity or irritation, does not induce an allergic response, and permits an earlier diagnosis of

CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Gaps 0;
 Matches 6; Conservative 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 DB 1 KVFVFA 6

RESULT 17
 ABM89186
 ID ABM89186 standard; protein; 336 AA.

AC ABM89186;
 DT 02-JUN-2005 (first entry)

DE Rice abiotic stress responsive polypeptide SEQ ID NO:7432.

XX
 KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
 OS Oryza sativa.

PN WO2003008540-A2.

XX 30-JAN-2003.

XX 21-JUN-2002; 2002WO-US019668.

XX 22-JUN-2001; 2001US-0300112P.

XX 24-AUG-2001; 2001US-0314662P.

XX 26-SEP-2001; 2001US-0325277P.

XX 21-NOV-2001; 2001US-0332132P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
 PI Moughamer T, Provart N, Ricke D, Zhu T;
 XX WPI; 2003-248011/24.

XX
 PT New stress-responsive nucleic acid, useful for altering the
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
 PT stress, salt stress or osmotic stress.

XX Claim 1; SEQ ID NO 7432; 89pp; English.

XX
 CC The invention relates to novel abiotic stress responsive polynucleotides
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated
 CC polynucleotide expression in a plant cell, and to identify a homolog or
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention

XX Sequence 336 AA;

Query Match 100.0%; Score 31; DB 7; Length 336;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 DB 80 KVFVFA 85

RESULT 18
 ADK35620
 ID ADK35620 standard; protein; 202 AA.

AC ADK35620;

XX 06-MAY-2004 (first entry)

XX Novel human polypeptide SeqID7702.

XX
 KW antiarthritic; antiparkinsonian; neuroprotective; nootropic;
 KW immunosuppressive; cytostatic; antiposrotic; antiinflammatory;
 KW antibacterial; antiviral; antifungal; antiparasitic; gene therapy;
 KW arthritis; Parkinson's; Alzheimer's; autoimmune disease; cancer;
 KW psoriasis; inflammatory bowel disease; infection; bacteria; virus;
 KW fungus; parasite; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1..202

FT /label= OTHER

FT /note= "OTHER= All Xaa's in this sequence are unknown

FT amino acids or the site of a stop codon within the DNA

XX WO200216439-A2.

XX 28-FEB-2002.

XX 05-MAR-2001; 2001WO-US004941.

XX 07-MAR-2000; 2000US-00519705.

XX 19-MAY-2000; 2000US-00574454.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2002-280918/32.

XX Isolated polynucleotide encoding bone marrow derived polypeptides useful
 PT for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's
 PT disease, and inflammatory bowel disease.

XX Claim 20; SEQ ID NO 7702; 504pp; English.

XX This invention relates to a novel isolated polynucleotide comprising a
 CC nucleotide sequence selected from one of 1680 sequences, a mature protein
 CC coding portion of them, an active domain of them and their complementary
 CC sequences. The invention may be useful for the production of compounds
 CC with an antiarthritic, antiparkinsonian, neuroprotective, nootropic,
 CC immunosuppressive, cytostatic, antiposrotic, antiinflammatory, In
 CC antibacterial, antiviral, antifungal or antiparasitic activity. In
 CC addition, the disclosed sequences may be useful for gene therapy. The
 CC polypeptides or their antibodies are useful for treating many diseases
 CC such as arthritis, Parkinson's, Alzheimer's, autoimmune diseases, cancer,
 CC psoriasis, inflammatory bowel disease and infections caused by bacteria,
 CC viruses, fungi or parasites. The present sequence is that of a human
 CC polypeptide of the invention.

XX Sequence 202 AA;

Query Match 96.8%; Score 30; DB 5; Length 202;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KVFPPA 6
Db 35 KFIFFA 40

RESULT 19
ABBI7989
ID ABB17989 standard; protein; 75 AA.
XX ABB17989;
XX 23-JAN-2002 (first entry)
XX Human nervous system related polypeptide SEQ ID NO 6646.
XX Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antischlicking; antianemic; antiarthritic; cancer;
KW antineumatic; hepatotropic; cerebroprotective; antinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
OS Homo sapiens.
XX WO200159063-A2.
XX 16-AUG-2001.
XX 17-JAN-2001; 2001WO-US001334.
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225277P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226688P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.

PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 01-DEC-2000; 2000US-0251160P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 PI WPI; 2001-541565/60.
 DR N-PSDB; ABA14315.
 XX
 XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system cancers
 PT and metastases.
 XX
 PS Claim 11; SEQ ID NO 6646; 1701pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (ABBI4678-ABBI8001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at fip.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 75 AA;
 Query Match 90.3%; Score 28; DB 4; Length 75;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFFA 6
 ||:||||
 Db 5 KFLFFA 10
 RESULT 20
 ADN23626
 ID ADN23626 standard; protein; 452 AA.
 XX
 AC ADN23626;
 XX
 DT 02-DEC-2004 (first entry)
 XX

DE Bacterial polypeptide #6279.
 XX
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.
 XX
 PN US2003233675-A1.
 XX
 PD 18-DEC-2003.
 XX
 PF 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX
 XX WPI; 2004-061375/06.
 DR
 XX
 PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1; SEQ ID NO 6279; 122pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 452 AA;
 Query Match 90.3%; Score 28; DB 8; Length 452;
 Best Local Similarity 83.3%; Pred. No. 9.3e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFFA 6
 :|||||
 Db 291 RVVFFA 296

RESULT 21

ADN46740
ID ADN46740 standard; protein; 485 AA.
XX
XX AC ADN46740;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Thermococcus kodakaraensis KOD1 protein sequence SeqID618.
XX
XX KW gene disruption; gene targeting; marker gene; transformation;
KW homologous recombination; hyperthermostable archaeobacterium; KOD1;
KW gene structure; gene function; enzyme activity; medicine;
KW forensic science; food; drug inspection; molecular biology; immunology.
XX
XX OS Thermococcus kodakaraensis.
XX
XX PN WO2004022736-A1.
XX
XX PD 18-MAR-2004.
XX
XX PF 29-AUG-2003; 2003WO-IB003597.
XX
XX PR 30-AUG-2002; 2002JP-00319011.
XX
XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
XX PI Inanaka T, Atomi H;
XX
XX DR WPI; 2004-257583/24.
XX
XX PT Method for disrupting targeted gene in genome of organism particularly
PT thermostable bacterium and with genome chips for analysis, applicable in
PT studying gene structure and functions.
XX
XX PS Claim 9; SEQ ID NO 618; 598pp; Japanese.
XX
XX CC This invention relates to a novel method for targeting disruption of an
CC arbitrary gene in a genome of an organism which comprises providing the
CC whole sequential data of the genome of such organism, selecting at least
CC 1 arbitrary region in the sequence, providing a vector that contains a
CC sequence homologous with the selected region and a marker gene,
CC transformation, and homologous recombination. The genome is preferably
CC the genome of a hyperthermostable archaeobacterium, particularly
CC Thermococcus kodakaraensis KOD1. The method is for targeting the
CC disruption of a gene in the genome of an organism, which is applicable in
CC studying gene structure and functions as well as enzyme activities of
CC encoded proteins and useful in medicine, forensic science, food or drug
CC inspection, molecular biology and immunology. With this method, the
CC disruption of a gene at an arbitrary position in a genome can be achieved
CC efficiently and reliably. The present sequence is that of a protein
CC encoded by the genome of Thermococcus kodakaraensis which was derived
CC using the method of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SO Sequence 485 AA;

Query Match 90.3%; Score 28; DB 8; Length 485;
Best Local Similarity 83.3%; Pred. No. 9.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	KFVFFA	6
		:	
Db	339	RFVFFA	344

RESULT 22
 AAY1993
 ID AAY1993 standard; protein; 490 AA.
 XX
 AC AAY1993;
 XX

DT	19-JUL-1999	(first entry)
XX	B. burgdorferi	antigenic protein, t752.aa.
XX	Antigenic protein;	vaccine; Lyme disease; infection; detection.
XX	Borrelia burgdorferi.	
OS	W09859071-A1.	
FN	30-DEC-1998.	
XX	18-JUN-1998;	98WO-US012718.
XX	20-JUN-1997;	97US-0050359P.
PR	22-JUL-1997;	97US-0053344P.
PR	22-JUL-1997;	97US-0053377P.
PR	03-SEP-1997;	97US-0057483P.
XX	(HUMA-) HUMAN GENOME SCI INC.	
FA	(MEDI-) MEDIMMUNE INC.	
XX	Choi GH, Erwin AL, Hanson MS, Lathigra R;	
PI	WPI; 1999-189980/16.	
XX	N-ESDB; AAX61690.	
DR	New isolated Borrelia burgdorferi nucleic acids - used to develop	
PT	products for the diagnosis, prevention and treatment of diseases caused	
PT	by Borrelia, particularly Lyme disease.	
XX	Claim 12; Page 153; 275pp; English.	
FS	This sequence represents a Borrelia burgdorferi (Bb) protein of the	
XX	invention, which is suitable for use in a vaccine. The Bb polypeptides	
CC	can be used in vaccines for eliciting protective antibodies to members of	
CC	the Borrelia genus, particularly for the use against Lyme disease in	
CC	humans and animals. They can be used for preventing or attenuating an	
CC	infection caused by a member of the Borrelia genus. The products can also	
CC	be used for detection of members of the Borrelia genus	
XX	Sequence 490 AA;	
SQ	Query Match	90.3%; Score 28; DB 2; Length 490;
	Best Local Similarity	83.3%; Pred. No. 1e+03;
	Matches	5; Conservative 1; Mismatches 0; Indels 0; Gaps 0
OY	1 KFVFFA 6	
	:	
DB	23 RFVFFA 28	
RESULT 23		
AAR95594		
ID	AAR95594 standard; protein; 506 AA.	
XX	AC	AAR95594;
XX	16-OCT-2003 (revised)	
DT	14-OCT-1996 (first entry)	
XX	Arabidopsis fatty acid elongation FAE1 enzyme.	
DE	Fatty acid elongation gene; FAE1; transgenic plant; seed oil;	
XX	vegetable oil; Brassica napus; canola; oilseed rape; eicosenoic acid;	
KW	erucic acid.	
KW	Arabidopsis thaliana; ecotype ws.	
XX	W09613582-A1.	
XX	09-MAY-1996.	
PD		

PF 23-OCT-1995; 95WO-US013918.
 XX
 XX 26-OCT-1994; 94US-00329603.
 XX
 XX (DNAP) DNA PLANT TECHNOLOGY CORP.
 XX
 XX James DW, Lim E, Keller J, Dooner HK;
 XX
 XX WPI; 1996-239495/24.
 DR N-PSDB; AAT27036.
 DR
 XX
 XX New DNA constructs contg. FAE1 gene sequences - used to produce
 PT transgenic plants with modified fatty acid content in plant organs or
 PT parts, esp. seeds.
 XX
 XX Example 1; Page 36; 48pp; English.
 XX
 XX Arabidopsis fatty acid elongation enzyme FAE1 (AAR95594) catalyses the
 CC conversion of oleic acid (18:1) to eicosenoic acid (20:1) and of
 CC eicosenoic acid to erucic acid (22:1). Its amino acid sequence was
 CC deduced from that of a clone (AAT27036) isolated from a cDNA library
 CC prep'd. from Arabidopsis green siliques. Expression of the FAE1 enzyme in
 CC transgenic plants, e.g. Brassica napus, can be used to modulate the fatty
 CC acid content of the plant, partic. the seed oil. Use of antisense DNA
 CC constructs suppresses the native FAE1 gene, allowing prodn. of edible
 CC oils with reduced content of very long chain fatty acids (VLCFA). Use of
 CC sense DNA constructs allows prodn. of oils with raised VLCFA content for
 CC industrial use. (Updated on 16-OCT-2003 to standardise OS field)
 XX
 XX Sequence 506 AA;
 SQ

Query Match 90.3%; Score 28; DB 2; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFFA 6
 ||:||||
 Db 356 KFLFFA 361

RESULT 24
 AAE17850
 ID AAE17850 standard; protein; 506 AA.
 XX
 AC AAE17850;
 XX
 DT 29-AUG-2003 (revised)
 DT 22-APR-2002 (first entry)
 XX
 DE Alternative version of At399 protein.
 XX
 XX Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; FAE1 protein; chimeric.
 KW
 XX Arabidopsis thaliana.
 OS Brassica napus.
 OS Chimeric.
 XX
 XX Key Location/Qualifiers
 FH Region 1..399
 FT /note= "Arabidopsis thaliana elongase KCS protein"
 FT Region 400..506
 FT /note= "Brassica napus elongase KCS protein"
 FT Misc-difference 502
 FT /note= "Encoded by CMA"
 XX
 XX WO200194565-A2.
 XX
 XX 13-DEC-2001.
 XX
 XX 08-JUN-2001; 2001WO-US018737.
 XX
 XX 08-JUN-2000; 2000US-0210326P.
 XX
 XX 08-JUN-2000; 2000US-0210326P.
 XX
 XX

XX (UYMI-) UNIV MIAMI.
 PA
 XX Jaworski JG, Blacklock BJ;
 PI
 XX WPI; 2002-154572/20.
 DR N-PSDB; AAD28537.
 DR
 XX
 XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids.
 XX
 XX Example 1; Page 114-115; 139pp; English.
 PS
 XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalysing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of
 CC C20 fatty acyl CoA. They are especially useful for producing very long
 CC chain fatty acids (VLCFA) and may be used in the development of reagents
 CC for various purposes, e.g., immunological reagents to monitor expression
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor
 CC inheritance of an elongase KCS gene in plant breeding programs. The
 CC present sequence is an alternative version of Arabidopsis thaliana FAE1-
 CC Brassica napus elongase KCS chimeric protein designated as At399.
 CC (Updated on 29-AUG-2003 to standardise OS field)
 XX
 XX Sequence 506 AA;
 SQ

Query Match 90.3%; Score 28; DB 5; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFFA 6
 ||:||||
 Db 356 KFLFFA 361

RESULT 25
 AAE17622
 ID AAE17622 standard; protein; 506 AA.
 XX
 AC AAE17622;
 XX
 DT 29-AUG-2003 (revised)
 DT 22-APR-2002 (first entry)
 XX
 DE A. thaliana FAE1-Brassica napus elongase KCS chimeric protein, At399.
 XX
 XX Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; FAE1 protein; chimeric.
 KW
 XX Arabidopsis thaliana.
 OS Brassica napus.
 OS Chimeric.
 XX
 XX Key Location/Qualifiers
 FH Region 1..399
 FT /note= "Arabidopsis thaliana elongase KCS protein"
 FT Region 400..506
 FT /note= "Brassica napus elongase KCS protein"
 XX
 XX WO200194565-A2.
 XX
 XX 13-DEC-2001.
 XX
 XX 08-JUN-2001; 2001WO-US018737.
 XX
 XX 08-JUN-2000; 2000US-0210326P.
 XX
 XX (UYMI-) UNIV MIAMI.
 PA
 XX

PI Jaworski JG, Blacklock BJ;
 XX WPI; 2002-154572/20.
 DR N-PSDB; AAD28514.
 XX
 PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids.
 XX
 PS Example 1; Fig 1-5; 139pp; English.
 XX
 CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalyzing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of
 CC C20 fatty acyl CoA. They are especially useful for producing very long
 CC chain fatty acids (VLCFA) and may be used in the development of reagents
 CC for various purposes, e.g., immunological reagents to monitor expression
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor
 CC inheritance of an elongase KCS gene in plant breeding programs. The
 CC present sequence is Arabidopsis thaliana FAE1- Brassica napus elongase
 CC KCS chimeric protein designated as At399. (Updated on 29-AUG-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 506 AA;

Query Match 90.3%; Score 28; DB 5; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
 ||:||||
 Db 356 KFLFFA 361

RESULT 26
 AAEL17625
 ID AAEL17625 standard; protein; 506 AA.
 XX
 AC AAEL17625;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE Arabidopsis thaliana FAE1 protein mutant, At K92R.
 XX
 KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; FAE1 gene; mutant; mutain.
 XX
 OS Arabidopsis thaliana.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 92
 FT /note= "Wild-type Lys substituted with Arg"
 XX
 XX WO200194565-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 08-JUN-2001; 2001WO-US018737.
 XX
 PR 08-JUN-2000; 2000US-0210326P.
 XX
 PA (UTMI-) UNIV MIAMI.
 XX
 PI Jaworski JG, Blacklock BJ;
 XX WPI; 2002-154572/20.
 DR N-PSDB; AAD28517.
 XX
 PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids.

XX Claim 7; Fig 1-6; 139pp; English.
 XX
 CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalyzing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of
 CC C20 fatty acyl CoA. They are especially useful for producing very long
 CC chain fatty acids (VLCFA) and may be used in the development of reagents
 CC for various purposes, e.g., immunological reagents to monitor expression
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor
 CC inheritance of an elongase KCS gene in plant breeding programs. The
 CC present sequence is a mutant of Arabidopsis thaliana elongase KCS
 CC protein/FAE1 protein designated as At K92R
 XX
 SQ Sequence 506 AA;

Query Match 90.3%; Score 28; DB 5; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
 ||:||||
 Db 356 KFLFFA 361

RESULT 27
 AAEL17621
 ID AAEL17621 standard; protein; 506 AA.
 XX
 AC AAEL17621;
 XX
 DT 22-AUG-2003 (revised)
 DT 29-APR-2002 (first entry)
 XX
 DE Brassica napus elongase KCS-A. thaliana FAE1 chimeric protein, Bn176.
 XX
 KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; FAE1 gene; chimeric.
 XX
 OS Brassica napus.
 OS Arabidopsis thaliana.
 OS Chimeric.
 XX
 XX Key Location/Qualifiers
 FH Region 1. .176
 FT /note= "Brassica napus elongase KCS protein"
 FT Region 177. .506
 FT /note= "Arabidopsis thaliana FAE1 protein"
 XX
 XX WO200194565-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 08-JUN-2001; 2001WO-US018737.
 XX
 PR 08-JUN-2000; 2000US-0210326P.
 XX
 PA (UTMI-) UNIV MIAMI.
 XX
 PI Jaworski JG, Blacklock BJ;
 XX WPI; 2002-154572/20.
 DR N-PSDB; AAD28513.
 XX
 PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids.
 XX
 PS Example 1; Fig 1-5; 139pp; English.
 XX
 CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase

CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalysing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of
 CC C20 fatty acyl CoA. They are especially useful for producing very long
 CC chain fatty acids (VLCFA) and may be used in the development of reagents
 CC for various purposes, e.g., immunological reagents to monitor expression
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor
 CC inheritance of an elongase KCS gene in plant breeding programs. The
 CC present sequence is *Brassica napus* elongase KCS- Arabidopsis thaliana
 CC FAE1 chimeric protein designated as Bn176. (Updated on 29-AUG-2003 to
 CC standardise OS field)
 XX

SQ Sequence 506 AA;
 Query Match 90.3%; Score 28; DB 5; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVFFPA 6
 ||:||||
 Db 356 KFLFFPA 361

RESULT 28
 AAE17608
 ID AAE17608 standard; protein; 506 AA.
 XX
 AC AAE17608;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE Arabidopsis thaliana elongase KCS protein.
 XX
 KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; FAE1 protein.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO2001194565-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 08-JUN-2001; 2001WO-US018737.
 XX
 PR 08-JUN-2000; 2000US-0210326P.
 XX
 PA (UYMT-) UNIV MIAMI.
 XX
 PI Jaworski JG, Blacklock BJ;
 XX
 DR WPI; 2002-154572/20.
 DR N-PSDB; AAD28500.
 XX

XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids.
 XX

PS Example 3; Fig 1-1; 139pp; English.
 XX
 CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalysing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of
 CC C20 fatty acyl CoA. They are especially useful for producing very long
 CC chain fatty acids (VLCFA) and may be used in the development of reagents
 CC for various purposes, e.g., immunological reagents to monitor expression
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor
 CC inheritance of an elongase KCS gene in plant breeding programs. The
 CC present sequence is Arabidopsis thaliana elongase KCS protein encoded by
 CC FAE1 gene
 CC

SQ Sequence 506 AA;
 Query Match 90.3%; Score 28; DB 5; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVFFPA 6
 ||:||||
 Db 356 KFLFFPA 361
 RESULT 29
 AEA37517
 ID AEA37517 standard; protein; 506 AA.
 XX
 AC AEA37517;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DE Arabidopsis sp. fatty acid elongase 1 (FAE1) protein.
 XX
 KW vector; transformation; plant; fatty acid elongase 1;
 KW 3-ketoacyl-CoA synthase; promoter; gene expression; seed; oil; enzyme.
 XX
 OS Arabidopsis sp.
 XX
 PN WO2005052162-A1.
 XX
 PD 09-JUN-2005.
 XX
 PF 24-NOV-2004; 2004WO-CA002021.
 XX
 PR 25-NOV-2003; 2003US-0524645P.
 XX
 PA (CANA) NAT RES COUNCIL CANADA.
 XX
 PI Mietkiewska E, Taylor DC, Katavic V;
 XX
 DR WPI; 2005-418004/42.
 DR N-PSDB; AEA37518.
 XX
 PT New expression vector for transforming a cell comprising a gene coding
 PT for a plant fatty acid elongase, useful for altering erucic acid content
 PT or the very long chain fatty acid content (C20 or greater) in a plant.
 XX
 PS Disclosure; SEQ ID NO 26; 72pp; English.
 XX
 CC The invention relates to an expression vector for transforming a cell.
 CC The expression vector comprises a gene coding for a plant fatty acid
 CC elongase (FAE, also designated 3-ketoacyl-CoA synthase (KCS)) in reading
 CC frame alignment with a promoter capable of increasing the expression of
 CC the gene, when the transformed cell is in a seed, sufficient to increase
 CC the proportion of very long chain monounsaturated fatty acid when
 CC compared with a control cell. Also described are: (1) a cell comprising a
 CC heterologous gene coding for a heterologous plant fatty acid elongase or
 CC its allelic variant, the cell being capable of producing an increase in
 CC proportion of a very long chain monounsaturated fatty acid when compared
 CC a control cell lacking the heterologous gene; (2) a seed comprising the
 CC plant cells above; (3) a plant comprising the plant cells; and (4) a
 CC method of altering erucic acid content of a plant-derived oil. The gene
 CC coding for a plant fatty acid elongase is a Nasturtium, Crambe, or
 CC Arabidopsis fatty acid elongase gene. The cell is a fungal cell,
 CC preferably yeast cell, or a plant cell, specifically a plant seed cell.
 CC The plant cell additionally comprises a further heterologous gene coding
 CC for an additional heterologous plant fatty acid elongase or its allelic
 CC variant or a heterologous plant desaturase gene or its allelic variant.
 CC It is capable of producing oil with an increased content of erucic acid
 CC or other very long chain fatty acid (C20 or greater). The heterologous
 CC gene codes for a 3-ketoacyl-CoA synthase. The very long chain
 CC monounsaturated fatty acid comprises erucic acid. The heterologous plant
 CC fatty acid elongase gene is useful for altering erucic acid content in a
 CC plant or the very long chain fatty acid content (C20 or greater) in a
 CC plant. The vector is useful for altering erucic acid content in a plant.

CC This sequence represents a *Arabidopsis* sp. FAE1.

XX Sequence 506 AA;

Query Match 90.3%; Score 28; DB 9; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6

Db 356 KFLFFA 361

RESULT 30

AAV1992
 ID AAV1992 standard; protein; 508 AA.

XX AC AAV1992;

DT 19-JUL-1999 (first entry)

DE B. burgdorferi antigenic protein, f752.aa.

KW Antigenic protein; vaccine; Lyme disease; infection; detection.

XX OS Borrelia burgdorferi.

XX PN W09859071-A1.

XX PD 30-DEC-1998.

XX PF 18-JUN-1998; 98WO-US012718.

XX PR 20-JUN-1997; 97US-0050359P.

XX PR 22-JUL-1997; 97US-0053344P.

XX PR 22-JUL-1997; 97US-0053377P.

XX PR 03-SEP-1997; 97US-0057483P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (MEDI-) MEDIMUNE INC.

PI Choi GH, Erwin AL, Hanson MS, Lathigra R;

DR WPI; 1999-189980/16.

DR N-PSDB; AAX61689.

XX PT New isolated Borrelia burgdorferi nucleic acids - used to develop products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease.

XX PS Claim 12; Page 153; 275pp; English.

CC This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus

XX SQ Sequence 508 AA;

Query Match 90.3%; Score 28; DB 2; Length 508;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6

Db 41 RFVFFA 46

RESULT 31

ABU19128

ID ABU19128 standard; protein; 508 AA.

XX AC ABU19128;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #4655.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX KW Borrelia burgdorferi.

XX OS WO200277183-A2.

XX PN 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA22998.

XX New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 47052; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 508 AA;

Query Match

90.3%; Score 28; DB 6; Length 508;

Best Local Similarity 83.3%; Pred. No. 1e+03; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
Db 41 RFVFFA 46

RESULT 32
ABU24005
ID ABU24005 standard; protein; 571 AA.
XX
AC ABU24005;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #9532.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Clostridium acetobutylicum.
XX
PN WO20027183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
DR N-PSDB; ACA27875.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 51929; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 571 AA;

Query Match 90.3%; Score 28; DB 6; Length 571;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
Db 314 KFMFFA 319

RESULT 33
ADN19501
ID ADN19501 standard; protein; 1089 AA.
XX
AC ADN19501;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #2154.

XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 2154; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX

SQ Sequence 1089 AA;

Query Match 90.3%; Score 28; DB 8; Length 1089;

Best Local Similarity 83.3%; Pred. No. 2.2e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6

Db 13 KVFVFS 18

RESULT 34

AAG61668

ID AAG61668 standard; protein; 52 AA.

XX AC AAG61668;

XX AC AAG61668;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 80017.

XX KW Protein identification; signal transduction pathway; metabolic pathway;

XX KW hybridisation assay; Genetic mapping; gene expression control; promoter;

XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 23-MAR-1999; 99US-0123548P.

XX PR 25-MAR-1999; 99US-0125788P.

XX PR 29-MAR-1999; 99US-0126264P.

XX PR 01-APR-1999; 99US-0126785P.

XX PR 06-APR-1999; 99US-0127462P.

XX PR 08-APR-1999; 99US-0128234P.

XX PR 16-APR-1999; 99US-0128714P.

XX PR 19-APR-1999; 99US-0129845P.

XX PR 21-APR-1999; 99US-0130077P.

XX PR 23-APR-1999; 99US-0130449P.

XX PR 28-APR-1999; 99US-0130891P.

XX PR 30-APR-1999; 99US-0131449P.

XX PR 04-MAY-1999; 99US-0132048P.

XX PR 06-MAY-1999; 99US-0132484P.

XX PR 07-MAY-1999; 99US-0132486P.

XX PR 11-MAY-1999; 99US-0132863P.

XX PR 14-MAY-1999; 99US-0134256P.

XX PR 14-MAY-1999; 99US-0134218P.

XX PR 14-MAY-1999; 99US-0134219P.

XX PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.

PR 19-MAY-1999; 99US-0134941P.

PR 20-MAY-1999; 99US-0135124P.

PR 21-MAY-1999; 99US-0135353P.

PR 24-MAY-1999; 99US-0135629P.

PR 25-MAY-1999; 99US-0136021P.

PR 27-MAY-1999; 99US-0136392P.

PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-0137222P.

PR 03-JUN-1999; 99US-0137528P.

PR 04-JUN-1999; 99US-0137502P.

PR 07-JUN-1999; 99US-0137724P.

PR 08-JUN-1999; 99US-0138094P.

PR 10-JUN-1999; 99US-0138540P.

PR 10-JUN-1999; 99US-0138847P.

PR 14-JUN-1999; 99US-0139119P.

PR 16-JUN-1999; 99US-0139452P.

PR 16-JUN-1999; 99US-0139453P.

PR 17-JUN-1999; 99US-0139492P.

PR 18-JUN-1999; 99US-0139454P.

PR 18-JUN-1999; 99US-0139455P.

PR 18-JUN-1999; 99US-0139456P.

PR 18-JUN-1999; 99US-0139457P.

PR 18-JUN-1999; 99US-0139458P.

PR 18-JUN-1999; 99US-0139459P.

PR 18-JUN-1999; 99US-0139460P.

PR 18-JUN-1999; 99US-0139461P.

PR 18-JUN-1999; 99US-0139462P.

PR 18-JUN-1999; 99US-0139463P.

PR 18-JUN-1999; 99US-0139750P.

PR 18-JUN-1999; 99US-0139763P.

PR 21-JUN-1999; 99US-0139817P.

PR 22-JUN-1999; 99US-0139899P.

PR 23-JUN-1999; 99US-0140353P.

PR 24-JUN-1999; 99US-0140354P.

PR 28-JUN-1999; 99US-0140895P.

PR 29-JUN-1999; 99US-0140823P.

PR 30-JUN-1999; 99US-0141287P.

PR 01-JUL-1999; 99US-0141842P.

PR 02-JUL-1999; 99US-0142154P.

PR 06-JUL-1999; 99US-0142390P.

PR 08-JUL-1999; 99US-0142803P.

PR 09-JUL-1999; 99US-0142920P.

PR 12-JUL-1999; 99US-0142977P.

PR 13-JUL-1999; 99US-0143542P.

PR 14-JUL-1999; 99US-0143624P.

PR 15-JUL-1999; 99US-0144005P.

PR 16-JUL-1999; 99US-0144085P.

PR 16-JUL-1999; 99US-0144086P.

PR 19-JUL-1999; 99US-0144325P.

PR 19-JUL-1999; 99US-0144331P.

PR 19-JUL-1999; 99US-0144332P.

PR 19-JUL-1999; 99US-0144333P.

PR 19-JUL-1999; 99US-0144334P.

PR 19-JUL-1999; 99US-0144335P.

PR 20-JUL-1999; 99US-0144352P.

PR 20-JUL-1999; 99US-0144632P.

PR 20-JUL-1999; 99US-0144684P.

PR 21-JUL-1999; 99US-0144814P.

PR 21-JUL-1999; 99US-0145086P.

PR 21-JUL-1999; 99US-0145088P.

PR 22-JUL-1999; 99US-0145085P.

PR 22-JUL-1999; 99US-0145087P.

PR 22-JUL-1999; 99US-0145089P.

PR 23-JUL-1999; 99US-0145192P.

PR 23-JUL-1999; 99US-0145145P.

PR 23-JUL-1999; 99US-0145218P.

PR 23-JUL-1999; 99US-0145224P.

PR 26-JUL-1999; 99US-0145276P.

PR 27-JUL-1999; 99US-0145913P.

PR 27-JUL-1999; 99US-0145918P.
 PR 27-JUL-1999; 99US-0145919P.
 PR 28-JUL-1999; 99US-0145951P.
 PR 02-AUG-1999; 99US-0146386P.
 PR 02-AUG-1999; 99US-0146388P.
 PR 02-AUG-1999; 99US-0146389P.
 PR 03-AUG-1999; 99US-0147038P.
 PR 04-AUG-1999; 99US-0147202P.
 PR 04-AUG-1999; 99US-0147302P.
 PR 05-AUG-1999; 99US-0147192P.
 PR 05-AUG-1999; 99US-0147260P.
 PR 06-AUG-1999; 99US-0147303P.
 PR 06-AUG-1999; 99US-0147416P.
 PR 09-AUG-1999; 99US-0147493P.
 PR 09-AUG-1999; 99US-0147935P.
 PR 10-AUG-1999; 99US-0148171P.
 PR 11-AUG-1999; 99US-0148319P.
 PR 12-AUG-1999; 99US-0148341P.
 PR 13-AUG-1999; 99US-0148565P.
 PR 13-AUG-1999; 99US-0148684P.
 PR 16-AUG-1999; 99US-0149368P.
 PR 17-AUG-1999; 99US-0149175P.
 PR 18-AUG-1999; 99US-0149426P.
 PR 20-AUG-1999; 99US-0149722P.
 PR 20-AUG-1999; 99US-0149723P.
 PR 20-AUG-1999; 99US-0149929P.
 PR 23-AUG-1999; 99US-0149902P.
 PR 23-AUG-1999; 99US-0149930P.
 PR 25-AUG-1999; 99US-0150566P.
 PR 26-AUG-1999; 99US-0150884P.
 PR 27-AUG-1999; 99US-0151065P.
 PR 27-AUG-1999; 99US-0151066P.
 PR 27-AUG-1999; 99US-0151080P.
 PR 30-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151330P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
 PR 16-SEP-1999; 99US-0154039P.
 PR 20-SEP-1999; 99US-0154779P.
 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-0155659P.
 PR 28-SEP-1999; 99US-0156458P.
 PR 29-SEP-1999; 99US-0156596P.
 PR 04-OCT-1999; 99US-0157117P.
 PR 05-OCT-1999; 99US-0157753P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 18-OCT-1999; 99US-0159638P.
 PR 21-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161040P.
 PR 25-OCT-1999; 99US-0161405P.

PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161992P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRVFF 5
 |||||
 Db 31 KRVFF 35

RESULT 35
 ADX67964
 ID ADX67964 standard; protein; 57 AA.
 XX
 AC ADX67964;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polypeptide seqid 38807.
 XX
 KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX
 OS Unidentified.
 XX
 PN US2004034888-A1.
 XX
 PD 19-FEB-2004.
 XX
 PF 28-APR-2003; 2003US-00425114.
 XX
 PR 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX
 PA (LIU//) LIU J.
 PA (ZHOU//) ZHOU Y.
 PA (KOVA//) KOVALIC D K.
 PA (SCRE//) SCREEN S E.
 PA (TABAS//) TABASKA J E.
 PA (CAOY//) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX
 DR WPI; 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 38807; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme

CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.

XX
SQ Sequence 57 AA;

Query Match 87.1%; Score 27; DB 8; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5

DB 29 KPVFF 33

RESULT 36

ABB03189
ID ABB03189 standard; protein; 62 AA.

XX
AC ABB03189;

XX
DT 08-JAN-2002 (first entry)

XX
DE Human musculoskeletal system related polypeptide SEQ ID NO 1136.

XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW anti-allergic; hepatotropic; antidiabetic; antinflammatory; antiulcer;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein;
KW musculoskeletal system.

XX
OS Homo sapiens.

XX
FN WO200155367-A1.

XX
PD 02-AUG-2001.

XX
PF 17-JAN-2001; 2001WO-US001138.

XX
PR 31-JAN-2000; 2000US-0179065P.

PR
04-FEB-2000; 2000US-0180628P.

PR
24-FEB-2000; 2000US-0184664P.

PR
02-MAR-2000; 2000US-0186350P.

PR
16-MAR-2000; 2000US-0189874P.

PR
17-MAR-2000; 2000US-0190078P.

PR
18-APR-2000; 2000US-0198123P.

PR
19-MAY-2000; 2000US-0205518P.

PR
07-JUN-2000; 2000US-0209467P.

PR
28-JUN-2000; 2000US-0214886P.

PR
30-JUN-2000; 2000US-0215135P.

PR
07-JUL-2000; 2000US-0216647P.

PR
07-JUL-2000; 2000US-0216880P.

PR
11-JUL-2000; 2000US-0217487P.

PR
11-JUL-2000; 2000US-0217496P.

PR
14-JUL-2000; 2000US-0219290P.

PR
26-JUL-2000; 2000US-0220963P.

PR
26-JUL-2000; 2000US-0220964P.

PR
14-AUG-2000; 2000US-0224518P.

PR
14-AUG-2000; 2000US-0224519P.

PR
14-AUG-2000; 2000US-0225213P.

PR
14-AUG-2000; 2000US-0225214P.

PR
14-AUG-2000; 2000US-0225266P.

PR
14-AUG-2000; 2000US-0225267P.

PR
14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249298P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-451937/48.
XX N-PSDB; AAL34771.
XX
XX Isolated polypeptide for treating, preventing and/ or prognosing
XX disorders related to the musculoskeletal system including musculoskeletal
XX cancers and also for testing and detection e.g. diagnosis.
XX
XX Claim 11; SEQ ID NO 1136; 781pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (AAL34669-AAL37666) and proteins
XX (ABR03087-ABR04109) associated with the musculoskeletal system useful for
XX preventing, treating or ameliorating medical conditions e.g. by protein
XX or gene therapy. The genes are isolated from a range of human tissues
XX disclosed in the specification. The nucleic acids, proteins, antibodies
XX and (ant)agonists are useful in the diagnosis, treatment and prevention
XX of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
XX adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
XX lung, or urogenital; (b) immune disorders e.g. Addison's disease,
XX allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
XX diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
XX arthritis and ulcerative colitis; (c) cardiovascular disorders such as
XX myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.
XX cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
XX bacterial, fungal and parasitic infections. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 62 AA;

Query Match 87.1%; Score 27; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVFF 5
Db 31 KPVFF 35
RESULT 37
ABU12483
ID ABU12483 standard; protein; 62 AA.
XX
AC ABU12483;
XX
DT 26-FEB-2003 (first entry)
XX
DE Novel human musculoskeletal system antigen #103.
XX
KW Musculoskeletal system antigen; cancer; metastasis; re-vascularisation;
KW thrombosis; arteriosclerosis; mineral content; cardiovascular condition;
KW wound; injury; burn; angiogenesis; ulcer; post-operative tissue repair;
KW limb regeneration; neuronal growth; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; AIDS-related complex;
KW chondrocyte growth; bone regeneration; periodontal regeneration;
KW tissue transport; bone graft; skin aging; keratinocyte growth; hair loss;
KW melanocyte growth; cell proliferation; cell growth; organ transplant;
KW cell differentiation; body height; weight; hair colour; eye colour; skin;
KW percentage of adipose tissue; pigmentation; cosmetic surgery; metabolism;
KW biorhythm; circadian rhythm; depression; tendency for violence; pain;
KW reproductive capability; hormone level; endocrine level; appetite;
KW libido; memory; stress; storage capability; fat content; lipid content;
KW protein content; carbohydrate content; vitamin content; cofactor content;
KW nutritional component.
XX
XX Homo sapiens.
XX
XX OS
XX US2002147140-A1.
XX
XX 10-OCT-2002.
XX
XX 17-JAN-2001; 2001US-00764877.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 28-JUN-2000; 2000US-0214886P.
XX 07-JUL-2000; 2000US-0216647P.
XX 07-JUL-2000; 2000US-0216880P.
XX 11-JUL-2000; 2000US-0217487P.
XX 14-JUL-2000; 2000US-0218290P.
XX 26-JUL-2000; 2000US-0220963P.
XX 26-JUL-2000; 2000US-0220964P.
XX 14-AUG-2000; 2000US-0224518P.
XX 14-AUG-2000; 2000US-0224519P.
XX 14-AUG-2000; 2000US-0225267P.
XX 14-AUG-2000; 2000US-0225268P.
XX 14-AUG-2000; 2000US-0225270P.
XX 14-AUG-2000; 2000US-0225447P.
XX 14-AUG-2000; 2000US-0225757P.
XX 14-AUG-2000; 2000US-0225758P.
XX 22-AUG-2000; 2000US-0226868P.
XX 30-AUG-2000; 2000US-0228924P.
XX 01-SEP-2000; 2000US-0229287P.
XX 01-SEP-2000; 2000US-0229343P.
XX 01-SEP-2000; 2000US-0229344P.
XX 01-SEP-2000; 2000US-0229345P.
XX 05-SEP-2000; 2000US-0229509P.
XX 05-SEP-2000; 2000US-0229513P.
XX 08-SEP-2000; 2000US-0231413P.
XX 21-SEP-2000; 2000US-0234223P.
XX 21-SEP-2000; 2000US-0234274P.
XX 25-SEP-2000; 2000US-0234997P.


```
PR 08-SEP-2000; 2000US-0231342P.
PR 08-SEP-2000; 2000US-02311243P.
PR 08-SEP-2000; 2000US-02311244P.
PR 08-SEP-2000; 2000US-02311413P.
PR 08-SEP-2000; 2000US-02311414P.
PR 08-SEP-2000; 2000US-02320801P.
PR 08-SEP-2000; 2000US-02320801P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0232063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246533P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249247P.
PR 17-NOV-2000; 2000US-0249248P.
PR 17-NOV-2000; 2000US-0249249P.
PR 17-NOV-2000; 2000US-0249250P.
PR 17-NOV-2000; 2000US-0249251P.
PR 17-NOV-2000; 2000US-0249252P.
PR 17-NOV-2000; 2000US-0249253P.
PR 17-NOV-2000; 2000US-0249254P.
PR 17-NOV-2000; 2000US-0249255P.
PR 17-NOV-2000; 2000US-0249256P.
PR 17-NOV-2000; 2000US-0249257P.
PR 17-NOV-2000; 2000US-0249258P.
PR 17-NOV-2000; 2000US-0249259P.
PR 17-NOV-2000; 2000US-0249260P.
PR 17-NOV-2000; 2000US-0249261P.
PR 17-NOV-2000; 2000US-0249262P.
PR 17-NOV-2000; 2000US-0249263P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249266P.
PR 17-NOV-2000; 2000US-0249267P.
PR 17-NOV-2000; 2000US-0249268P.
PR 17-NOV-2000; 2000US-0249269P.
PR 17-NOV-2000; 2000US-0249270P.
PR 17-NOV-2000; 2000US-0249271P.
PR 17-NOV-2000; 2000US-0249272P.
PR 17-NOV-2000; 2000US-0249273P.
PR 17-NOV-2000; 2000US-0249274P.
PR 17-NOV-2000; 2000US-0249275P.
PR 17-NOV-2000; 2000US-0249276P.
PR 17-NOV-2000; 2000US-0249277P.
PR 17-NOV-2000; 2000US-0249278P.
PR 17-NOV-2000; 2000US-0249279P.
PR 17-NOV-2000; 2000US-0249280P.
PR 17-NOV-2000; 2000US-0249281P.
PR 17-NOV-2000; 2000US-0249282P.
PR 17-NOV-2000; 2000US-0249283P.
PR 17-NOV-2000; 2000US-0249284P.
PR 17-NOV-2000; 2000US-0249285P.
PR 17-NOV-2000; 2000US-0249286P.
PR 17-NOV-2000; 2000US-0249287P.
PR 17-NOV-2000; 2000US-0249288P.
PR 17-NOV-2000; 2000US-0249289P.
PR 17-NOV-2000; 2000US-0249290P.
PR 17-NOV-2000; 2000US-0249291P.
PR 17-NOV-2000; 2000US-0249292P.
PR 17-NOV-2000; 2000US-0249293P.
PR 17-NOV-2000; 2000US-0249294P.
PR 17-NOV-2000; 2000US-0249295P.
PR 17-NOV-2000; 2000US-0249296P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249298P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250160P.
PR 05-DEC-2000; 2000US-0250303P.
PR 05-DEC-2000; 2000US-0250303P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764877.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Barash SC;
PI N-PSDB; ADJ27486.
XX
XX WPI; 2004-090458/09.
DR N-PSDB; ADJ27486.
XX
XX New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g., cancer of
PT musculoskeletal tissues or osteoporosis.
XX
XX Claim 11; SEQ ID NO 1136; 289pp; English.
XX
XX The invention relates to a novel isolated musculoskeletal system-
CC associated nucleic acid molecule. The nucleic acid of the invention
CC demonstrates cytostatic and osteopathic activities and may be useful for
CC preparing a medicament for preventing, treating or ameliorating a medical
CC condition such as cancer of the musculoskeletal tissues or osteoporosis,
CC possibly via gene therapy or vaccine production. The current sequence is
CC that of the human musculoskeletal system-associated polypeptide of the
CC invention. The current sequence is not shown within the specification per
CC se but is available on the USPTO web-site
CC http:seqdata.uspto.gov/sequence.html?DocID=20040009488.
XX
XX Sequence 62 AA;
SQ
Query Match 87.1%; Score 27; DB 8; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KRVFF 5
Db 31 KRVFF 35
RESULT 39
AAG00778
ID AAG00778 standard; protein; 82 AA.
XX
XX AAG00778;
XX
XX 06-OCT-2000 (first entry)
XX
XX Human secreted protein, SEQ ID NO: 4859.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping.
XX
XX Homo sapiens.
XX
XX EP1033401-A2.
XX
```

PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-00200610.
 XX
 PR 26-FEB-1999; 99US-0122487P.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI; 2000-500381/45.
 DR N-PSDB; AAC00784.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 PS Claim 13; SEQ ID NO 4859; 71pp + Sequence Listing; English.
 XX
 CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX
 SQ Sequence 82 AA;
 Query Match 87.1%; Score 27; DB 3; Length 82;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVFF 5
 Db 32 KVFVF 36
 |||||
 |||||
 RESULT 40
 ABG13797
 ID ABG13797 standard; protein; 82 AA.
 XX
 AC ABG13797;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #13788.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 XX WPI; 2001-639362/73.
 DR

DR N-PSDB; AAS77984.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 44156; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have application in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 82 AA;
 Query Match 87.1%; Score 27; DB 4; Length 82;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFF 6
 Db 11 EFVFFA 16
 :|||
 |||||
 RESULT 41
 AAO12276
 ID AAO12276 standard; protein; 91 AA.
 XX
 AC AAO12276;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 26168.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US004927.
 XX
 PR 28-FEB-2000; 2000US-00515126.
 PR 18-MAY-2000; 2000US-00577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 XX WPI; 2001-514838/56.
 DR

DR N-PSDB; AAI92207.
 XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 XX
 PS Claim 20; SEQ ID NO 26168; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC actvity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 91 AA;

Query Match 87.1%; Score 27; DB 4; Length 91;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 |||||
 DB 17 KVFVF 21

RESULT 42
 AAO10108
 ID AAO10108 standard; protein; 99 AA.

XX AAO10108;
 XX
 XX 06-NOV-2001 (first entry)
 XX Human polypeptide SEQ ID NO 24000.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US004927.

XX 28-FEB-2000; 2000US-00515126.

XX 18-MAY-2000; 2000US-00577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

XX N-PSDB; AAI90039.

XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.

XX Claim 20; SEQ ID NO 24000; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce

CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC actvity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 99 AA;

Query Match 87.1%; Score 27; DB 4; Length 99;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 |||||
 DB 39 KVFVF 43

RESULT 43

AAE12897
 ID AAE12897 standard; protein; 104 AA.

XX AAE12897;

XX 15-JAN-2002 (first entry)

XX Human recombinant beta-amyloid precursor protein (betaAPP) C-83.

XX Human; Alzheimer's disease; Gamma-secretase; integral-membrane protein;
 KW beta-amyloid precursor protein; betaAPP.

XX Homo sapiens.

XX WO200175435-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US010453.

XX 03-APR-2000; 2000US-0194495P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Roberts SB, Hendrick JP, Vinitzky A, Lewis M, Smith DW, Pak R;

XX WPI; 2001-648575/74.

XX N-PSDB; AAD20982.

XX Novel gamma secretase protein, useful in the production of amyloids, is
 PT capable of cleaving beta-amyloid precursor protein to produce beta
 PT amyloid peptide.

XX Claim 83; Fig 3; 127pp; English.

XX The invention relates to the field of plaque amyloid deposits that are
 CC the hallmarks of Alzheimer's disease. In particular, the invention
 CC relates to an isolated, functionally-active protein that has gamma-
 CC secretase activity. Gamma-secretase activity is necessary for amyloid
 CC production. The present invention also relates to methods for isolating
 CC integral-membrane proteins and protein complexes, including the gamma-
 CC secretase protein of the invention. The method is useful for monitoring
 CC the cleavage of beta-amyloid precursor protein (betaAPP) by gamma-
 CC secretase. The present sequence is human recombinant betaAPP protein (C-
 CC 83)

XX Sequence 104 AA;

Query Match 87.1%; Score 27; DB 4; Length 104;
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
:|||||
Db 21 EFVFFA 26

RESULT 44
AAB93728
ID AAB93728 standard; protein; 114 AA.
AC AAB93728;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:13358.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
FN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PP 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-0018776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
(HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Negai K, Otsuki T;
XX
WPI; 2001-318749/34.
XX
Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
XX
Claim 8; SEQ ID NO 13358; 2537pp + Sequence Listing; English.
XX
The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH03166 to AAH05893 represent human amino acid sequences; and AAH13629 to AAH13632 represent polynucleotides, all of which are used in the exemplification of the present invention
XX
Sequence 114 AA;

Query Match 87.1%; Score 27; DB 4; Length 114;

Best Local Similarity 66.7%; Pred. No. 4e+02; Mismatches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
:|||||
Db 24 KTIFFS 29

RESULT 45
ABP33134
ID ABP33134 standard; protein; 115 AA.
XX
AC ABP33134;
XX
DT 09-JUL-2002 (first entry)
XX
DE Human isomerase-like ORF2107 protein, SEQ ID NO:4214.
XX
KW Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnery; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.
XX
OS Homo sapiens.
XX
WO200190366-A2.
XX
PN
XX
PD 29-NOV-2001.
XX
XX
24-MAY-2001; 2001WO-US017076.
XX
XX
24-MAY-2000; 2000US-0206690P.
XX
XX
(CURA-) CURAGEN CORP.
XX
PI Leach MD, Shinkets RA;
XX
WPI; 2002-106200/14.
XX
N-PSDB; ABN77160.
XX
Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation.
XX
Claim 10; Page 1311; 2508pp; English.
XX
Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN79587 represent cDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX polynucleotides or polypeptides, methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haematopoiesis regulation, tissue growth, angiogenesis, activin or inhibin activity, chemotactic/chemokinetic activity, haemostatic activity, thrombolytic activity, receptor/ligand, antiinflammatory activity, tumour inhibition activity, and antiinfective activity, and may also be involved in the determination

Query Match 87.1%; Score 27; DB 4; Length 132;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5
 |||||
 Db 22 KPVFF 26

RESULT 48
 ABG26562
 ID ABG26562 standard; protein; 144 AA.
 XX
 AC ABG26562;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #26553.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
 KW
 XX Homo sapiens.
 OS
 XX WO200175067-A2.
 PN
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US008631.
 PF
 XX 31-MAR-2000; 2000US-00540217.
 PR
 XX 23-AUG-2000; 2000US-00649167.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR
 XX N-PSDB; AAS90749.
 DR
 XX New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
 PT
 PT
 PT
 PT
 PS Claim 20; SEQ ID NO 56921; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The CC polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic CC amino acid sequences of the invention. Note: The sequence data for this CC patent did not appear in the printed specification, but was obtained in CC electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences CC
 XX SQ Sequence 144 AA;

Query Match 87.1%; Score 27; DB 4; Length 144;
 Best Local Similarity 66.7%; Pred. No. 5e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 6
 :|||
 Db 111 RPIFFA 116

RESULT 49
 AAO07503
 ID AAO07503 standard; protein; 146 AA.
 XX
 AC AAO07503;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 21395.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
 KW
 XX Homo sapiens.
 OS
 XX WO200164835-A2.
 PN
 XX 07-SEP-2001.
 PD
 XX 26-FEB-2001; 2001WO-US004927.
 PF
 XX 28-FEB-2000; 2000US-00515126.
 PR
 XX 18-MAY-2000; 2000US-00577409.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX WPI; 2001-514838/56.
 DR
 XX N-PSDB; AAI87434.
 DR
 XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing PT and treating e.g. leukemia, inflammation and immune disorders.
 PT
 PT
 XX Claim 20; SEQ ID NO 21395; 1399pp + Sequence Listing; English.
 PS
 CC The invention relates to human polynucleotides (AAI79941-AAI93941) and CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to CC cytokine cell proliferation or cell differentiation or which may induce CC production of other cytokines in other cell populations. The CC polynucleotides and polypeptides are useful in gene therapy, vaccines or CC peptide therapy. The polypeptides have various cytokine-like activities, CC e.g. stem cell growth factor activity, haematopoiesis regulating CC activity, tissue growth factor activity, immunomodulatory activity and CC activin/inhibin activity and may be useful in the diagnosis and/or CC treatment of cancer, leukaemia, nervous system disorders, arthritis and CC inflammation. Note: The sequence data for this patent did not form part CC of the printed specification, but was obtained in electronic format CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences CC
 XX SQ Sequence 146 AA;

Query Match 87.1%; Score 27; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5
 |||||
 Db 24 KPVFF 28

RESULT 50
 ADQ6558
 ID ADQ6558 standard; protein; 148 AA.

```

XX ADQ66558;
AC
XX 07-OCT-2004 (first entry)
DT
XX Novel human protein sequence #1531.
DE
XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW Gene therapy; diagnostic marker; morbid state; osteoporosis;
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW cancer.
XX
XX Homo sapiens.
OS
XX EP1440981-A2.
PN
XX 28-JUL-2004.
PR
XX 21-JAN-2004; 2004EP-00001196.
PF
XX 21-JAN-2003; 2003JP-00102206.
PR
XX 09-MAY-2003; 2003JP-00131392.
PR
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
PA
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Nagai K, Irie R;
PI
XX WPI; 2004-535376/52.
DR
XX N-PSDB; ADQ64370.
DR
XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
PT
XX Claim 1; SEQ ID NO 3719; 2449pp; English.
PS
XX The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a protein
CC sequence of the invention.
XX
XX Sequence 148 AA;
SQ
Query Match 87.1%; Score 27; DB 8; Length 148;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVF 5
Db 17 KVFVF 21
RESULT 51
AAU27710
ID AAU27710 standard; protein; 173 AA.
AC
XX AAU27710;
XX
XX 18-DEC-2001 (first entry)
DT
XX Human full-length polypeptide sequence #35.
DE
XX Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
KW nervous system disorder; inflammatory disorder; cell differentiation;
KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;

```

```

KW cytostatic; antirheumatic; antiarthritic; vulnery; antiinflammatory;
KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
KW neuroprotective; osteopathic; antidiabetic; antiasthmatic; antiallergic;
KW immunostimulant; analgesic; gene therapy.
XX
XX Homo sapiens.
OS
XX WO200164834-A2.
PN
XX 07-SEP-2001.
PD
XX 26-FEB-2001; 2001WO-US004926.
PF
XX 28-FEB-2000; 2000US-00515126.
PR
XX 18-MAY-2000; 2000US-00577409.
PR
XX 17-JUN-2000; 2000US-00597707.
PR
XX 14-JUL-2000; 2000US-00616807.
PR
XX 19-SEP-2000; 2000US-00664641.
XX
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
XX Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
PI Drmanac R;
PI
XX WPI; 2001-589862/66.
DR
XX N-PSDB; AAS44610.
DR
XX Novel polypeptides and nucleic acids obtained from cDNA libraries
PT prepared from various human tissues, for diagnosis, treatment of cancer,
PT neurological, inflammatory disorders and for use in arrays for detection.
PT
XX Claim 10; SEQ ID NO 207; 153pp; English.
XX
XX Sequences AAU27676-AAU28019 represent full-length polypeptides and contig
CC polypeptides of the invention. The proteins and their associated DNA
CC sequences are useful for the treatment, diagnosis and prevention of
CC various types of disorder in a mammalian subject such as a human, dog,
CC monkey, mouse, hamster or rat. The disorders include cancers such as
CC leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as
CC multiple sclerosis, connective tissue disease, rheumatoid arthritis,
CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
CC Wernicke disease, inflammatory disorders such as nephritis, Crohn's
CC disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
CC bowel disease. The sequences exhibit activity relating to angiogenesis,
CC cell proliferation, cell differentiation, stem cell growth factor,
CC activin or inhibin. Therefore, they can be used to manipulate stem cells
CC in culture to give rise to neuroepithelial cells that can be used to
CC augment or replace cells damaged by illness, accidental damage or genetic
CC disorders. The sequences may also be used for regeneration of bone,
CC cartilage, tendons and ligaments and in tissue repair and burn healing.
CC Note: Some sequences for this patent did not form part of the printed
CC specification, but were obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 173 AA;
SQ
Query Match 87.1%; Score 27; DB 4; Length 173;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVF 5
Db 46 KVFVF 50
RESULT 52
AAU77842
ID AAU77842 standard; protein; 173 AA.
XX
XX AAU77842;
AC

```



```

XX DT 05-JUN-2002 (first entry)
XX DE Oestrogen receptor associated protein 19.03.
XX KW Oestrogen receptor associated protein 19.03; cytostatic; antiinfertility;
XX KW reproductive system; tumour; sex growth impediment.
XX OS Unidentified.
XX PN WO200212317-A1.
XX PD 14-FEB-2002.
XX PF 11-JUN-2001; 2001WO-CN000930.
XX PR 12-JUN-2000; 2000CN-00116442.
XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PI Mao Y, Xie Y;
XX PS WPI; 2002-172145/22.
XX DR N-PSDB; ABK12230.
XX PT Estrogen receptor associated protein 19.03 and encoded polynucleotide,
XX PT used in diagnosis and treatment of reproductive system tumors.
XX PS Claim 1; Page 30; 38pp; Chinese.
XX CC This invention relates to the cDNA and protein sequences of a novel
XX CC isolated protein estrogen receptor associated protein 19.03 and a method
XX CC for producing the protein by recombinant means. The protein of the
XX CC invention may have cytostatic and antiinfertility activities. The DNA and
XX CC protein sequences of the invention may be used in the diagnosis and
XX CC treatment of reproductive system tumors and sex growth impediment in the
XX CC adolescence. The present sequence represents the estrogen receptor
XX CC associated protein 19.03 of the invention
XX SQ Sequence 173 AA;
Query Match 87.1%; Score 27; DB 5; Length 173;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVFVF 5
Db 46 KVFVF 50
RESULT 53
ADJ69976
ID ADJ69976 standard; protein; 173 AA.
AC ADJ69976;
XX 06-MAY-2004 (first entry)
XX DE Human heat mitochondrial protein as a therapeutic target SeqID1782.
XX KW mitochondrial; human; screening assay; diabetes mellitus;
XX KW Huntington's disease; osteoarthritis;
XX KW Leber's hereditary optic neuropathy; LHON;
XX KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
XX KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
XX KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
XX KW osteopathic; ophthalmological; cytostatic.
XX OS Homo sapiens.
XX PN WO2003087768-A2.
XX PD 23-OCT-2003.

```

```

XX PF 04-APR-2003; 2003WO-US010870.
XX PR 12-APR-2002; 2002US-0372843P.
XX PR 17-JUN-2002; 2002US-0389987P.
XX PR 20-SEP-2002; 2002US-0412418P.
XX PA (MITO-) MITOKOR.
XX PA (BUCK-) BUCK INST AGE RES.
XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
XX PI Warnock DE;
XX PD WPI; 2003-845369/78.
XX PT Identifying a mitochondrial target for drug screening assays and for
XX PT treating diseases associated with altered mitochondrial function,
XX PT comprises detecting a modified polypeptide in a sample and correlating
XX PT with the disease.
XX PS Claim 1; SEQ ID NO 1782; 180pp; English.
XX CC This invention relates to novel mitochondrial targets that can be used
XX CC for therapeutic intervention in treating a disease associated with
XX CC altered mitochondrial function. Specifically, it refers to a method for
XX CC identifying proteins of the human heart mitochondrial proteome that are
XX CC useful for drug screening assays, as well as therapeutic targets. The
XX CC present invention describes a method for identifying such proteins that
XX CC can be used in the treatment of various diseases associated with altered
XX CC mitochondrial function including diabetes mellitus, Huntington's disease,
XX CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
XX CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
XX CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
XX CC compositions have neuroprotective, nontropic, antidiabetic,
XX CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
XX CC cytostatic activities. This polypeptide sequence is a human heart
XX CC mitochondrial protein of the invention.
XX SQ Sequence 173 AA;
Query Match 87.1%; Score 27; DB 7; Length 173;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVFVF 5
Db 46 KVFVF 50
RESULT 54
AAG47987
ID AAG47987 standard; protein; 184 AA.
AC AAG47987;
XX 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 60548.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.

```

PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139750P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 02-JUL-1999; 99US-0142154P.
PR 06-JUL-1999; 99US-0142055P.
PR 08-JUL-1999; 99US-0142390P.
PR 09-JUL-1999; 99US-0142803P.
PR 12-JUL-1999; 99US-0142920P.
PR 13-JUL-1999; 99US-0142977P.
PR 14-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144684P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154775P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156566P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.

PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 184;

Best Local Similarity 66.7%; Pred. No. 6.4e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 ||:|:
 Db 29 KFIFFS 34

RESULT 55

ABB38594
 ID AEB38594 standard; protein; 186 AA.

AC AEB38594;

XX 08-SEP-2005 (first entry)

DE L. pneumophila protein SEQ ID NO 2926.

XX detection; infection; Antibacterial; Vaccine.

XX Legionella pneumophila.

OS WO2005049642-A2.

XX 02-JUN-2005.

PF 23-SEP-2004; 2004WO-IB003578.

XX 21-NOV-2003; 2003FR-00013687.

PA (INSP) INST PASTEUR.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.

PA (CNRS) CNRS CENT NAT RECH SCI.

XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;

PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst P, Vandenesch P;

PI Jarraud S;

XX

DR WPI; 2005-388305/40.
 XX New genome of Legionella pneumophila Paris strain and derived
 PT polypeptides, useful for detection or identification of the strain and
 for treatment and prevention of infections.
 XX
 PS Claim 3; SEQ ID NO 2926; 660pp; English.
 XX
 CC The invention relates to an isolated or purified nucleotide sequences (I)
 from Legionella pneumophila Paris strain. (I), and their related
 CC sequences or fragments, are useful as primers and probes for detection
 CC and amplification, including differentiation between the Paris and
 CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
 CC (hybrid) polypeptides (II). (II) are also useful for preparation of
 CC specific antibodies (Ab), also used for detection/identification of
 CC Legionella, and some (I), specifically those involved in synthesis of
 CC surface proteins, are targets for identification of inhibitors. (II), or
 CC vectors that contain (I), are useful as vaccines and immunogenic
 CC compositions, for treatment and prevention of infections by L.
 CC pneumophila. The present sequence represents the amino acid sequence of a
 CC L. pneumophila protein.
 XX
 SQ Sequence 186 AA;

Query Match 87.1%; Score 27; DB 9; Length 186;

Best Local Similarity 66.7%; Pred. No. 6.4e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 :||:
 Db 7 RFIFFA 12

RESULT 56

AAU79255
 ID AAU79255 standard; protein; 189 AA.

AC AAU79255;

XX 13-AUG-2002 (first entry)

XX Human membrane-bound matrix metalloprotease 1 (MT1-MMP) related protein.

XX Membrane-bound matrix metalloprotease; MT-MMP; MT1-MMP; enzyme; human;

KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;

KW cytostatic; antiallergic; nootropic; neuroprotective.

XX Homo sapiens.

XX WO200241000-A1.

XX 23-MAY-2002.

XX 20-NOV-2001; 2001WO-JP010136.

XX 20-NOV-2000; 2000JP-00352491.

XX (DAII-) DAIICHI FINE CHEM CO LTD.

XX Aoki T, Yonezawa K, Fijimoto N, Ogawa M, Iwata K;

XX WPI; 2002-435988/46.

XX Immunoassay method for membrane-bound matrix metalloprotease with

PT quantitation using its antibody, applicable in diagnosis of cancer and

PT cancer metastasis, and in drug development.

XX Disclosure; Fig 9; 93pp; Japanese.

XX The invention relates to a method for quantitative immunoassay of a

CC membrane-bound matrix metalloprotease (MT-MMP), involving using an

CC antibody against MT-MMP selected from groups containing MT-MMPs. The

CC method involves releasing and/or solubilising MT-MMP from a cell membrane

CC among a group of MT-MMPs by using a surfactant and reductant. Such a
 CC method is for detecting a membrane-bound matrix metalloprotease with
 CC quantitation, which is applicable in diagnosis of cancer and cancer
 CC metastasis as well as in drug development, and is also used to monitor
 CC progress of rheumatoid arthritis and Alzheimer's disease. This sequence
 CC represents a human MTL-MMP related protein
 XX

SQ Sequence 189 AA;

Query Match 87.1%; Score 27; DB 5; Length 189;

Best Local Similarity 100.0%; Pred. No. 6.5e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

QY 1 KVFVF 5

Db 60 KVFVF 64
 |||||

RESULT 57

AAU79257
 ID AAU79257 standard; protein; 189 AA.

AC AAU79257;

DT 13-AUG-2002 (first entry)

DE Rat membrane-bound matrix metalloprotease 1 (MT1-MMP) related protein.

KW Membrane-bound matrix metalloprotease; MT-MMP; MT1-MMP; enzyme; rat;
 KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;
 KW cytostatic; antiallergic; neutrotropic; neuroprotective.

OS Rattus sp.

PN WO200241000-A1.

PD 23-MAY-2002.

PF 20-NOV-2001; 2001WO-JP010136.

PR 20-NOV-2000; 2000JP-00352491.

PA (DAIIT-) DAIICHI FINE CHEM CO LTD.

PI Aoki T, Yonezawa K, Fijimoto N, Ogawa M, Iwata K;

DR WPI; 2002-435988/46.

PT Immunoassay method for membrane-bound matrix metalloprotease with
 PT quantitation using its antibody, applicable in diagnosis of cancer and
 PT cancer metastasis, and in drug development.

PS Disclosure; Fig 9; 93pp; Japanese.

CC The invention relates to a method for quantitative immunoassay of a
 CC membrane-bound matrix metalloprotease (MT-MMP), involving using an
 CC antibody against MT-MMP selected from groups containing MT-MMPs. The
 CC method involves releasing and/or solubilising MT-MMP from a cell membrane
 CC among a group of MT-MMPs by using a surfactant and reductant. Such a
 CC method is for detecting a membrane-bound matrix metalloprotease with
 CC quantitation, which is applicable in diagnosis of cancer and cancer
 CC metastasis as well as in drug development, and is also used to monitor
 CC progress of rheumatoid arthritis and Alzheimer's disease. This sequence
 CC represents a rat MT1-MMP related protein

SQ Sequence 189 AA;

Query Match 87.1%; Score 27; DB 5; Length 189;

Best Local Similarity 100.0%; Pred. No. 6.5e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

QY 1 KVFVF 5

|||||

Db 60 KVFVF 64

RESULT 58

AAU79258
 ID AAU79258 standard; protein; 189 AA.

AC AAU79258;

DT 13-AUG-2002 (first entry)

DE Rabbit membrane-bound matrix metalloprotease 1 (MT1-MMP) related protein.

KW Membrane-bound matrix metalloprotease; MT-MMP; MT1-MMP; enzyme; rabbit;
 KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;
 KW cytostatic; antiallergic; neutrotropic; neuroprotective.

OS Oryctolagus cuniculus.

PN WO200241000-A1.

PD 23-MAY-2002.

PF 20-NOV-2001; 2001WO-JP010136.

PR 20-NOV-2000; 2000JP-00352491.

PA (DAIIT-) DAIICHI FINE CHEM CO LTD.

PI Aoki T, Yonezawa K, Fijimoto N, Ogawa M, Iwata K;

DR WPI; 2002-435988/46.

PT Immunoassay method for membrane-bound matrix metalloprotease with
 PT quantitation using its antibody, applicable in diagnosis of cancer and
 PT cancer metastasis, and in drug development.

PS Disclosure; Fig 9; 93pp; Japanese.

CC The invention relates to a method for quantitative immunoassay of a
 CC membrane-bound matrix metalloprotease (MT-MMP), involving using an
 CC antibody against MT-MMP selected from groups containing MT-MMPs. The
 CC method involves releasing and/or solubilising MT-MMP from a cell membrane
 CC among a group of MT-MMPs by using a surfactant and reductant. Such a
 CC method is for detecting a membrane-bound matrix metalloprotease with
 CC quantitation, which is applicable in diagnosis of cancer and cancer
 CC metastasis as well as in drug development, and is also used to monitor
 CC progress of rheumatoid arthritis and Alzheimer's disease. This sequence
 CC represents a rabbit MT1-MMP related protein

SQ Sequence 189 AA;

Query Match 87.1%; Score 27; DB 5; Length 189;

Best Local Similarity 100.0%; Pred. No. 6.5e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

QY 1 KVFVF 5

Db 60 KVFVF 64
 |||||

RESULT 59

AAU79256
 ID AAU79256 standard; protein; 189 AA.

AC AAU79256;

DT 13-AUG-2002 (first entry)

DE Murine membrane-bound matrix metalloprotease 1 (MT1-MMP) related protein.

KW Membrane-bound matrix metalloprotease; MT-MMP; MT1-MMP; enzyme; mouse;
 KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;

KW cytostatic; antiallergic; nootropic; neuroprotective.

XX Mus sp.

XX WO200241000-A1.

XX 23-MAY-2002.

XX 20-NOV-2001; 2001WO-JP010136.

XX 20-NOV-2000; 2000JP-00352491.

XX (DAI-I-) DAIICHI FINE CHEM CO LTD.

XX Aoki T, Yonezawa K, Fijimoto N, Ogawa M, Iwata K;

XX WPI; 2002-435988/46.

XX Immunoassay method for membrane-bound matrix metalloprotease with quantitation using its antibody, applicable in diagnosis of cancer and cancer metastasis, and in drug development.

XX Disclosure; Fig 9; 93pp; Japanese.

XX The invention relates to a method for quantitative immunoassay of a membrane-bound matrix metalloprotease (MT-MMP), involving using an antibody against MT-MMP selected from groups containing MT-MMPs. The method involves releasing and/or solubilising MT-MMP from a cell membrane among a group of MT-MMPs by using a surfactant and reductant. Such a method is for detecting a membrane-bound matrix metalloprotease with quantitation, which is applicable in diagnosis of cancer and cancer metastasis as well as in drug development, and is also used to monitor progress of rheumatoid arthritis and Alzheimer's disease. This sequence represents a mouse MT1-MMP related protein

XX Sequence 189 AA;

Query Match 87.1%; Score 27; DB 5; Length 189;

Best Local Similarity 100.0%; Pred. No. 6.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVPP 5

Db 60 KFVPP 64

RESULT 60

ABM73888

ID ABM73888 standard; protein; 197 AA.

XX ABM73888;

XX 17-OCT-2003 (first entry)

XX DNA clone originating in barley containing SNP sequence #298.

XX Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.

XX Hordeum vulgare.

XX WO2003057877-A1.

XX 17-JUL-2003.

XX 16-DEC-2002; 2002WO-1B005403.

XX 20-DEC-2001; 2001JP-00387059.

XX 20-DEC-2001; 2001JP-00387131.

XX 20-DEC-2001; 2001JP-00403299.

XX 20-DEC-2001; 2001JP-00403300.

XX 27-SEP-2002; 2002JP-00327515.

XX (UTNI-) UNIV JAPAN OKAYAMA.

XX

PI Sato K, Takeda K, Kohara Y;

XX WPI; 2003-587127/55.

XX Single nucleotide polymorphism sites in barley varieties and DNA sequences containing them for analysis and identification of barley varieties and production of barley transformants with desired characteristics.

XX Disclosure; SEQ ID XX; 284pp; Japanese.

XX The present invention relates to oligonucleotide clones originating in barley (Hordeum vulgare) which contain single nucleotide polymorphisms (SNP). The oligonucleotides may be used for analysis of SNPs among barley varieties, identification of particular varieties and genotype-phenotype analysis, isolation of specific genes and creation of new varieties by transformation of barley varieties with them and production of new barley varieties with desired properties. The present sequence represents an oligonucleotide clone sequence featured in the specification. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published-pct-sequences

XX Sequence 197 AA;

Query Match 87.1%; Score 27; DB 7; Length 197;

Best Local Similarity 66.7%; Pred. No. 6.8e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVPPA 6

Db 140 KPIFYA 145

RESULT 61

ABBS2559

ID ABBS2559 standard; protein; 206 AA.

XX AC ABBS2559;

XX 11-FEB-2002 (first entry)

XX Escherichia coli polypeptide SEQ ID NO 489.

XX Escherichia coli; B2/D+A-; antiinflammatory; antibacterial; immunosuppressive; extra-intestinal infection; phylogeny; meningitis; systemic infection; non-diarrhoeal infection; septicaemia; pyelonephritis; antibiotic resistance.

XX OS Escherichia coli.

XX WO200166572-A2.

XX 13-SEP-2001.

XX 12-MAR-2001; 2001WO-EP003445.

XX 10-MAR-2000; 2000EP-00003145.

XX 02-FEB-2001; 2001EP-00001449.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;

XX WPI; 2001-550253/61.

XX A library of DNA fragments of Escherichia coli strains for the phylogenetic determination of a given strain comprises polynucleotides of nature B2/D+A-.

XX Example 6; Fig 6; 646pp; English.

XX

CC The invention relates to a library of DNA fragments of Escherichia coli
 CC strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533) and
 CC encoded proteins (AB852459-AB852919 and AB852954-AB853094) of nature
 CC B2/D-A-. The polynucleotides have potential antiinflammatory,
 CC antibacterial and immunosuppressive activity as part of pharmaceutical
 CC compositions used to treat, palliate or prevent extra-intestinal E. coli
 CC infections. The polypeptides are useful for determining the phylogenetic
 CC group of a given E. coli strain. These polypeptides can detect and treat
 CC an undesired development of E. coli, particularly an extra-intestinal
 CC infection that include systemic and non-diarrhoeal infections such as
 CC septicæmia, pyelonephritis and meningitis this is particularly
 CC advantageous as bacterial resistance is increasing with the more frequent
 CC use of broad spectrum antibiotics
 XX
 SQ Sequence 206 AA;

Query Match 87.1%; Score 27; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 |||||
 Db 25 KVFVF 29

RESULT 62
 ABG22983
 ID ABG22983 standard; protein; 221 AA.
 XX
 AC ABG22983;
 XX

DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #22974.
 XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX

OS Homo sapiens.
 XX

PN WO200175067-A2.
 XX

PD 11-OCT-2001.
 XX

PF 30-MAR-2001; 2001WO-US008631.
 XX

PR 31-MAR-2000; 2000US-00540217.
 XX

PR 23-AUG-2000; 2000US-00649167.
 XX

PA (HYSE-) HYSEQ INC.
 XX

PI Drmanac RT, Liu C, Tang YT;
 XX

XX WPI; 2001-639362/73.
 DR N-PSDB; AAS87170.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX

PS Claim 20; SEQ ID NO 53342; 103pp; English.
 XX

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 221 AA;

Query Match 87.1%; Score 27; DB 4; Length 221;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 |||||
 Db 36 KVFVF 40

RESULT 63
 ABG06994
 ID ABG06994 standard; protein; 221 AA.
 XX

AC ABG06994;
 XX

DT 13-FEB-2002 (first entry)
 XX

DE Novel human diagnostic protein #6985.
 XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX

OS Homo sapiens.
 XX

PN WO200175067-A2.
 XX

PD 11-OCT-2001.
 XX

PF 30-MAR-2001; 2001WO-US008631.
 XX

PR 31-MAR-2000; 2000US-00540217.
 XX

PR 23-AUG-2000; 2000US-00649167.
 XX

PA (HYSE-) HYSEQ INC.
 XX

PI Drmanac RT, Liu C, Tang YT;
 XX

XX WPI; 2001-639362/73.
 DR N-PSDB; AAS71181.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX

PS Claim 20; SEQ ID NO 37353; 103pp; English.
 XX

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. NOTE: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

XX SQ Sequence 221 AA;

Query Match 87.1%; Score 27; DB 4; Length 221;
 Best Local Similarity 83.3%; Pred. No. 7.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6

Db 11 EFVFFA 16

RESULT 64

ADH45453
 ID ADH45453 standard; protein; 227 AA.

XX AC ADH45453;

XX DT 25-MAR-2004 (first entry)

XX DE Human molecule useful for disease detection and treatment, SEQ ID NO 47.

XX KW human; molecule; disease detection; treatment; MDDT; cytostatic;
 KW antiarteriosclerotic; anti-HIV; anti-allergic; cerebroprotective;
 KW antiparkinsonian; anticonvulsant; nootropic; neuroprotective;
 KW antiinflammatory; ophthalmological; antithyroid; antiarthritic;
 KW antibacterial; virucide; protozoacide; antiparasitic; fungicide;
 KW anorectic; cardiant; hypotensive; antiinfertility; hepatotropic;
 KW gene therapy.

XX OS Homo sapiens.

XX PN WO2003093427-A2.

XX PD 13-NOV-2003.

XX PF 30-APR-2003; 2003WO-US013629.

XX PR 30-APR-2002; 2002US-0376988P.

XX PR 14-JUN-2002; 2002US-0389095P.

XX PR 22-AUG-2002; 2002US-0405860P.

XX PR 27-AUG-2002; 2002US-0406512P.

XX PA (INCY-) INCYTE CORP.

XX PI Swarnakar A, Tran UK, Khare R, Marquis JP, Hafalia AJA;

XX PI Elliott VS, Becha SD, Ramkumar J, Kable AE, Wilson AD, Yue H;

XX PI Forsythe IJ, Griffin JA, Bulloch SA, Jin P, Jiang X, Jackson AA;

XX PI Mason PM, Chawla NK, Chang H, Richardson TW, Tang YT, Lee SY;

XX PI Gietzen KJ, Fu GK;

XX DR WPI; 2004-022653/02.

XX DR N-PSDB; ADH45507.

XX PT New human molecules for disease detection and treatment (MDDT) and
 PT encoding polynucleotides, useful for diagnosing, preventing or treating
 PT diseases associated with aberrant MDDT expression, e.g. cancer, stroke,
 PT obesity or AIDS.
 XX

XX PS Claim 1; SEQ ID NO 47; 267pp; English.

XX CC The invention relates to human molecules useful for disease detection and
 CC treatment (MDDT) and also the polynucleotides which encode and identify
 CC and encode MDDT. The MDDT polypeptides and encoding polynucleotides have

CC the following activities: cytostatic, antiarteriosclerotic, anti-HIV,
 CC antiallergic, cerebroprotective, antiparkinsonian, anticonvulsant,
 CC nootropic, neuroprotective, antiinflammatory, ophthalmological,
 CC antithyroid, antiarthritic, antibacterial, virucide, protozoacide,
 CC antiparasitic, fungicide, anorectic, cardiant, hypotensive,
 CC antiinfertility, and hepatotropic. The MDDT polynucleotide may be used in
 CC gene therapy to treat disorders. The polypeptides and polynucleotides are
 CC useful in diagnosing, preventing or treating diseases or conditions
 CC associated with the decreased expression or overexpression of MDDT, such
 CC as autoimmune/inflammatory disorders (AIDS, allergies, atopic dermatitis,
 CC arthritis or thyroiditis), infections (e.g. bacterial, viral, parasitic,
 CC protozoal or fungal), metabolic disorders (e.g. obesity), reproductive
 CC disorders (e.g. infertility), neurological disorders (Parkinson's
 CC disease, Alzheimer's disease, stroke, epilepsy), cardiovascular disorders
 CC (e.g. myocardial infarction or hypertension), eye disorders, or cell
 CC proliferative diseases (e.g. cancer, atherosclerosis, hepatitis). These
 CC are also useful in assessing the effects of exogenous compounds on the
 CC expression of nucleic acid and amino acid sequences of MDDT. The MDDT or
 CC its fragments are useful in screening compounds for effectiveness as
 CC agonist or antagonist of the polypeptides, or in altering the expression
 CC of the target polynucleotide and compounds that specifically bind to or
 CC modulate the activity of the polypeptide. The microarray of the invention
 CC is useful in monitoring or measuring protein-protein interactions, drug-
 CC target interactions, and gene expression profiles. This sequence
 CC represents an MDDT polypeptide of the invention.
 XX

XX SQ Sequence 227 AA;

Query Match 87.1%; Score 27; DB 8; Length 227;

Best Local Similarity 100.0%; Pred. No. 7.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5

Db 32 KPVFF 36

RESULT 65

ABM91660
 ID ABM91660 standard; protein; 238 AA.

XX AC ABM91660;

XX DT 02-JUN-2005 (first entry)

XX DE M. xanthus protein sequence, seq id 10859.

XX KW Transgenic plant; DNA replication; gene regulation; gene expression.

XX OS Myxococcus xanthus.

XX PN US6833447-B1.

XX PD 21-DEC-2004.

XX PF 10-JUL-2001; 2001US-00902540.

XX PR 10-JUL-2000; 2000US-0217883P.

XX PA (MONS) MONSANTO TECHNOLOGY LLC.

XX PI Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;

XX DR WPI; 2005-028716/03.

XX PT New substantially purified Myxococcus xanthus nucleic acid molecule
 PT encoding a nitrite reductase, useful for determining gene expression,
 PT identifying mutations in a gene of interest, and for constructing
 PT mutations in a gene of interest.
 XX

XX PS Example 2; SEQ ID NO 10859; 25pp; English.

XX CC The invention relates to a substantially purified nucleic acid molecule

CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
 CC recombinant DNA construct for expression of a nitrite reductase gene in a
 CC plant cell, and a plant cell comprising the recombinant DNA construct.
 CC The nucleic acid is useful for determining gene expression, identifying
 CC mutations in a gene of interest, and for constructing mutations in a gene
 CC of interest. Sequences given in records for SEQ IDs 9692-16825 represent
 CC a group of 7134 *Mycococcus xanthus* proteins and peptides. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 XX
 XX Sequence 238 AA;

Query Match 87.1%; Score 27; DB 9; Length 238;
 Best Local Similarity 100.0%; Pred. No. 8.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 Db 132 KVFVF 136

RESULT 66
 ABP40600
 ID ABP40600 standard; protein; 240 AA.
 XX
 AC ABP40600;
 XX
 XX 24-JUL-2002 (first entry)
 XX
 XX Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5445.

DE Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 XX antibacterial; gene therapy.
 KW Staphylococcus epidermidis.
 XX

OS Staphylococcus epidermidis.
 XX

XX US6380370-B1.
 FN

XX 30-APR-2002.
 PD

XX 13-AUG-1998; 98US-00134001.
 PF

XX 14-AUG-1997; 97US-0055779P.
 XX

PR 08-NOV-1997; 97US-0064964P.
 PR

XX (GENO-) GENOME THERAPEUTICS CORP.
 XX

XX Doucette-Stamm LA, Bush D;
 PI

XX WPI; 2002-381255/41.
 XX

DR N-PSDB; ABN93145.
 DR

XX Novel isolated nucleic acid encoding a Staphylococcus epidermis
 PT polypeptide, useful for diagnosing and treating bacterial infections.
 PT

XX Disclosure; SEQ ID NO 5445; 267pp; English.
 XX

PS ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
 CC antibacterial activity and can be used in gene therapy. The sequences can
 CC also be used in the diagnosis and treatment of bacterial infections,
 CC particularly S. epidermidis infections. The sequences can be used to
 CC screen for compounds able to interfere with the S. epidermidis life cycle
 CC or inhibit S. epidermidis infection. N.B. The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from the USPTO web site
 XX

XX Sequence 240 AA;

Query Match 87.1%; Score 27; DB 5; Length 240;
 Best Local Similarity 83.3%; Pred. No. 8.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 Db 168 QVFVFA 173

RESULT 67

ADS07805

ID ADS07805 standard; protein; 240 AA.

XX ADS07805;

XX 04-NOV-2004 (first entry)

XX Staphylococcus epidermis polypeptide seqid 7100.

XX antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;
 KW recombinant expression vector; infection; computer readable medium;
 KW computer based system.

XX Staphylococcus epidermidis.

XX US2004147734-A1.

XX 29-JUL-2004.

XX 01-DEC-2003; 2003US-00724972.

XX 08-NOV-1997; 97US-0064964P.

XX 13-AUG-1998; 98US-00134001.

XX 29-NOV-1999; 99US-00450969.

XX (DOUC/) DOUCETTE-STAMM L.

XX (BUSH/) BUSH D.

XX Doucette-Stamm L, Bush D;

XX WPI; 2004-580138/56.

XX N-PSDB; ADS04033.

XX New isolated polypeptide and encoding nucleic acid derived from
 PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or
 PT treating an S. epidermidis bacterial infection.

XX Claim 17; SEQ ID NO 7100; 741pp; English.

XX The invention describes an isolated nucleic acid comprising a nucleotide
 CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:
 CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any
 CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as
 CC given in the specification. Also described are: a recombinant expression
 CC vector; a cell comprising a recombinant expression vector of (1);
 CC producing an S. epidermidis polypeptide; an isolated nucleic acid
 CC comprising a nucleotide sequence of at least 8 nucleotides in length; a
 CC vaccine composition for prevention or treatment of an S. epidermidis
 CC infection, comprising a nucleic acid cited above and a carrier; treating
 CC a subject for S. epidermidis infection; a recombinant or substantially
 CC pure preparation of an S. epidermidis polypeptide or its fragment; a
 CC vaccine composition for prevention or treatment of an S. epidermidis
 CC infection; detecting the presence of a Staphylococcus nucleic acid in a
 CC sample; a computer readable medium having recorded in it the nucleotide
 CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based
 CC system for identifying fragments of the Staphylococcus genome of
 CC commercial importance; a computer based system for identifying fragments
 CC of the Staphylococcus plasmids of commercial importance; identifying
 CC commercially important nucleic acid fragments of the Staphylococcus
 CC genome and/or plasmids; and identifying an expression modulating fragment
 CC of the Staphylococcus genome and/or plasmids. The methods and
 CC compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of an Staphylococcal epidermidis bacterial
 CC infection. This is the amino acid sequence of a S. epidermidis protein of
 CC the invention.

XX


```
SQ Sequence 240 AA;
Query Match      87.1%; Score 27; DB 8; Length 240;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFPEFA 6
Db      168 QVFPEFA 173

RESULT 68
AAG10914
ID AAG10914 standard; protein; 248 AA.
XX AC AAG10914;
XX AC AAG10914;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 9429.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hydriisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 18-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137503P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 24-JUN-1999; 99US-0140354P.
PR 28-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142820P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 28-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
```

PR 09-AUG-1999;	99US-0147935P.	Db	: :	206 KEIFYA 211
PR 10-AUG-1999;	99US-0148171P.			
PR 11-AUG-1999;	99US-0148319P.			
PR 12-AUG-1999;	99US-0148341P.			
PR 13-AUG-1999;	99US-0148565P.			
PR 13-AUG-1999;	99US-0148584P.			
PR 16-AUG-1999;	99US-0149368P.			
PR 17-AUG-1999;	99US-0149175P.			
PR 18-AUG-1999;	99US-0149426P.			
PR 20-AUG-1999;	99US-0149722P.			
PR 20-AUG-1999;	99US-0149829P.			
PR 23-AUG-1999;	99US-0149902P.			
PR 23-AUG-1999;	99US-0149930P.			
PR 25-AUG-1999;	99US-0150566P.			
PR 26-AUG-1999;	99US-0150884P.			
PR 27-AUG-1999;	99US-0151065P.			
PR 27-AUG-1999;	99US-0151066P.			
PR 27-AUG-1999;	99US-0151080P.			
PR 30-AUG-1999;	99US-0151303P.			
PR 31-AUG-1999;	99US-0151438P.			
PR 01-SEP-1999;	99US-0151930P.			
PR 07-SEP-1999;	99US-0152363P.			
PR 10-SEP-1999;	99US-0153070P.			
PR 13-SEP-1999;	99US-0153758P.			
PR 15-SEP-1999;	99US-0154018P.			
PR 16-SEP-1999;	99US-0154039P.			
PR 20-SEP-1999;	99US-0154779P.			
PR 22-SEP-1999;	99US-0155139P.			
PR 23-SEP-1999;	99US-0155486P.			
PR 24-SEP-1999;	99US-0155659P.			
PR 28-SEP-1999;	99US-0156458P.			
PR 29-SEP-1999;	99US-0156596P.			
PR 04-OCT-1999;	99US-0157117P.			
PR 05-OCT-1999;	99US-0157753P.			
PR 06-OCT-1999;	99US-0157865P.			
PR 07-OCT-1999;	99US-0158029P.			
PR 08-OCT-1999;	99US-0158232P.			
PR 12-OCT-1999;	99US-0158369P.			
PR 13-OCT-1999;	99US-0159293P.			
PR 13-OCT-1999;	99US-0159294P.			
PR 14-OCT-1999;	99US-0159429P.			
PR 14-OCT-1999;	99US-0159330P.			
PR 14-OCT-1999;	99US-0159331P.			
PR 14-OCT-1999;	99US-0159637P.			
PR 14-OCT-1999;	99US-0159638P.			
PR 18-OCT-1999;	99US-0159864P.			
PR 21-OCT-1999;	99US-0160741P.			
PR 21-OCT-1999;	99US-0160767P.			
PR 21-OCT-1999;	99US-0160768P.			
PR 21-OCT-1999;	99US-0160770P.			
PR 21-OCT-1999;	99US-0160814P.			
PR 21-OCT-1999;	99US-0160815P.			
PR 22-OCT-1999;	99US-0160980P.			
PR 22-OCT-1999;	99US-0160981P.			
PR 22-OCT-1999;	99US-0160989P.			
PR 25-OCT-1999;	99US-0161404P.			
PR 25-OCT-1999;	99US-0161405P.			
PR 25-OCT-1999;	99US-0161406P.			
PR 26-OCT-1999;	99US-0161359P.			
PR 26-OCT-1999;	99US-0161360P.			
PR 26-OCT-1999;	99US-0161361P.			
PR 28-OCT-1999;	99US-0161920P.			
PR 28-OCT-1999;	99US-0161922P.			
PR 28-OCT-1999;	99US-0161933P.			
PR 29-OCT-1999;	99US-0162142P.			
<p>Query Match 87.1%; Score 27; DB 3; Length 248; Best Local Similarity 66.7%; Pred. No. 8.5e+02; Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;</p>				
<p>1 KVFVFA 6</p>				
PR 09-AUG-1999;	99US-0147935P.	Db	: :	206 KEIFYA 211
PR 10-AUG-1999;	99US-0148171P.			
PR 11-AUG-1999;	99US-0148319P.			
PR 12-AUG-1999;	99US-0148341P.			
PR 13-AUG-1999;	99US-0148565P.			
PR 13-AUG-1999;	99US-0148584P.			
PR 16-AUG-1999;	99US-0149368P.			
PR 17-AUG-1999;	99US-0149175P.			
PR 18-AUG-1999;	99US-0149426P.			
PR 20-AUG-1999;	99US-0149722P.			
PR 20-AUG-1999;	99US-0149829P.			
PR 23-AUG-1999;	99US-0149902P.			
PR 23-AUG-1999;	99US-0149930P.			
PR 25-AUG-1999;	99US-0150566P.			
PR 26-AUG-1999;	99US-0150884P.			
PR 27-AUG-1999;	99US-0151065P.			
PR 27-AUG-1999;	99US-0151066P.			
PR 27-AUG-1999;	99US-0151080P.			
PR 30-AUG-1999;	99US-0151303P.			
PR 31-AUG-1999;	99US-0151438P.			
PR 01-SEP-1999;	99US-0151930P.			
PR 07-SEP-1999;	99US-0152363P.			
PR 10-SEP-1999;	99US-0153070P.			
PR 13-SEP-1999;	99US-0153758P.			
PR 15-SEP-1999;	99US-0154018P.			
PR 16-SEP-1999;	99US-0154039P.			
PR 20-SEP-1999;	99US-0154779P.			
PR 22-SEP-1999;	99US-0155139P.			
PR 23-SEP-1999;	99US-0155486P.			
PR 24-SEP-1999;	99US-0155659P.			
PR 28-SEP-1999;	99US-0156458P.			
PR 29-SEP-1999;	99US-0156596P.			
PR 04-OCT-1999;	99US-0157117P.			
PR 05-OCT-1999;	99US-0157753P.			
PR 06-OCT-1999;	99US-0157865P.			
PR 07-OCT-1999;	99US-0158029P.			
PR 08-OCT-1999;	99US-0158232P.			
PR 12-OCT-1999;	99US-0158369P.			
PR 13-OCT-1999;	99US-0159293P.			
PR 13-OCT-1999;	99US-0159294P.			
PR 14-OCT-1999;	99US-0159429P.			
PR 14-OCT-1999;	99US-0159330P.			
PR 14-OCT-1999;	99US-0159331P.			
PR 14-OCT-1999;	99US-0159637P.			
PR 14-OCT-1999;	99US-0159638P.			
PR 18-OCT-1999;	99US-0159864P.			
PR 21-OCT-1999;	99US-0160741P.			
PR 21-OCT-1999;	99US-0160767P.			
PR 21-OCT-1999;	99US-0160768P.			
PR 21-OCT-1999;	99US-0160770P.			
PR 21-OCT-1999;	99US-0160814P.			
PR 21-OCT-1999;	99US-0160815P.			
PR 22-OCT-1999;	99US-0160980P.			
PR 22-OCT-1999;	99US-0160981P.			
PR 22-OCT-1999;	99US-0160989P.			
PR 25-OCT-1999;	99US-0161404P.			
PR 25-OCT-1999;	99US-0161405P.			
PR 25-OCT-1999;	99US-0161406P.			
PR 26-OCT-1999;	99US-0161359P.			
PR 26-OCT-1999;	99US-0161360P.			
PR 26-OCT-1999;	99US-0161361P.			
PR 28-OCT-1999;	99US-0161920P.			
PR 28-OCT-1999;	99US-0161922P.			
PR 28-OCT-1999;	99US-0161933P.			
PR 29-OCT-1999;	99US-0162142P.			
PR 25-FEB-2000;	2000EP-00301439.			
PR 25-FEB-1999;	99US-0121825P.			
PR 05-MAR-1999;	99US-0123180P.			
PR 09-MAR-1999;	99US-0123548P.			
PR 23-MAR-1999;	99US-0125788P.			
PR 25-MAR-1999;	99US-0126264P.			
PR 29-MAR-1999;	99US-0126785P.			
PR 01-APR-1999;	99US-0127462P.			
PR 06-APR-1999;	99US-0128234P.			
PR 08-APR-1999;	99US-0128714P.			
PR 16-APR-1999;	99US-0129845P.			
PR 19-APR-1999;	99US-0130077P.			
PR 21-APR-1999;	99US-0130449P.			
PR 23-APR-1999;	99US-0130510P.			
PR 23-APR-1999;	99US-0130891P.			
PR 28-APR-1999;	99US-0131445P.			
PR 30-APR-1999;	99US-0132048P.			
PR 30-APR-1999;	99US-0132407P.			
PR 04-MAY-1999;	99US-0132484P.			
PR 05-MAY-1999;	99US-0132485P.			
PR 06-MAY-1999;	99US-0132486P.			
PR 06-MAY-1999;	99US-0132487P.			
PR 07-MAY-1999;	99US-0132863P.			
PR 11-MAY-1999;	99US-0134256P.			
PR 14-MAY-1999;	99US-0134218P.			
PR 14-MAY-1999;	99US-0134219P.			
PR 14-MAY-1999;	99US-0134221P.			
PR 14-MAY-1999;	99US-0134370P.			
PR 18-MAY-1999;	99US-0134768P.			
PR 19-MAY-1999;	99US-0134941P.			
PR 20-MAY-1999;	99US-0135124P.			
PR 21-MAY-1999;	99US-0135353P.			
PR 24-MAY-1999;	99US-0135629P.			
PR 25-MAY-1999;	99US-0136021P.			
PR 27-MAY-1999;	99US-0136392P.			
PR 28-MAY-1999;	99US-0136782P.			
PR 01-JUN-1999;	99US-0137222P.			
PR 03-JUN-1999;	99US-0137528P.			
PR 04-JUN-1999;	99US-0137503P.			
PR 07-JUN-1999;	99US-0137724P.			
PR 08-JUN-1999;	99US-0138094P.			
PR 10-JUN-1999;	99US-0138540P.			
PR 10-JUN-1999;	99US-0138847P.			
PR 14-JUN-1999;	99US-0139119P.			
PR 16-JUN-1999;	99US-0139452P.			
PR 16-JUN-1999;	99US-0139453P.			
PR 17-JUN-1999;	99US-0139492P.			
PR 18-JUN-1999;	99US-0139454P.			

PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 28-JUN-1999; 99US-0140981P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 27-JUL-1999; 99US-0145951P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149369P.

PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 23-AUG-1999; 99US-0150566P.
PR 25-AUG-1999; 99US-0150884P.
PR 26-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 11-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 252;
Best Local Similarity 66.7%; Pred. No. 8.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPPA 6
Db 210 KPIFYA 215

RESULT 70
AAG10912
ID AAG10912 standard; protein; 270 AA.

XX AAG10912; PR 18-JUN-1999; 99US-0139462P.
AC PR 18-JUN-1999; 99US-0139463P.
XX PR 18-JUN-1999; 99US-0139750P.
DT PR 18-JUN-1999; 99US-0139763P.
XX PR 21-JUN-1999; 99US-0139817P.
DE PR 22-JUN-1999; 99US-0139899P.
XX PR 23-JUN-1999; 99US-0140353P.
KW PR 24-JUN-1999; 99US-0140354P.
KW PR 24-JUN-1999; 99US-0140695P.
XX PR 28-JUN-1999; 99US-0140823P.
KW PR 29-JUN-1999; 99US-0140991P.
OS PR 30-JUN-1999; 99US-0141287P.
XX PR 01-JUL-1999; 99US-0141842P.
PN PR 01-JUL-1999; 99US-0142154P.
XX PR 02-JUL-1999; 99US-0142055P.
PD PR 06-JUL-1999; 99US-0142390P.
XX PR 08-JUL-1999; 99US-0142803P.
XX PR 09-JUL-1999; 99US-0142920P.
XX PR 12-JUL-1999; 99US-0142977P.
XX PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144384P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147491P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 23-AUG-1999; 99US-0149930P.

XX 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9427.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132487P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.

PR 25-AUG-1999; 99US-0150566P.
 PR 26-AUG-1999; 99US-0150884P.
 PR 27-AUG-1999; 99US-0151065P.
 PR 27-AUG-1999; 99US-0151066P.
 PR 27-AUG-1999; 99US-0151080P.
 PR 30-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151930P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
 PR 16-SEP-1999; 99US-0154039P.
 PR 20-SEP-1999; 99US-0154779P.
 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-015659P.
 PR 28-SEP-1999; 99US-0156458P.
 PR 29-SEP-1999; 99US-0156596P.
 PR 04-OCT-1999; 99US-0157117P.
 PR 05-OCT-1999; 99US-0157753P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161992P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 270;
 Best Local Similarity 66.7%; Pred. NO. 9.2e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
 |||:|:
 DB 228 KPIFYA 233

RESULT 71
 AAU80872
 ID AAU80872 standard; protein; 297 AA.
 XX
 AC AAU80872;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human CLAN NACHT.
 XX

QY 1 KPVFFA 6
 |||:|:
 DB 228 KPIFYA 233

KW Caspase recruitment domain; CARD; NB-ARC; ANGIO-R; LRR; SAM;
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
 KW leukemia; allergy; arthritis; lupus; Schrogen's syndrome;
 KW Crohn's disease; graft-versus-host disease; stroke;
 KW myocardial infarction; heart failure; neurodegenerative disease;
 KW Parkinson's disease; Alzheimer's disease; HIV;
 KW human immunodeficiency virus infection.

OS Homo sapiens.

XX WO200190156-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US017158.

XX 24-MAY-2000; 2000US-00579240.

PR 10-OCT-2000; 2000US-00686347.

PR 14-MAR-2001; 2001US-0275980P.

XX 23-MAY-2001; 2001US-00864921.

PA (BURN-) BURNHAM INST.

XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;

PI Oliveira VAM, Hayashi H, Pawlowski K;

XX WPI; 2002-083086/11.

DR N-PSDB; ABK22766.

XX New caspase recruitment domain (CARD)-containing polypeptides and

PS Claim 9; Page 201-202; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD) -
 containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
 from it, and the polynucleotides encoding them. Also included are a
 recombinant vector comprising the polynucleotide, recombinant cells
 containing the vector (e.g. bacteria, yeast, plant, animal, mammalian and
 insect cells) and an anti-CARD antibody. The CARD-containing polypeptide
 CC and CARD-encoding nucleic acid are useful for treating a pathology
 CC characterised by abnormal cell proliferation (e.g. cancer), abnormal cell
 CC death (apoptosis), autoimmune diseases or inflammation. In particular,
 CC the polypeptide and nucleic acid are useful for treating keratinocyte
 CC hyperplasia, inflammatory hyperplasia, fibrosis, smooth muscle cell
 CC proliferation in arteries following balloon angioplasty (restenosis),
 CC gliomas, carcinomas, sarcomas, melanomas, leukemias, allergies,
 CC arthritis, lupus, Schrogen's syndrome, Crohn's disease, graft-versus-host
 CC diseases, stroke, myocardial infarction, heart failure, neurodegenerative
 CC diseases (e.g. Parkinson's disease or Alzheimer's disease) or
 CC immunodeficiency associated disease (e.g. human immunodeficiency virus
 CC (HIV) infection). The nucleic acids are useful in a variety of diagnostic
 CC applications. The present sequence is a CARD domain containing protein

XX Sequence 297 AA;

Query Match 87.1%; Score 27; DB 5; Length 297;
 Best Local Similarity 100.0%; Pred. NO. 1e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
 |||:
 DB 38 KPVFF 42

RESULT 72
 ABU81731
 ID ABU81731 standard; protein; 297 AA.

XX AC ABU81731;
 XX DT 26-JUN-2003 (first entry)
 XX DE Human caspase recruitment domain-containing polypeptide #15.
 XX KW Human; caspase recruitment domain-containing polypeptide; CARD; NB-ARC;
 KW ANGIO-R; leucine rich repeat; LRR; S-adenosyl methionine domain;
 KW apoptosis; NF-kappaB induction; cytokine processing; SAM; transcription;
 KW cJun N-terminal kinase induction; caspase-mediated proteolysis; cancer;
 KW inflammation; cell adhesion; cell proliferation; abnormal cell death;
 KW keratinocyte hyperplasia; neoplasia; benign prostatic hypertrophy; lupus;
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
 KW angioplasty; artery; keloid; restenosis; autoimmune disease; allergy;
 KW arthritis; Sjogren's syndrome; Crohn's disease; ulcerative colitis;
 KW allograft rejection; graft versus host disease; myocardial infarction;
 KW heart failure; neurodegenerative disease; stroke; HIV.
 XX OS Homo sapiens.
 XX US2002176853-A1.
 XX 28-NOV-2002.
 XX 23-MAY-2001; 2001US-00864921.
 XX 24-MAY-2000; 2000US-0325756P.
 XX 10-OCT-2000; 2000US-0367337P.
 XX 14-MAR-2001; 2001US-0275980P.
 XX (REED/) REED J C.
 XX (PIOF/) PIO F F.
 XX (GODZ/) GODZIK A.
 XX (STEH/) STEHLIK C.
 XX (DAMI/) DAMIANO J S.
 XX (LEES/) LEE S H.
 XX (OLIV/) OLIVEIRA V A.
 XX (HAYA/) HAYASHI H.
 XX (PAWL/) PAWLOWSKI K.
 XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
 XX Oliveira VA, Hayashi H, Pawlowski K;
 XX WPI; 2002-083086/11.
 XX N-PSDB; ACA68180.
 XX New caspase recruitment domain (CARD)-containing polypeptides and
 XX encoding nucleic acids, useful for treating abnormal cell proliferation
 XX or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
 XX arthritis or stroke.
 XX Claim 1; Page 85-86; 106pp; English.
 XX The invention relates to an isolated caspase recruitment domain (CARD)-
 XX containing polypeptide, or its CARD, NB-ARC, ANGIO-R, leucine rich repeat
 XX (LRR) or S-adenosyl methionine (SAM) domain, and its associated
 XX polynucleotide. The DNA is useful for altering the level of a biochemical
 XX process (including apoptosis, NF-kappaB induction, cytokine processing,
 XX cJun N-terminal kinase induction, caspase-mediated proteolysis,
 XX transcription, inflammation and cell adhesion) modulated by the DNA. The
 XX sequences are useful for treating a pathology characterised by abnormal
 XX cell proliferation, abnormal cell death or inflammation. The treatable
 XX diseases include cancer, keratinocyte hyperplasia, neoplasia, keloids,
 XX benign prostatic hypertrophy, inflammatory hyperplasia, fibrosis, smooth
 XX muscle cell proliferation in arteries following angioplasty, restenosis,
 XX autoimmune diseases including allergies, inflammatory diseases including
 XX arthritis, lupus, Sjogren's syndrome, Crohn's disease, ulcerative
 XX colitis, allograft rejection such as graft versus host disease, stroke,
 XX myocardial infarction, heart failure, neurodegenerative diseases such as
 XX Parkinson's disease and Alzheimer's disease and immunodeficiency
 XX associated diseases such as human immunodeficiency virus (HIV) infection.
 XX Sequences ABU81714-ABU81735 represent human CARD-containing polypeptides

CC of the invention
 XX Sequence 297 AA;
 SQ
 Query Match 87.1%; Score 27; DB 5; Length 297;
 Best Local Similarity 100.0%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;
 QY 1 KPVFF 5
 |||||
 DB 38 KPVFF 42
 RESULT 73
 ADP47907
 ID ADP47907 standard; protein; 312 AA.
 XX AC ADP47907;
 XX 12-AUG-2004 (first entry)
 XX Human CATERPILLER Ipaf nucleotide binding domain (NBD) protein.
 XX Monarch-1; CATERPILLER 11.2; caspase recruitment domain;
 KW CARD, transcription enhancer, R-binding, pyrin, lots of leucine repeat;
 KW CATERPILLER 11.3; CATERPILLER 16.1; CATERPILLER 16.2; CIAS1;
 KW cold-induced autoinflammatory syndrome 1; antiinflammatory; cytostatic;
 KW inflammatory disease; cancer; gene therapy; human; purine;
 KW nucleotide binding domain; NBD; Ipaf.
 XX OS Homo sapiens.
 XX WO2004034093-A2.
 XX 22-APR-2004.
 XX 30-APR-2003; 2003WO-US013562.
 XX 30-APR-2002; 2002US-0376626P.
 XX (UYNC-) UNIV NORTH CAROLINA.
 XX Ting JY, Linhoff MW, Harton JA, Williams KL, Lich J, O'Connor W;
 XX Moore CB, Davis B, Brickey J, Conti B, Zhang J, Zhu X;
 XX WPI; 2004-348215/32.
 XX New nucleic acid encoding Monarch-1, CATERPILLER 11.2, CATERPILLER 11.3,
 XX CATERPILLER 16.1, CATERPILLER 16.2 or CIAS1 polypeptide, useful in
 XX preparing a composition for treating inflammatory disease or cancer.
 XX Example 1; Fig 3; 205pp; English.
 XX The invention relates to a novel isolated nucleic acid encoding a Monarch
 XX -1, CATERPILLER (CARD [caspase recruitment domain], transcription
 XX enhancer, R(purine)-binding, pyrin, lots of leucine repeats) 11.2,
 XX CATERPILLER 11.3, CATERPILLER 16.1, CATERPILLER 16.2 or CIAS1 (cold-
 XX induced autoinflammatory syndrome 1) polypeptide comprising the amino
 XX acids encoded by exon 6 and lacking the amino acids encoded by exon 4 or
 XX its fragment. The nucleic acid of the invention demonstrates
 XX antiinflammatory and cytostatic activities and may be useful in preparing
 XX a composition for treating an inflammatory disease or cancer, possibly
 XX via gene therapy. The current sequence is that of a human CATERPILLER
 XX nucleotide binding domain (NBD) protein of the invention.
 XX Sequence 312 AA;
 SQ
 Query Match 87.1%; Score 27; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVFF 5
 |||||

Db 51 KVFVF 55

RESULT 74
AAG33404
ID AAG33404 standard; protein; 313 AA.
XX AAG33404;
AC AAG33404;
XX 18-OCT-2000 (first entry)
XX Zea mays protein fragment SEQ ID NO: 40468.
DE Zea mays protein fragment SEQ ID NO: 40468.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; generic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX Zea mays subsp. mays.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130501P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137503P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 21-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 23-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145242P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.

```
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 18-OCT-1999; 99US-0159584P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
Db 86 KVVFF 90

RESULT 75
ADT58396
ID ADT58396 standard; protein; 335 AA.
XX
```

```
AC ADT58396;
XX 13-JAN-2005 (first entry)
XX Plant polypeptide, SEQ ID 8473.
XX
XX Plant; transgenic; cold tolerance; growth rate; drought tolerance;
XX disease resistance; galactomannan production; plant growth regulator;
XX heat tolerance; herbicide tolerance; lignin production;
XX extreme osmotic condition tolerance; pathogens resistance;
XX pest resistance; yield improvement; seed oil yield; seed protein yield.
XX Viridiplantae.
OS
XX US2004216190-A1.
XX
XX 28-OCT-2004.
XX
XX 18-DEC-2003; 2003US-00739930.
XX
XX 28-APR-2003; 2003US-00424599.
XX 28-APR-2003; 2003US-00425115.
XX (KOVA/) KOVALIC D K.
XX
XX Kovalic DK;
XX
XX WPI; 2004-757369/74.
XX
XX New recombinant DNA constructs useful in the field of biochemistry and
XX genetics, and in particular for producing transgenic plants with improved
XX biological characteristics.
XX
XX Claim 2; SEQ ID NO 8473; 14pp; English.
XX
XX The invention relates a recombinant DNA construct comprising a
XX polynucleotide having any of 5544 nucleotide sequences (CDNAS SEQ ID NO:
XX 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
XX (SEQ ID NO: 5545-11088). The CDNAS and proteins are from corn, soybean,
XX Arabidopsis, wheat and rape but the specification does not indicate which
XX sequences is derived from which organism. Also included is a method of
XX producing a plant having an improved property, comprising transforming a
XX plant with a recombinant DNA construct comprising a promoter region
XX functional in a plant cell operably joined to a polynucleotide encoding a
XX polypeptide associated with the property, and growing the transformed
XX plant. The property is selected from improving plant cold tolerance, for
XX manipulating growth rate in plant cells by modification of the cell cycle
XX pathway, for improving plant drought tolerance, for providing increased
XX resistance to plant disease, for galactomannan production, for production
XX of plant growth regulators, for improving plant heat tolerance, for
XX improving plant tolerance to herbicides, for increasing the rate of
XX homologous recombination in plants, for lignin production, for improving
XX plant tolerance to extreme osmotic conditions, for improving plant
XX tolerance to pathogens or pests, for yield improvement by modification of
XX photosynthesis, for modifying seed oil yield and/or content, for
XX modifying seed protein yield and/or content, for yield improvement by
XX modification of carbohydrate, nitrogen or phosphorus use and/or uptake
XX and for yield improvement by providing improved plant growth and
XX development under at least one stress condition. The polynucleotide may
XX also encode a plant transcription factor. The methods and compositions of
XX the present invention are useful in the field of biochemistry and
XX genetics, in particular for producing transgenic plants with improved
XX biological characteristics such as increased yield, improved nitrogen
XX flow, increasing plant tolerance to cold or heat, improving plant
XX tolerance to extreme osmotic and drought conditions, and improving plant
XX tolerance to plant pests or pathogens. They can also be used in physical
XX arrays of molecules, plant breeding markers, computer-based storage and
XX analysis systems. The present sequence is one of the 5544 plant protein
XX sequences of the invention. Note: The sequence data for this patent did
XX not form part of the printed specification, but was obtained in
XX electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?docID=20040216190.
```

XX

SQ Sequence 335 AA;

Query Match 87.1%; Score 27; DB 8; Length 335;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
| | | |
Db 80 KPAFFA 85

Search completed: December 29, 2005, 17:33:26
Job time : 93.7742 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 77.3387 Seconds
(without alignments)
37.818 Million cell updates/sec

Title: US-10-009-122-2

Perfect score: 34

Sequence: 1 KKLVFPA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications AA_Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	7	3	US-09-867-847-12
2	34	100.0	7	3	US-09-915-092-2
3	34	100.0	7	3	US-09-747-408-2
4	34	100.0	7	5	US-10-728-028-2
5	34	100.0	7	5	US-10-825-958-10
6	34	100.0	9	4	US-10-235-483-64
7	31	91.2	1640	4	US-10-437-963-109646
8	30	88.2	7	3	US-09-972-475-7
9	30	88.2	7	4	US-10-463-729-7
10	30	88.2	7	5	US-10-810-881A-128
11	30	88.2	8	3	US-09-972-475-5
12	30	88.2	8	4	US-10-463-729-5
13	30	88.2	9	3	US-09-867-847-9
14	30	88.2	9	3	US-09-747-408-20
15	30	88.2	9	4	US-10-235-483-54
16	30	88.2	9	4	US-10-619-454-28
17	30	88.2	10	3	US-09-867-847-29
18	30	88.2	10	3	US-09-915-092-19
19	30	88.2	10	5	US-10-889-999-20
20	30	88.2	10	5	US-10-889-999-21
21	30	88.2	10	5	US-10-889-999-22
22	30	88.2	10	5	US-10-889-999-23
23	30	88.2	10	5	US-10-890-070-20
24	30	88.2	10	5	US-10-890-070-21
25	30	88.2	10	5	US-10-890-070-22
26	30	88.2	10	5	US-10-890-070-23
27	30	88.2	10	5	US-10-890-000-20
28	30	88.2	10	5	US-10-890-000-21
29	30	88.2	10	5	US-10-890-000-22
30	30	88.2	10	5	US-10-823-463-20
31	30	88.2	10	5	US-10-823-463-21
32	30	88.2	10	5	US-10-823-463-22
33	30	88.2	10	5	US-10-823-463-23
34	30	88.2	10	5	US-10-728-028-19
35	30	88.2	10	5	US-10-822-968-20
36	30	88.2	10	5	US-10-822-968-21
37	30	88.2	10	5	US-10-822-968-22
38	30	88.2	10	5	US-10-822-968-23
39	30	88.2	10	5	US-10-777-792-20
40	30	88.2	10	5	US-10-777-792-21
41	30	88.2	10	5	US-10-777-792-22
42	30	88.2	10	5	US-10-777-792-23
43	30	88.2	10	5	US-10-825-958-27
44	30	88.2	10	5	US-10-890-071-20
45	30	88.2	10	5	US-10-890-071-21
46	30	88.2	10	5	US-10-890-071-22
47	30	88.2	10	5	US-10-890-071-23
48	30	88.2	10	5	US-10-890-024-20
49	30	88.2	10	5	US-10-890-024-21
50	30	88.2	10	5	US-10-890-024-22
51	30	88.2	10	5	US-10-890-024-23
52	30	88.2	10	5	US-10-828-926-20
53	30	88.2	10	5	US-10-828-926-21
54	30	88.2	10	5	US-10-828-926-22
55	30	88.2	10	5	US-10-828-926-23
56	30	88.2	10	6	US-11-058-757-20
57	30	88.2	10	6	US-11-058-757-21
58	30	88.2	10	6	US-11-058-757-22
59	30	88.2	10	6	US-11-058-757-23
60	30	88.2	11	3	US-09-988-842-9
61	30	88.2	11	3	US-09-988-842-25
62	30	88.2	11	4	US-10-235-483-14
63	30	88.2	11	4	US-10-050-200-33
64	30	88.2	11	5	US-10-464-117-13
65	30	88.2	11	5	US-10-772-230-9
66	30	88.2	11	5	US-10-772-230-25
67	30	88.2	12	6	US-11-012-797A-33
68	30	88.2	12	5	US-10-867-847-8
69	30	88.2	12	5	US-10-810-881A-115
70	30	88.2	12	5	US-10-508-586-2
71	30	88.2	12	5	US-10-508-586-3
72	30	88.2	12	5	US-10-625-854-139
73	30	88.2	12	6	US-10-012-797A-33
74	30	88.2	13	4	US-10-281-458-1
75	30	88.2	13	5	US-10-625-854-127
76	30	88.2	13	5	US-10-625-854-140
77	30	88.2	14	3	US-09-992-800-5
78	30	88.2	14	3	US-09-992-994-5
79	30	88.2	14	4	US-10-385-065-5
80	30	88.2	14	5	US-10-810-881A-114
81	30	88.2	14	5	US-10-505-313-2
82	30	88.2	14	5	US-10-625-854-115
83	30	88.2	14	5	US-10-625-854-128
84	30	88.2	14	5	US-10-625-854-141
85	30	88.2	14	6	US-11-063-350-5
86	30	88.2	15	4	US-10-235-483-56
87	30	88.2	15	4	US-10-235-483-57
88	30	88.2	15	4	US-10-235-483-60
89	30	88.2	15	4	US-10-235-483-61
90	30	88.2	15	4	US-10-235-483-63
91	30	88.2	15	4	US-10-235-483-65
92	30	88.2	15	5	US-10-625-854-103
93	30	88.2	15	5	US-10-625-854-116
94	30	88.2	15	5	US-10-625-854-129
95	30	88.2	15	5	US-10-625-854-142
96	30	88.2	16	5	US-10-625-854-91
97	30	88.2	16	5	US-10-625-854-104
98	30	88.2	16	5	US-10-625-854-117
99	30	88.2	16	5	US-10-625-854-130
100	30	88.2	16	5	US-10-625-854-143

101	30	88.2	17	3	US-09-992-800-3	Sequence 3, Appli	174	30	88.2	30	4	US-10-666-423-1	Sequence 1, Appli
102	30	88.2	17	3	US-09-992-994-3	Sequence 3, Appli	175	30	88.2	30	4	US-10-617-876-9	Sequence 9, Appli
103	30	88.2	17	3	US-09-998-491-8	Sequence 8, Appli	176	30	88.2	30	4	US-10-619-454-24	Sequence 24, Appli
104	30	88.2	17	4	US-10-385-065-3	Sequence 3, Appli	177	30	88.2	30	4	US-10-301-448-1	Sequence 1, Appli
105	30	88.2	17	4	US-10-451-367-26	Sequence 26, Appli	178	30	88.2	30	5	US-10-775-562-5	Sequence 5, Appli
106	30	88.2	17	4	US-10-475-281-8	Sequence 8, Appli	179	30	88.2	32	4	US-09-732-862A-99	Sequence 99, Appli
107	30	88.2	17	4	US-10-810-919-3	Sequence 3, Appli	180	30	88.2	33	3	US-09-930-915A-295	Sequence 295, App
108	30	88.2	17	5	US-10-684-346-24	Sequence 24, Appli	181	30	88.2	33	4	US-10-082-014-84	Sequence 84, Appli
109	30	88.2	17	5	US-10-997-078-46	Sequence 46, Appli	182	30	88.2	33	4	US-10-372-076-85	Sequence 85, Appli
110	30	88.2	17	5	US-10-997-700-19	Sequence 19, Appli	183	30	88.2	33	4	US-10-732-862A-98	Sequence 98, Appli
111	30	88.2	17	6	US-11-063-350-3	Sequence 3, Appli	184	30	88.2	33	4	US-10-806-006-295	Sequence 295, App
112	30	88.2	17	6	US-11-066-697-950	Sequence 950, App	185	30	88.2	33	4	US-10-677-074-85	Sequence 85, Appli
113	30	88.2	17	6	US-11-066-697-983	Sequence 983, App	186	30	88.2	33	4	US-10-805-913-295	Sequence 295, App
114	30	88.2	19	3	US-09-825-242-5	Sequence 5, Appli	187	30	88.2	35	3	US-09-867-847-3	Sequence 3, Appli
115	30	88.2	19	4	US-10-429-216-5	Sequence 5, Appli	188	30	88.2	35	3	US-09-972-475-16	Sequence 16, Appli
116	30	88.2	19	4	US-10-816-022-5	Sequence 5, Appli	189	30	88.2	35	4	US-10-463-729-16	Sequence 16, Appli
117	30	88.2	19	4	US-10-816-523-5	Sequence 5, Appli	190	30	88.2	35	5	US-10-825-958-3	Sequence 3, Appli
118	30	88.2	19	4	US-10-815-353-5	Sequence 5, Appli	191	30	88.2	35	6	US-11-066-697-979	Sequence 979, App
119	30	88.2	19	4	US-10-815-391-5	Sequence 5, Appli	192	30	88.2	35	6	US-11-066-697-1006	Sequence 1006, App
120	30	88.2	19	5	US-10-828-548-5	Sequence 5, Appli	193	30	88.2	36	3	US-09-861-847-6	Sequence 6, Appli
121	30	88.2	19	5	US-10-816-380-5	Sequence 5, Appli	194	30	88.2	36	3	US-09-861-847-11	Sequence 11, Appli
122	30	88.2	19	5	US-10-889-999-75	Sequence 75, Appli	195	30	88.2	36	4	US-10-301-488A-6	Sequence 6, Appli
123	30	88.2	19	5	US-10-890-070-75	Sequence 75, Appli	196	30	88.2	36	4	US-10-301-488A-11	Sequence 11, Appli
124	30	88.2	19	5	US-10-890-000-75	Sequence 75, Appli	197	30	88.2	36	4	US-10-666-423-6	Sequence 6, Appli
125	30	88.2	19	5	US-10-788-666-5	Sequence 5, Appli	198	30	88.2	36	4	US-10-666-423-11	Sequence 11, Appli
126	30	88.2	19	5	US-10-923-471-5	Sequence 5, Appli	199	30	88.2	36	4	US-10-301-448-6	Sequence 6, Appli
127	30	88.2	19	5	US-10-923-463-5	Sequence 5, Appli	200	30	88.2	36	4	US-10-301-448-11	Sequence 11, Appli
128	30	88.2	19	5	US-10-923-463-5	Sequence 5, Appli	201	30	88.2	36	4	US-10-732-862A-436	Sequence 436, App
129	30	88.2	19	5	US-10-933-559-5	Sequence 5, Appli	202	30	88.2	38	4	US-10-425-115-290955	Sequence 290955, App
130	30	88.2	19	5	US-10-915-404-5	Sequence 5, Appli	203	30	88.2	38	6	US-11-066-697-975	Sequence 975, App
131	30	88.2	19	5	US-10-934-609-5	Sequence 5, Appli	204	30	88.2	38	6	US-11-066-697-1002	Sequence 1002, App
132	30	88.2	19	5	US-10-923-474-5	Sequence 5, Appli	205	30	88.2	39	4	US-10-051-496-5	Sequence 5, Appli
133	30	88.2	19	5	US-10-884-892-5	Sequence 5, Appli	206	30	88.2	39	4	US-10-190-548A-5	Sequence 5, Appli
134	30	88.2	19	5	US-10-822-968-75	Sequence 75, Appli	207	30	88.2	40	3	US-09-861-847-7	Sequence 7, Appli
135	30	88.2	19	5	US-10-777-792-75	Sequence 75, Appli	208	30	88.2	40	3	US-09-861-847-8	Sequence 8, Appli
136	30	88.2	19	5	US-10-890-071-75	Sequence 75, Appli	209	30	88.2	40	3	US-09-867-847-2	Sequence 2, Appli
137	30	88.2	19	5	US-10-890-024-75	Sequence 75, Appli	210	30	88.2	40	3	US-09-988-842-3	Sequence 3, Appli
138	30	88.2	19	5	US-10-934-819-5	Sequence 5, Appli	211	30	88.2	40	3	US-09-851-071-3	Sequence 3, Appli
139	30	88.2	19	5	US-10-923-267-5	Sequence 5, Appli	212	30	88.2	40	3	US-09-962-955C-36	Sequence 36, Appli
140	30	88.2	19	5	US-10-928-926-75	Sequence 75, Appli	213	30	88.2	40	3	US-09-792-079-12	Sequence 12, Appli
141	30	88.2	19	6	US-11-058-757-75	Sequence 75, Appli	214	30	88.2	40	4	US-10-007-779A-1	Sequence 1, Appli
142	30	88.2	19	6	US-11-108-102-5	Sequence 5, Appli	215	30	88.2	40	4	US-10-051-496-4	Sequence 4, Appli
143	30	88.2	20	3	US-09-908-943A-25	Sequence 25, Appli	216	30	88.2	40	4	US-10-217-584-3	Sequence 3, Appli
144	30	88.2	20	5	US-10-801-487-25	Sequence 25, Appli	217	30	88.2	40	4	US-10-169-580-1	Sequence 1, Appli
145	30	88.2	20	5	US-10-801-938-25	Sequence 25, Appli	218	30	88.2	40	4	US-10-143-534-3	Sequence 3, Appli
146	30	88.2	20	5	US-10-801-509-25	Sequence 25, Appli	219	30	88.2	40	4	US-10-190-548A-4	Sequence 4, Appli
147	30	88.2	20	5	US-10-801-486-25	Sequence 25, Appli	220	30	88.2	40	4	US-10-051-663-3	Sequence 3, Appli
148	30	88.2	20	5	US-10-801-493-25	Sequence 25, Appli	221	30	88.2	40	4	US-10-151-614-1	Sequence 1, Appli
149	30	88.2	24	5	US-10-728-246-6	Sequence 5, Appli	222	30	88.2	40	4	US-10-159-279-12	Sequence 12, Appli
150	30	88.2	24	5	US-10-728-246-6	Sequence 6, Appli	223	30	88.2	40	4	US-10-301-488A-7	Sequence 7, Appli
151	30	88.2	26	4	US-09-792-079-11	Sequence 11, Appli	224	30	88.2	40	4	US-10-301-488A-8	Sequence 8, Appli
152	30	88.2	26	4	US-10-159-279-11	Sequence 11, Appli	225	30	88.2	40	4	US-10-455-218-1	Sequence 1, Appli
153	30	88.2	28	3	US-09-867-847-4	Sequence 4, Appli	226	30	88.2	40	4	US-10-366-125-27	Sequence 27, Appli
154	30	88.2	28	3	US-09-865-294-66	Sequence 66, Appli	227	30	88.2	40	4	US-10-337-261-1	Sequence 1, Appli
155	30	88.2	28	3	US-09-792-079-5	Sequence 5, Appli	228	30	88.2	40	4	US-10-666-423-7	Sequence 7, Appli
156	30	88.2	28	4	US-10-159-279-5	Sequence 5, Appli	229	30	88.2	40	4	US-10-666-423-8	Sequence 8, Appli
157	30	88.2	28	4	US-10-363-082-2	Sequence 2, Appli	230	30	88.2	40	4	US-10-301-448-7	Sequence 7, Appli
158	30	88.2	28	4	US-10-433-385-7	Sequence 7, Appli	231	30	88.2	40	4	US-10-301-448-8	Sequence 8, Appli
159	30	88.2	28	4	US-10-390-472-4	Sequence 4, Appli	232	30	88.2	40	4	US-10-683-815-1	Sequence 1, Appli
160	30	88.2	28	4	US-10-741-205-36	Sequence 36, Appli	233	30	88.2	40	4	US-10-683-815-14	Sequence 14, Appli
161	30	88.2	28	4	US-10-416-262B-7	Sequence 7, Appli	234	30	88.2	40	4	US-10-683-815-15	Sequence 15, Appli
162	30	88.2	28	4	US-10-478-308-4	Sequence 4, Appli	235	30	88.2	40	4	US-10-683-815-16	Sequence 16, Appli
163	30	88.2	28	4	US-10-478-307-4	Sequence 4, Appli	236	30	88.2	40	4	US-10-683-815-17	Sequence 17, Appli
164	30	88.2	28	5	US-10-861-614-66	Sequence 66, Appli	237	30	88.2	40	4	US-10-683-815-18	Sequence 18, Appli
165	30	88.2	28	5	US-10-825-958-4	Sequence 4, Appli	238	30	88.2	40	4	US-10-810-919-1	Sequence 1, Appli
166	30	88.2	28	6	US-11-091-309-3	Sequence 3, Appli	239	30	88.2	40	5	US-10-864-107-1	Sequence 1, Appli
167	30	88.2	28	6	US-11-066-697-959	Sequence 959, App	240	30	88.2	40	5	US-10-485-310-18	Sequence 18, Appli
168	30	88.2	28	6	US-11-066-697-965	Sequence 965, App	241	30	88.2	40	5	US-10-481-387-1	Sequence 1, Appli
169	30	88.2	28	6	US-11-066-697-976	Sequence 976, App	242	30	88.2	40	5	US-10-481-954-5	Sequence 5, Appli
170	30	88.2	28	6	US-11-066-697-992	Sequence 992, App	243	30	88.2	40	5	US-10-698-259A-1	Sequence 1, Appli
171	30	88.2	28	6	US-11-066-697-1003	Sequence 1003, App	244	30	88.2	40	5	US-10-884-729-1	Sequence 1, Appli
172	30	88.2	30	3	US-09-861-847-1	Sequence 1, Appli	245	30	88.2	40	5	US-10-728-246-4	Sequence 4, Appli
173	30	88.2	30	4	US-10-301-488A-1	Sequence 1, Appli	246	30	88.2	40	5	US-10-772-230-3	Sequence 3, Appli

```

247 30 88.2 40 5 US-10-933-206-36
248 30 88.2 40 5 US-10-825-358-2
249 30 88.2 40 5 US-10-775-562-2
250 30 88.2 40 5 US-10-296-168-1
251 30 88.2 40 6 US-11-004-053-36
252 30 88.2 40 6 US-11-007-643-36
253 30 88.2 40 6 US-11-007-644-36
254 30 88.2 40 6 US-11-007-669-36
255 30 88.2 40 6 US-11-066-697-956
256 30 88.2 40 6 US-11-066-697-962
257 30 88.2 40 6 US-11-066-697-968
258 30 88.2 40 6 US-11-066-697-978
259 30 88.2 40 6 US-11-066-697-989
260 30 88.2 40 6 US-11-066-697-995
261 30 88.2 40 6 US-11-066-697-1005
262 30 88.2 41 4 US-10-051-496-3
263 30 88.2 41 4 US-10-190-548A-3
264 30 88.2 41 4 US-10-683-815-13
265 30 88.2 42 2 US-08-922-930-2
266 30 88.2 42 2 US-08-923-055-2
267 30 88.2 42 3 US-09-867-847-1
268 30 88.2 42 3 US-09-956-625-26
269 30 88.2 42 3 US-09-731-460-1
270 30 88.2 42 3 US-09-899-815-1
271 30 88.2 42 3 US-09-962-955C-37
272 30 88.2 42 3 US-09-848-616-174
273 30 88.2 42 3 US-09-865-294-65
274 30 88.2 42 3 US-09-792-079-13
275 30 88.2 42 3 US-09-825-242-1
276 30 88.2 42 3 US-09-930-915A-293
277 30 88.2 42 4 US-10-051-496-2
278 30 88.2 42 4 US-10-082-804-7
279 30 88.2 42 4 US-10-217-584-2
280 30 88.2 42 4 US-10-217-584-8
281 30 88.2 42 4 US-10-217-584-9
282 30 88.2 42 4 US-10-217-584-10
283 30 88.2 42 4 US-10-217-584-11
284 30 88.2 42 4 US-10-169-580-2
285 30 88.2 42 4 US-10-278-181-1
286 30 88.2 42 4 US-10-143-534-2
287 30 88.2 42 4 US-10-190-548A-1
288 30 88.2 42 4 US-10-051-663-2
289 30 88.2 42 4 US-10-159-279-13
290 30 88.2 42 4 US-10-318-302-4
291 30 88.2 42 4 US-10-050-902-220
292 30 88.2 42 4 US-10-050-898-220
293 30 88.2 42 4 US-10-082-014-81
294 30 88.2 42 4 US-10-372-076-82
295 30 88.2 42 4 US-10-455-218-2
296 30 88.2 42 4 US-10-231-298B-15
297 30 88.2 42 4 US-10-231-470C-15
298 30 88.2 42 4 US-10-231-063C-15
299 30 88.2 42 4 US-10-366-125-28
300 30 88.2 42 4 US-10-411-544-2

```

ALIGNMENTS

```

RESULT 1
US-09-867-847-12
; Sequence 12, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

```

```

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-12

Query Match 100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 1 KKLVPFA 7

RESULT 2
US-09-915-092-2
; Sequence 2, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-2

Query Match 100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 1 KKLVPFA 7

RESULT 3
US-09-747-408-2
; Sequence 2, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-2

Query Match 100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. NO. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
|||
Db 1 KKLVEFA 7

RESULT 4

US-10-728-028-2
; Sequence 2, Application US/10728028
; Publication NO. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xiangci
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-2

Query Match 100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. NO. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
|||
Db 1 KKLVEFA 7

RESULT 5

US-10-825-958-10
; Sequence 10, Application US/10825958
; Publication NO. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangci
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-10-825-958-10

Query Match 100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. NO. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
|||
Db 1 KKLVEFA 7

RESULT 6

US-10-235-483-64
; Sequence 64, Application US/10235483
; Publication No. US20030087407A1
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; BAUMANN, Marc
; FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIK
; DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/235,483
; FILING DATE: 06-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-10-235-483-64

Query Match 100.0%; Score 34; DB 4; Length 9;


```
/ MOLECULE TYPE: peptide
US-10-463-729-7

Query Match      88.2%; Score 30; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVEFFA 7
Db 1 QKLVEFFA 7

RESULT 10
US-10-810-881A-128
; Sequence 128, Application US/10810881A
; Publication No. US20050129695A1
; GENERAL INFORMATION:
; APPLICANT: Mercken, Marc; Benson, Jacqueline M.
; TITLE OF INVENTION: ANTI-AMYLLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CENS021 NP
; CURRENT APPLICATION NUMBER: US/10/810,881A
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/458,474
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,469
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,509
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,510
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 128
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PEPTIDE
US-10-810-881A-128

Query Match      88.2%; Score 30; DB 5; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVEFFA 7
Db 1 QKLVEFFA 7

RESULT 11
US-09-972-475-5
; Sequence 5, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
```


; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-463-729-5

Query Match 88.2%; Score 30; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 2 QKLVPFA 8

RESULT 13
US-09-867-847-9
; Sequence 9, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-09-867-847-9

Query Match 88.2%; Score 30; DB 3; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 3 QKLVPFA 9

RESULT 14
US-09-747-408-20
; Sequence 20, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-058
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 9

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-20

Query Match 88.2%; Score 30; DB 3; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 3 QKLVPFA 9

RESULT 15
US-10-235-483-54
; Sequence 54, Application US/10235483
; Publication No. US20030087407A1
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; BAUMANN, Marc
; FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASE
; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LI
; DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/235,483
; FILING DATE: 06-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-10-235-483-54

Query Match 88.2%; Score 30; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPF 6
Db 1 KKLVPF 6

```
RESULT 16
US-10-619-454-28
; Sequence 28, Application US/10619454
; Publication No. US20040091945A1
; GENERAL INFORMATION:
; APPLICANT: Mindset
; APPLICANT: Pitzer Attas, Cheryl
; APPLICANT: Chain, Daniel
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES A
; FILE REFERENCE: P-5202-US
; CURRENT APPLICATION NUMBER: US/10/619,454
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: US 60/396,245
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: algorithm generated
US-10-619-454-28
Query Match      88.2%; Score 30; DB 4; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 3 QKLVPFA 9

RESULT 17
US-09-867-847-29
; Sequence 29, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangl
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-29
Query Match      88.2%; Score 30; DB 3; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 3 QKLVPFA 9

RESULT 18
US-09-915-092-19
; Sequence 19, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NEI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-915-092-19
Query Match      88.2%; Score 30; DB 3; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 3 QKLVPFA 9

RESULT 19
US-10-889-999-20
; Sequence 20, Application US/10889999
; Publication No. US20040247590A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/889,999
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-889-999-20
Query Match      88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 4 QKLVPFA 10

RESULT 20
US-10-889-999-21
```

; Sequence 21, Application US/10889999
; Publication No. US20040247590A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/889,999
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-889-999-21

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KQLVFFA 7
:|||||
Db 3 QKLVFFA 9

RESULT 21

US-10-889-999-22
; Sequence 22, Application US/10889999
; Publication No. US20040247590A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/889,999
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-889-999-22

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KQLVFFA 7
:|||||
Db 2 QKLVFFA 8

RESULT 22

US-10-889-999-23
; Sequence 23, Application US/10889999
; Publication No. US20040247590A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/889,999
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-889-999-23

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KQLVFFA 7
:|||||
Db 1 QKLVFFA 7

RESULT 23

US-10-890-070-20
; Sequence 20, Application US/10890070
; Publication No. US20040247591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,070
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-070-20

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KQLVFFA 7
:|||||
Db 4 QKLVFFA 10

RESULT 24
US-10-890-070-21
; Sequence 21, Application US/10890070
; Publication No. US20040247591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,070
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-070-21

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 3 QKLVPFA 9

RESULT 25
US-10-890-070-22
; Sequence 22, Application US/10890070
; Publication No. US20040247591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,070
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-070-22

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 2 QKLVPFA 8

RESULT 26
US-10-890-070-23
; Sequence 23, Application US/10890070
; Publication No. US20040247591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,070
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-070-23

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 1 QKLVPFA 7

RESULT 27
US-10-890-000-20
; Sequence 20, Application US/10890000
; Publication No. US20040265301A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,000
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-000-20

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 4 QKLVPFA 10

RESULT 28
US-10-890-000-21
; Sequence 21, Application US/10890000
; Publication No. US20040265301A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,000
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-000-21

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 3 QKLVPFA 9

RESULT 29
US-10-890-000-22
; Sequence 22, Application US/10890000
; Publication No. US20040265301A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,000
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-000-22

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 3 QKLVPFA 9

Db 2 QKLVPFA 8
RESULT 30
US-10-890-000-23
; Sequence 23, Application US/10890000
; Publication No. US20040265301A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,000
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-000-23

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 1 QKLVPFA 7

RESULT 31
US-10-823-463-20
; Sequence 20, Application US/10823463
; Publication No. US20050019328A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/823,463
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

```
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-823-463-20

Query Match      88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7
   :|||||
Db 4 QKLVEFFA 10

RESULT 32
US-10-823-463-21
; Sequence 21, Application US/10823463
; Publication No. US20050019328A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/823,463
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-823-463-21

Query Match      88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7
   :|||||
Db 3 QKLVEFFA 9

RESULT 33
US-10-823-463-22
; Sequence 22, Application US/10823463
; Publication No. US20050019328A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/823,463
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/580,015
```

```
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-823-463-22

Query Match      88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7
   :|||||
Db 2 QKLVEFFA 8

RESULT 34
US-10-823-463-23
; Sequence 23, Application US/10823463
; Publication No. US20050019328A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/823,463
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-823-463-23

Query Match      88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 KKLVFPA 7
Db 1 OKLVFPA 7

RESULT 35

US-10-728-028-19

; Sequence 19, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-19

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
Db 3 OKLVFPA 9

RESULT 36

US-10-822-968-20

; Sequence 20, Application US/10822968
; Publication No. US20050059591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/822,968
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10

; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-822-968-20

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
Db 4 OKLVFPA 10

RESULT 37

US-10-822-968-21

; Sequence 21, Application US/10822968
; Publication No. US20050059591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/822,968
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-822-968-21

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
Db 3 OKLVFPA 9

RESULT 38

US-10-822-968-22

; Sequence 22, Application US/10822968
; Publication No. US20050059591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
US-10-822-968-22

```
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/822,968
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-822-968-22

Query Match      88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
       :|||||
Db      2 QKLVPFA 8

RESULT 39
US-10-822-968-23
; Sequence 23, Application US/10822968
; Publication No. US20050059591A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/822,968
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-822-968-23
```

```
Query Match      88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
       :|||||
Db      1 QKLVPFA 7

RESULT 40
US-10-777-792-20
; Sequence 20, Application US/10777792
; Publication No. US20050059802A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/777,792
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-777-792-20

Query Match      88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
       :|||||
Db      4 QKLVPFA 10

RESULT 41
US-10-777-792-21
; Sequence 21, Application US/10777792
; Publication No. US20050059802A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/777,792
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-777-792-21
```


Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
:|||||
Db 3 QKLVPFA 9

RESULT 42

US-10-777-792-22
; Sequence 22, Application US/10777792
; Publication No. US20050059802A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/777,792
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-777-792-22

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
:|||||
Db 2 QKLVPFA 8

RESULT 43

US-10-777-792-23
; Sequence 23, Application US/10777792
; Publication No. US20050059802A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/777,792
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)

US-10-777-792-23

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
:|||||
Db 1 QKLVPFA 7

RESULT 44

US-10-825-958-27
; Sequence 27, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-27

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
:|||||
Db 3 QKLVPFA 9

RESULT 45

US-10-890-071-20
; Sequence 20, Application US/10890071
; Publication No. US20050123544A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,071
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-071-20

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
:|||||
Db 4 QKLVEFA 10

RESULT 46

US-10-890-071-21
; Sequence 21, Application US/10890071
; Publication No. US20050123544A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,071
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-071-21

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
:|||||
Db 3 QKLVEFA 9

RESULT 47

US-10-890-071-22
; Sequence 22, Application US/10890071
; Publication No. US20050123544A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,071
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-071-22

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
:|||||
Db 2 QKLVEFA 8

RESULT 48

US-10-890-071-23
; Sequence 23, Application US/10890071
; Publication No. US20050123544A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,071
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-071-23

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
:|||||
Db 1 QKLVEFA 7

RESULT 49

US-10-890-024-20
; Sequence 20, Application US/10890024
; Publication No. US20050158304A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,024
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-024-20

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
:|||||
Db 4 QKLVFPA 10

RESULT 50

US-10-890-024-21
; Sequence 21, Application US/10890024
; Publication No. US20050158304A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,024
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-024-21

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
:|||||
Db 3 QKLVFPA 9

RESULT 51

US-10-890-024-22
; Sequence 22, Application US/10890024
; Publication No. US20050158304A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,024
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-024-22

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
:|||||
Db 2 QKLVFPA 8

RESULT 52

US-10-890-024-23
; Sequence 23, Application US/10890024
; Publication No. US20050158304A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/10/890,024
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-890-024-23

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
:|||||
Db 1 QKLVFPA 7

RESULT 53

US-10-928-926-20
; Sequence 20, Application US/10928926
; Publication No. US20050196399A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/928,926
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430

```
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-928-926-20

Query Match      88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
       :|||||
DB      4 QKLVPFA 10

RESULT 54
US-10-928-926-21
; Sequence 21, Application US/10928926
; Publication No. US20050196399A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/928,926
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-928-926-22

Query Match      88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
       :|||||
DB      2 QKLVPFA 8

RESULT 56
US-10-928-926-23
; Sequence 23, Application US/10928926
; Publication No. US20050196399A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/928,926
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
```

```
DB      3 QKLVPFA 9

RESULT 55
US-10-928-926-22
; Sequence 22, Application US/10928926
; Publication No. US20050196399A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/928,926
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-928-926-22

Query Match      88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
       :|||||
DB      2 QKLVPFA 8

RESULT 56
US-10-928-926-23
; Sequence 23, Application US/10928926
; Publication No. US20050196399A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/928,926
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
```

; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-10-928-926-23

Query Match 88.2%; Score 30; DB 5; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
:|||||
Db 1 QKLVFPA 7

RESULT 57
US-11-058-757-20
; Sequence 20, Application US/11058757
; Publication No. US20050142132A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004760US
; CURRENT APPLICATION NUMBER: US/11/058,757
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-11-058-757-20

Query Match 88.2%; Score 30; DB 6; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
:|||||
Db 4 QKLVFPA 10

RESULT 58
US-11-058-757-21
; Sequence 21, Application US/11058757
; Publication No. US20050142132A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004760US

; CURRENT APPLICATION NUMBER: US/11/058,757
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-11-058-757-21

Query Match 88.2%; Score 30; DB 6; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
:|||||
Db 3 QKLVFPA 9

RESULT 59
US-11-058-757-22
; Sequence 22, Application US/11058757
; Publication No. US20050142132A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004760US
; CURRENT APPLICATION NUMBER: US/11/058,757
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-11-058-757-22

Query Match 88.2%; Score 30; DB 6; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
:|||||
Db 2 QKLVFPA 8

RESULT 60
US-11-058-757-23
; Sequence 23, Application US/11058757
; Publication No. US20050142132A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004760US

```
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/11/058,757
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-11-058-757-23

Query Match      88.2%; Score 30; DB 6; Length 10;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
Db      1 QKLVPFA 7

RESULT 61
US-09-988-842-9
; Sequence 9, Application US/09988842
; Patent No. US20020143105A1
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

Query Match      88.2%; Score 30; DB 3; Length 11;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
Db      1 QKLVPFA 7

RESULT 62
US-09-988-842-25
; Sequence 25, Application US/09988842
; Patent No. US20020143105A1
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
```

```
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

Query Match      88.2%; Score 30; DB 3; Length 11;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
Db      1 QKLVPFA 7

RESULT 63
US-10-235-483-14
; Sequence 14, Application US/10235483
; Publication No. US20030087407A1
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; BAUMANN, Marc
; FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIK
; DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/235,483
; FILING DATE: 06-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
```

SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-235-463-14

Query Match 88.2%; Score 30; DB 4; Length 11;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 1 QKLVPFA 7

RESULT 64

US-10-050-200-33
; Sequence 33, Application US/10050200
; Publication No. US20030166037A1
; GENERAL INFORMATION:
; APPLICANT: Fourie, Anne
; APPLICANT: Coles, Fawn
; APPLICANT: Karisson, Lars
; TITLE OF INVENTION: AggreCanase-1 and -2 Peptide Substrates and Methods
; FILE REFERENCE: ORT-1417
; CURRENT APPLICATION NUMBER: US/10/050,200
; CURRENT FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide substrate
US-10-050-200-33

Query Match 88.2%; Score 30; DB 4; Length 11;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 5 QKLVPFA 11

RESULT 65

US-10-464-117-13
; Sequence 13, Application US/10464117
; Publication No. US20050014193A1
; GENERAL INFORMATION:
; APPLICANT: Palatin Technologies, Inc.
; APPLICANT: Sharma, Shubh D.
; APPLICANT: Shi, Yi-Qun
; TITLE OF INVENTION: Identification of Target-Specific Folding Sites in Peptides and
; FILE REFERENCE: 70025-UT-50075
; CURRENT APPLICATION NUMBER: US/10/464,117
; CURRENT FILING DATE: 2003-06-17
; PRIOR APPLICATION NUMBER: PCT/US01/50075
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 60/256,842
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/304,835
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 60/327,835
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 171
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amyloid beta-protein related peptide
US-10-464-117-13

Query Match 88.2%; Score 30; DB 5; Length 11;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 2 EKLVPFA 8

RESULT 66

US-10-772-230-9
; Sequence 9, Application US/10772230
; Publication No. US20050059084A1
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/10/772,230
; CURRENT FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US/09/988,842
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-772-230-9

Query Match 88.2%; Score 30; DB 5; Length 11;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 1 QKLVPFA 7

RESULT 67

US-10-772-230-25
; Sequence 25, Application US/10772230
; Publication No. US20050059084A1
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/10/772,230
; CURRENT FILING DATE: 2004-02-04
; PRIOR APPLICATION NUMBER: US/09/988,842
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-772-230-25

```
Query Match      88.2%; Score 30; DB 5; Length 11;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 1 QKLVPFA 7

RESULT 68
US-09-867-847-8
; Sequence 8, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangdi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-8

Query Match      88.2%; Score 30; DB 3; Length 12;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 6 QKLVPFA 12

RESULT 69
US-10-810-881A-115
; Sequence 115, Application US/10810881A
; Publication No. US20050129695A1
; GENERAL INFORMATION:
; APPLICANT: Marcken, Marc; Benson, Jacqueline M.
; TITLE OF INVENTION: ANTI-AMYLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5021 NP
; CURRENT APPLICATION NUMBER: US/10/810,881A
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/458,474
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,469
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,509
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,510
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 115
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PEPTIDE

Query Match      88.2%; Score 30; DB 5; Length 11;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 1 QKLVPFA 7

RESULT 68
US-09-867-847-8
; Sequence 8, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangdi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-8

Query Match      88.2%; Score 30; DB 3; Length 12;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 6 QKLVPFA 12

RESULT 69
US-10-810-881A-115
; Sequence 115, Application US/10810881A
; Publication No. US20050129695A1
; GENERAL INFORMATION:
; APPLICANT: Marcken, Marc; Benson, Jacqueline M.
; TITLE OF INVENTION: ANTI-AMYLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5021 NP
; CURRENT APPLICATION NUMBER: US/10/810,881A
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/458,474
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,469
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,509
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,510
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 115
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PEPTIDE

Query Match      88.2%; Score 30; DB 5; Length 12;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 6 QKLVPFA 12

RESULT 70
US-10-508-586-2
; Sequence 2, Application US/10508586
; Publication No. US20050164361A1
; GENERAL INFORMATION:
; APPLICANT: EMORY UNIVERSITY
; TITLE OF INVENTION: SELF-ASSEMBLING-PEPTIDE-BASED STRUCTURES AND PROCESSES FOR
; FILE REFERENCE: 050508-2230
; CURRENT APPLICATION NUMBER: US/10/508,586
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-508-586-2

Query Match      88.2%; Score 30; DB 5; Length 12;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 6 QKLVPFA 12

RESULT 71
US-10-508-586-3
; Sequence 3, Application US/10508586
; Publication No. US20050164361A1
; GENERAL INFORMATION:
; APPLICANT: EMORY UNIVERSITY
; TITLE OF INVENTION: SELF-ASSEMBLING-PEPTIDE-BASED STRUCTURES AND PROCESSES FOR
; FILE REFERENCE: 050508-2230
; CURRENT APPLICATION NUMBER: US/10/508,586
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-508-586-3

Query Match      88.2%; Score 30; DB 5; Length 12;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 6 QKLVPFA 12

RESULT 72
US-10-625-854-139
; Sequence 139, Application US/10625854
; Publication No. US20050175626A1
; GENERAL INFORMATION:
; APPLICANT: Delacourte, Andr
```



```
; APPLICANT: Sergeant, Nicolas
; TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
; FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
; CURRENT APPLICATION NUMBER: US/10/625,854
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/401,497
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
; LENGTH: 12
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-625-854-139
```

```
Query Match      88.2%; Score 30; DB 5; Length 12;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KKLVPFA 7
Db      6 QKLVPFA 12
```

RESULT 73

```
US-11-012-797A-33
; Sequence 33, Application US/11012797A
; Publication No. US20050164319A1
; GENERAL INFORMATION:
; APPLICANT: FOURIE, ANNE M.
; APPLICANT: KARLSSON, LARS
; APPLICANT: COLES, EAWN
; TITLE OF INVENTION: AGGREGANASE-1 AND -2 PEPTIDE SUBSTRATES AND METHODS
; FILE REFERENCE: ORT-1417-USCWT1
; CURRENT APPLICATION NUMBER: US/11/012,797A
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 10/050,200
; PRIOR FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn ver. 3.3
; SEQ ID NO 33
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: Aedans-Glu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: Dabcyl-Lys
US-11-012-797A-33
```

```
Query Match      88.2%; Score 30; DB 6; Length 12;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KKLVPFA 7
Db      5 QKLVPFA 11
```

RESULT 74

```
US-10-281-458-1
; Sequence 1, Application US/10281458
; Publication No. US20030108978A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Ciambrone, Gary J.
; APPLICANT: Gibbons, Ian
; TITLE OF INVENTION: Whole Cell Assay Systems for Cell
; TITLE OF INVENTION: Surface Proteases
; FILE REFERENCE: 50225-8093 US03
; CURRENT APPLICATION NUMBER: US/10/281,458
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/337,641
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 09/924,692
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-281-458-1
```

```
Query Match      88.2%; Score 30; DB 4; Length 13;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KKLVPFA 7
Db      5 QKLVPFA 11
```

RESULT 75

```
US-10-625-854-127
; Sequence 127, Application US/10625854
; Publication No. US20050175626A1
; GENERAL INFORMATION:
; APPLICANT: Delacourte, Andr
; APPLICANT: Sergeant, Nicolas
; TITLE OF INVENTION: Prevention, treatment and diagnosis of diseases associated with
; FILE REFERENCE: 11362.0039.NPUS01 (INNS039---)
; CURRENT APPLICATION NUMBER: US/10/625,854
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: European Patent Application No. 02447147.6
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/401,497
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-625-854-127
```

```
Query Match      88.2%; Score 30; DB 5; Length 13;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KKLVPFA 7
Db      7 QKLVPFA 13
```

```
Search completed: December 29, 2005, 18:49:35
Job time : 79.3387 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 23.371 Seconds
(without alignments)
24.763 Million cell updates/sec

Title: US-10-009-122-2

Perfect score: 34

Sequence: 1 KKLVFFA 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	7	2	US-09-747-408-2
2	34	100.0	9	2	US-08-766-596A-64
3	34	100.0	34	1	US-08-475-579A-4
4	30	88.2	6	2	US-09-242-724-33
5	30	88.2	7	1	US-08-612-785B-7
6	30	88.2	7	2	US-08-703-675C-30
7	30	88.2	7	2	US-08-617-267C-7
8	30	88.2	8	1	US-08-612-785B-5
9	30	88.2	8	2	US-08-703-675C-28
10	30	88.2	8	2	US-08-617-267C-5
11	30	88.2	9	2	US-08-766-596A-54
12	30	88.2	9	2	US-09-747-408-20
13	30	88.2	10	2	US-09-724-961-21
14	30	88.2	10	2	US-09-724-961-22
15	30	88.2	10	2	US-09-724-961-23
16	30	88.2	10	2	US-09-724-961-24
17	30	88.2	10	2	US-09-580-018-21
18	30	88.2	10	2	US-09-580-018-22
19	30	88.2	10	2	US-09-580-018-23
20	30	88.2	10	2	US-09-724-961-25
21	30	88.2	10	2	US-09-724-961-26
22	30	88.2	10	2	US-09-724-961-27
23	30	88.2	10	2	US-09-724-961-28
24	30	88.2	10	2	US-09-724-961-29
25	30	88.2	10	2	US-09-724-961-30
26	30	88.2	10	2	US-09-724-961-31
27	30	88.2	10	2	US-09-724-961-32

28	88.2	10	2	US-09-724-940-23	Sequence 23, Appl
29	88.2	11	1	US-08-630-645-14	Sequence 14, Appl
30	88.2	11	2	US-08-766-596A-14	Sequence 14, Appl
31	88.2	11	2	US-09-988-842-9	Sequence 9, Appl
32	88.2	11	4	PCT-US96-10220-14	Sequence 25, Appl
33	88.2	14	2	US-09-594-366-5	Sequence 14, Appl
34	88.2	14	2	US-09-594-366-5	Sequence 5, Appl
35	88.2	14	2	US-09-594-366-5	Sequence 5, Appl
36	88.2	15	1	US-08-612-785B-37	Sequence 37, Appl
37	88.2	15	2	US-08-766-596A-56	Sequence 56, Appl
38	88.2	15	2	US-08-766-596A-57	Sequence 57, Appl
39	88.2	15	2	US-08-766-596A-60	Sequence 60, Appl
40	88.2	15	2	US-08-766-596A-61	Sequence 61, Appl
41	88.2	15	2	US-08-766-596A-63	Sequence 63, Appl
42	88.2	15	2	US-08-766-596A-65	Sequence 65, Appl
43	88.2	17	2	US-09-264-709A-2	Sequence 2, Appl
44	88.2	17	2	US-09-594-366-3	Sequence 3, Appl
45	88.2	17	2	US-09-623-548A-950	Sequence 950, App
46	88.2	17	2	US-09-623-548A-983	Sequence 983, Appl
47	88.2	17	2	US-09-592-800-3	Sequence 3, Appl
48	88.2	17	2	US-09-657-276-950	Sequence 950, App
49	88.2	17	2	US-09-657-276-983	Sequence 983, App
50	88.2	19	2	US-08-970-833-11	Sequence 11, Appl
51	88.2	19	2	US-09-723-384-5	Sequence 5, Appl
52	88.2	19	2	US-09-724-961-75	Sequence 75, Appl
53	88.2	19	2	US-09-724-961-75	Sequence 5, Appl
54	88.2	19	2	US-09-580-018-75	Sequence 75, Appl
55	88.2	19	2	US-09-723-927-5	Sequence 5, Appl
56	88.2	19	2	US-09-724-489-5	Sequence 5, Appl
57	88.2	19	2	US-09-724-477-5	Sequence 5, Appl
58	88.2	19	2	US-09-723-762-5	Sequence 5, Appl
59	88.2	19	2	US-09-201-430-5	Sequence 5, Appl
60	88.2	19	2	US-09-724-551-75	Sequence 75, Appl
61	88.2	19	2	US-10-815-353-5	Sequence 5, Appl
62	88.2	19	2	US-10-816-529-5	Sequence 5, Appl
63	88.2	19	2	US-10-815-391-5	Sequence 5, Appl
64	88.2	19	2	US-10-816-022-5	Sequence 5, Appl
65	88.2	19	2	US-09-724-940-75	Sequence 75, Appl
66	88.2	19	2	US-10-934-609-5	Sequence 5, Appl
67	88.2	19	2	US-10-884-892-5	Sequence 5, Appl
68	88.2	20	2	US-08-970-833-10	Sequence 10, Appl
69	88.2	20	2	US-09-724-953-33	Sequence 33, Appl
70	88.2	20	2	US-09-724-567-33	Sequence 33, Appl
71	88.2	20	2	US-09-979-352-33	Sequence 33, Appl
72	88.2	20	2	US-09-585-817-33	Sequence 33, Appl
73	88.2	26	1	US-08-304-585-7	Sequence 7, Appl
74	88.2	28	1	US-08-346-849-4	Sequence 4, Appl
75	88.2	28	1	US-08-302-808-7	Sequence 7, Appl
76	88.2	28	1	US-08-609-090-2	Sequence 2, Appl
77	88.2	28	1	US-08-986-948-7	Sequence 7, Appl
78	88.2	28	1	US-08-293-284A-4	Sequence 4, Appl
79	88.2	28	1	US-08-461-216-2	Sequence 2, Appl
80	88.2	28	2	US-09-388-890-2	Sequence 2, Appl
81	88.2	28	2	US-09-388-890-3	Sequence 3, Appl
82	88.2	28	2	US-09-388-890-4	Sequence 4, Appl
83	88.2	28	2	US-09-388-890-5	Sequence 5, Appl
84	88.2	28	2	US-09-388-890-6	Sequence 6, Appl
85	88.2	28	2	US-09-388-890-7	Sequence 7, Appl
86	88.2	28	2	US-09-388-890-8	Sequence 8, Appl
87	88.2	28	2	US-09-388-890-9	Sequence 9, Appl
88	88.2	28	2	US-09-388-890-10	Sequence 10, Appl
89	88.2	28	2	US-09-388-890-12	Sequence 12, Appl
90	88.2	28	2	US-09-388-890-13	Sequence 13, Appl
91	88.2	28	2	US-09-388-890-14	Sequence 14, Appl
92	88.2	28	2	US-09-264-709A-1	Sequence 1, Appl
93	88.2	28	2	US-08-723-661B-2	Sequence 2, Appl
94	88.2	28	2	US-09-660-954-2	Sequence 2, Appl
95	88.2	28	2	US-09-660-954-3	Sequence 3, Appl
96	88.2	28	2	US-09-660-954-4	Sequence 4, Appl
97	88.2	28	2	US-09-660-954-5	Sequence 5, Appl
98	88.2	28	2	US-09-660-954-6	Sequence 6, Appl
99	88.2	28	2	US-09-660-954-7	Sequence 7, Appl
100	88.2	28	2	US-09-660-954-8	Sequence 8, Appl

101	30	88.2	28	2	US-09-660-954-9	Sequence 9, Appli	174	30	88.2	40	2	US-09-623-548A-995	Sequence 995, App
102	30	88.2	28	2	US-09-660-954-10	Sequence 10, Appli	175	30	88.2	40	2	US-09-623-548A-1005	Sequence 1005, Ap
103	30	88.2	28	2	US-09-660-954-11	Sequence 11, Appli	176	30	88.2	40	2	US-09-657-276-956	Sequence 956, App
104	30	88.2	28	2	US-09-660-954-12	Sequence 12, Appli	177	30	88.2	40	2	US-09-657-276-962	Sequence 962, App
105	30	88.2	28	2	US-09-660-954-13	Sequence 13, Appli	178	30	88.2	40	2	US-09-657-276-968	Sequence 968, App
106	30	88.2	28	2	US-08-898-300-4	Sequence 14, Appli	179	30	88.2	40	2	US-09-657-276-978	Sequence 978, App
107	30	88.2	28	2	US-08-824-513-4	Sequence 4, Appli	180	30	88.2	40	2	US-09-657-276-989	Sequence 989, App
108	30	88.2	28	2	US-09-623-548A-959	Sequence 959, App	181	30	88.2	40	2	US-09-657-276-995	Sequence 995, App
109	30	88.2	28	2	US-09-623-548A-965	Sequence 965, App	182	30	88.2	40	2	US-09-657-276-1005	Sequence 1005, Ap
110	30	88.2	28	2	US-09-623-548A-976	Sequence 976, App	183	30	88.2	40	2	US-09-657-276-1005	Sequence 1005, Ap
111	30	88.2	28	2	US-09-623-548A-992	Sequence 992, App	184	30	88.2	40	2	PCT-US92-06700-1	Sequence 1, Appli
112	30	88.2	28	2	US-09-623-548A-1003	Sequence 1003, Ap	185	30	88.2	41	4	US-08-302-808-4	Sequence 1, Appli
113	30	88.2	28	2	US-09-657-276-959	Sequence 959, App	186	30	88.2	41	1	US-08-302-808-4	Sequence 1, Appli
114	30	88.2	28	2	US-09-657-276-965	Sequence 965, App	187	30	88.2	41	1	US-08-302-808-4	Sequence 1, Appli
115	30	88.2	28	2	US-09-657-276-976	Sequence 976, App	188	30	88.2	41	1	US-08-302-808-4	Sequence 1, Appli
116	30	88.2	28	2	US-09-657-276-992	Sequence 992, App	189	30	88.2	41	1	US-08-302-808-4	Sequence 1, Appli
117	30	88.2	28	2	US-09-657-276-1003	Sequence 1003, Ap	190	30	88.2	42	1	US-07-744-767A-2	Sequence 2, Appli
118	30	88.2	28	2	US-08-865-294A-66	Sequence 66, Appli	191	30	88.2	42	1	US-08-179-574-1	Sequence 1, Appli
119	30	88.2	30	1	US-08-609-090-3	Sequence 3, Appli	192	30	88.2	42	1	US-08-271-162-5	Sequence 5, Appli
120	30	88.2	30	1	US-09-861-847A-1	Sequence 1, Appli	193	30	88.2	42	1	US-08-347-144-1	Sequence 1, Appli
121	30	88.2	33	1	US-08-609-090-4	Sequence 4, Appli	194	30	88.2	42	1	US-08-462-859A-19	Sequence 19, Appl
122	30	88.2	35	1	US-08-304-585-6	Sequence 6, Appli	195	30	88.2	42	1	US-08-123-659A-19	Sequence 19, Appl
123	30	88.2	35	1	US-08-612-785B-16	Sequence 16, Appli	196	30	88.2	42	1	US-08-464-247A-19	Sequence 19, Appl
124	30	88.2	35	1	US-08-612-785B-36	Sequence 36, Appli	197	30	88.2	42	1	US-08-464-248A-19	Sequence 19, Appl
125	30	88.2	35	1	US-08-612-785B-38	Sequence 38, Appli	198	30	88.2	42	1	US-08-476-464A-1	Sequence 1, Appli
126	30	88.2	35	1	US-08-612-785B-40	Sequence 40, Appli	199	30	88.2	42	1	US-08-304-585-2	Sequence 2, Appli
127	30	88.2	35	2	US-08-617-267C-16	Sequence 16, Appli	200	30	88.2	42	1	US-08-302-808-5	Sequence 5, Appli
128	30	88.2	35	2	US-09-623-548A-979	Sequence 979, App	201	30	88.2	42	1	US-08-268-348A-1	Sequence 1, Appli
129	30	88.2	35	2	US-09-623-548A-1006	Sequence 1006, Ap	202	30	88.2	42	1	US-08-268-348A-2	Sequence 2, Appli
130	30	88.2	35	2	US-09-657-276-979	Sequence 979, App	203	30	88.2	42	1	US-08-268-348A-3	Sequence 3, Appli
131	30	88.2	35	2	US-09-657-276-1006	Sequence 1006, Ap	204	30	88.2	42	1	US-08-268-348A-4	Sequence 4, Appli
132	30	88.2	36	1	US-08-609-090-6	Sequence 6, Appli	205	30	88.2	42	1	US-08-268-348A-5	Sequence 5, Appli
133	30	88.2	36	2	US-09-861-847A-6	Sequence 6, Appli	206	30	88.2	42	1	US-08-268-348A-6	Sequence 6, Appli
134	30	88.2	36	2	US-09-861-847A-11	Sequence 11, Appli	207	30	88.2	42	1	US-08-433-734-2	Sequence 2, Appli
135	30	88.2	38	1	US-08-302-808-1	Sequence 1, Appli	208	30	88.2	42	1	US-08-609-090-9	Sequence 9, Appli
136	30	88.2	38	1	US-07-737-371E-68	Sequence 68, Appli	209	30	88.2	42	1	US-07-737-371E-72	Sequence 72, Appli
137	30	88.2	38	1	US-08-986-948-1	Sequence 1, Appli	210	30	88.2	42	1	US-08-422-333-4	Sequence 4, Appli
138	30	88.2	38	1	US-09-623-548A-975	Sequence 975, App	211	30	88.2	42	1	US-08-682-245A-4	Sequence 4, Appli
139	30	88.2	38	2	US-09-623-548A-1002	Sequence 1002, Ap	212	30	88.2	42	1	US-08-986-948-5	Sequence 5, Appli
140	30	88.2	38	2	US-09-657-276-975	Sequence 975, App	213	30	88.2	42	2	US-08-717-551A-2	Sequence 2, Appli
141	30	88.2	38	2	US-09-657-276-1002	Sequence 1002, Ap	214	30	88.2	42	2	US-09-388-890-1	Sequence 1, Appli
142	30	88.2	39	1	US-08-304-585-5	Sequence 5, Appli	215	30	88.2	42	2	US-09-005-215-20	Sequence 20, Appli
143	30	88.2	39	1	US-08-302-808-2	Sequence 2, Appli	216	30	88.2	42	2	US-09-242-724-23	Sequence 23, Appli
144	30	88.2	39	1	US-08-609-090-7	Sequence 7, Appli	217	30	88.2	42	2	US-08-922-930-2	Sequence 2, Appli
145	30	88.2	39	1	US-08-682-245A-1	Sequence 1, Appli	218	30	88.2	42	2	US-09-660-954-1	Sequence 1, Appli
146	30	88.2	39	1	US-08-986-948-2	Sequence 2, Appli	219	30	88.2	42	2	US-08-923-055-2	Sequence 2, Appli
147	30	88.2	40	1	US-07-744-767A-1	Sequence 1, Appli	220	30	88.2	42	2	US-08-922-889-2	Sequence 2, Appli
148	30	88.2	40	1	US-08-235-400-2	Sequence 2, Appli	221	30	88.2	42	2	US-08-731-460-1	Sequence 1, Appli
149	30	88.2	40	1	US-08-476-464A-2	Sequence 2, Appli	222	30	88.2	42	2	US-09-133-866-2	Sequence 2, Appli
150	30	88.2	40	1	US-08-304-585-1	Sequence 1, Appli	223	30	88.2	42	2	US-09-723-384-1	Sequence 1, Appli
151	30	88.2	40	1	US-08-304-585-8	Sequence 8, Appli	224	30	88.2	42	2	US-09-724-961-42	Sequence 42, Appli
152	30	88.2	40	1	US-08-302-808-3	Sequence 3, Appli	225	30	88.2	42	2	US-09-724-961-42	Sequence 42, Appli
153	30	88.2	40	1	US-08-433-734-1	Sequence 1, Appli	226	30	88.2	42	2	US-10-455-218-2	Sequence 2, Appli
154	30	88.2	40	1	US-08-609-090-8	Sequence 8, Appli	227	30	88.2	42	2	US-09-723-429-1	Sequence 1, Appli
155	30	88.2	40	1	US-07-737-371E-69	Sequence 69, Appli	228	30	88.2	42	2	US-09-724-961-42	Sequence 42, Appli
156	30	88.2	40	1	US-08-682-245A-2	Sequence 2, Appli	229	30	88.2	42	2	US-09-723-429-1	Sequence 1, Appli
157	30	88.2	40	1	US-08-986-948-3	Sequence 3, Appli	230	30	88.2	42	2	US-09-723-762-1	Sequence 1, Appli
158	30	88.2	40	1	US-08-461-216-1	Sequence 1, Appli	231	30	88.2	42	2	US-09-201-430-1	Sequence 1, Appli
159	30	88.2	40	2	US-08-959-148-1	Sequence 1, Appli	232	30	88.2	42	2	US-09-724-961-42	Sequence 42, Appli
160	30	88.2	40	2	US-09-242-724-22	Sequence 22, Appli	233	30	88.2	42	2	US-10-815-353-1	Sequence 1, Appli
161	30	88.2	40	2	US-08-723-661B-1	Sequence 1, Appli	234	30	88.2	42	2	US-10-278-181-1	Sequence 1, Appli
162	30	88.2	40	2	US-09-062-365-3	Sequence 3, Appli	235	30	88.2	42	2	US-10-816-529-1	Sequence 1, Appli
163	30	88.2	40	2	US-09-133-866-1	Sequence 1, Appli	236	30	88.2	42	2	US-09-623-548A-955	Sequence 955, App
164	30	88.2	40	2	US-09-861-847A-7	Sequence 7, Appli	237	30	88.2	42	2	US-09-623-548A-961	Sequence 961, App
165	30	88.2	40	2	US-09-861-847A-8	Sequence 8, Appli	238	30	88.2	42	2	US-08-623-548A-967	Sequence 967, App
166	30	88.2	40	2	US-09-988-842-3	Sequence 3, Appli	239	30	88.2	42	2	US-09-623-548A-988	Sequence 988, App
167	30	88.2	40	2	US-10-455-218-1	Sequence 1, Appli	240	30	88.2	42	2	US-09-623-548A-994	Sequence 994, App
168	30	88.2	40	2	US-10-151-614-1	Sequence 1, Appli	241	30	88.2	42	2	US-10-815-391-1	Sequence 1, Appli
169	30	88.2	40	2	US-09-623-548A-956	Sequence 956, App	242	30	88.2	42	2	US-10-816-022-1	Sequence 1, Appli
170	30	88.2	40	2	US-09-623-548A-962	Sequence 962, App	243	30	88.2	42	2	US-09-724-961-42	Sequence 42, Appli
171	30	88.2	40	2	US-09-623-548A-968	Sequence 968, App	244	30	88.2	42	2	US-09-657-276-955	Sequence 955, App
172	30	88.2	40	2	US-09-623-548A-978	Sequence 978, App	245	30	88.2	42	2	US-09-657-276-961	Sequence 961, App
173	30	88.2	40	2	US-09-623-548A-989	Sequence 989, App	246	30	88.2	42	2	US-09-657-276-967	Sequence 967, App

247	30	88.2	42	2	US-09-657-276-988	Sequence 988, Appl
248	30	88.2	42	2	US-09-657-276-994	Sequence 994, Appl
249	30	88.2	42	2	US-09-724-567-34	Sequence 34, Appl
250	30	88.2	42	2	US-09-724-940-42	Sequence 42, Appl
251	30	88.2	42	2	US-09-865-294A-65	Sequence 65, Appl
252	30	88.2	42	2	US-09-979-952-34	Sequence 34, Appl
253	30	88.2	42	2	US-09-585-817-34	Sequence 34, Appl
254	30	88.2	42	2	US-09-962-955D-37	Sequence 37, Appl
255	30	88.2	42	2	US-09-706-574A-20	Sequence 20, Appl
256	30	88.2	42	2	US-10-934-609-1	Sequence 1, Appli
257	30	88.2	42	2	US-10-884-892-1	Sequence 1, Appli
258	30	88.2	42	4	PCT-US92-06700-2	Sequence 2, Appli
259	30	88.2	42	4	PCT-US93-00325-1	Sequence 1, Appli
260	30	88.2	42	4	PCT-US95-08302-5	Sequence 5, Appli
261	30	88.2	42	6	5220013-12	Patent No. 5220013
262	30	88.2	42	6	5220013-14	Patent No. 5220013
263	30	88.2	42	6	5223482-12	Patent No. 5223482
264	30	88.2	43	1	US-08-235-400-1	Sequence 1, Appli
265	30	88.2	43	1	US-08-437-067-1	Sequence 1, Appli
266	30	88.2	43	1	US-08-302-808-6	Sequence 6, Appli
267	30	88.2	43	1	US-08-079-511-1	Sequence 1, Appli
268	30	88.2	43	1	US-08-467-607-1	Sequence 1, Appli
269	30	88.2	43	1	US-08-404-831-1	Sequence 1, Appli
270	30	88.2	43	1	US-08-602-264A-3	Sequence 3, Appli
271	30	88.2	43	1	US-08-469-362-1	Sequence 1, Appli
272	30	88.2	43	1	US-08-612-785B-1	Sequence 1, Appli
273	30	88.2	43	1	US-08-475-579A-1	Sequence 1, Appli
274	30	88.2	43	1	US-08-850-392-1	Sequence 1, Appli
275	30	88.2	43	1	US-07-737-371B-70	Sequence 70, Appli
276	30	88.2	43	1	US-08-986-94B-6	Sequence 6, Appli
277	30	88.2	43	1	US-08-975-977-1	Sequence 1, Appli
278	30	88.2	43	1	US-08-817-423-1	Sequence 1, Appli
279	30	88.2	43	1	US-08-920-162A-1	Sequence 1, Appli
280	30	88.2	43	1	US-08-461-018A-3	Sequence 3, Appli
281	30	88.2	43	2	US-08-976-191-1	Sequence 1, Appli
282	30	88.2	43	2	US-08-339-141A-1	Sequence 1, Appli
283	30	88.2	43	2	US-08-976-179-1	Sequence 1, Appli
284	30	88.2	43	2	US-09-216-95B-3	Sequence 3, Appli
285	30	88.2	43	2	US-09-356-931-1	Sequence 1, Appli
286	30	88.2	43	2	US-08-733-202-1	Sequence 1, Appli
287	30	88.2	43	2	US-08-703-675C-1	Sequence 1, Appli
288	30	88.2	43	2	US-09-390-692-1	Sequence 1, Appli
289	30	88.2	43	2	US-08-617-267C-1	Sequence 1, Appli
290	30	88.2	43	2	US-09-303-655-1	Sequence 1, Appli
291	30	88.2	43	2	US-08-294-819-1	Sequence 1, Appli
292	30	88.2	43	2	US-09-408-283-1	Sequence 1, Appli
293	30	88.2	43	2	US-09-280-966-1	Sequence 1, Appli
294	30	88.2	43	2	US-09-032-019-1	Sequence 1, Appli
295	30	88.2	43	2	US-09-481-980A-1	Sequence 1, Appli
296	30	88.2	43	2	US-09-594-366-1	Sequence 1, Appli
297	30	88.2	43	2	US-08-665-649-1	Sequence 1, Appli
298	30	88.2	43	2	US-09-519-019A-1	Sequence 1, Appli
299	30	88.2	43	2	US-09-915-342-1	Sequence 1, Appli
300	30	88.2	43	2	US-08-996-442-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-747-408-2
; Sequence 2, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, France
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23

```

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-2

Query Match      100.0%; Score 34; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKLVEFA 7
Db      1 KKLVEFA 7

RESULT 2
US-08-766-596A-64
; Sequence 64, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-64

Query Match      100.0%; Score 34; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKLVEFA 7

```

```
Db          1 KKLVEFA 7
|||||
RESULT 3
US-08-475-579A-4
; Sequence 4, Application US/08475579A
; Patent No. 5854215
; GENERAL INFORMATION:
; APPLICANT: Mark A. Findeis et al.
; TITLE OF INVENTION: Modulators of (SYMBOL 98 \f "Symbol")-Amyloid Peptide Aggrega
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,579A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/404,831
; FILING DATE: 14-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: P41,106
; REFERENCE/DOCKET NUMBER: PPI-002CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-475-579A-4
Query Match      100.0%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KKLVEFA 7
|||||
Db          9 KKLVEFA 15
|||||
RESULT 4
US-09-242-724-33
; Sequence 33, Application US/09242724
; Patent No. 6316405
; GENERAL INFORMATION:
; APPLICANT: Solomon, Michael E.
; APPLICANT: Rich, Daniel H.
; TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
; FILE REFERENCE: Cyclosporin Analogs
; CURRENT APPLICATION NUMBER: US/09/242,724
; CURRENT FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 6
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: polypeptide
US-09-242-724-33
Query Match      88.2%; Score 30; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KKLVEFA 6
|||||
Db          1 KKLVEFA 6
|||||
RESULT 5
US-08-612-785B-7
; Sequence 7, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-7
Query Match      88.2%; Score 30; DB 1; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KKLVEFA 7
|||||
Db          1 KKLVEFA 7
|||||
```

```
RESULT 6
US-08-703-675C-30
; Sequence 30, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Fingels, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-703-675C-30

Query Match      88.2%; Score 30; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKLVFFA 7
Db      1 QKLVFFA 7

RESULT 7
US-08-617-267C-7
; Sequence 7, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Fingels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-617-267C-7

Query Match      88.2%; Score 30; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKLVFFA 7
Db      1 QKLVFFA 7

RESULT 8
US-08-612-785B-5
; Sequence 5, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Fingels, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-617-267C-7

Query Match      88.2%; Score 30; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKLVFFA 7
Db      1 QKLVFFA 7

Aggregation Comprising D-
```

```

; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-703-675C-28

Query Match      88.2%; Score 30; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
Db      2 QKLVPFA 8

RESULT 10
US-08-617-267C-5
; Sequence 5, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findex, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US88/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US88/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US88/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-617-267C-5

Query Match      88.2%; Score 30; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
Db      2 QKLVPFA 8

RESULT 11
US-08-766-596A-54

```



```
; Sequence 54, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEROP FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATIONS WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-766-596A-54

Query Match      88.2%; Score 30; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFF 6
        :|||||
Db      1 KKLVPFF 6

RESULT 12
US-09-747-408-20
; Sequence 20, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-747-408-20

Query Match      88.2%; Score 30; DB 2; Length 9;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFF 7
        :|||||
Db      3 QKLVPFF 9

RESULT 13
US-09-724-961-20
; Sequence 20, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid)
; OTHER INFORMATION: peptide)
; US-09-724-961-20

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFF 7
        :|||||
Db      4 QKLVPFF 10

RESULT 14
US-09-724-961-21
; Sequence 21, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
```

```
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-724-961-21

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
      :|||||
DB      3 QKLVPFA 9

RESULT 15
US-09-724-961-22
; Sequence 22, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-724-961-22

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
      :|||||
DB      3 QKLVPFA 9
```

```
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
      :|||||
DB      2 QKLVPFA 8

RESULT 16
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-09-724-961-23

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
      :|||||
DB      1 QKLVPFA 7

RESULT 17
US-09-580-018-20
; Sequence 20, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-20

Query Match 88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 4 QKLVPFA 10

RESULT 18
US-09-580-018-21
; Sequence 21, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-21

Query Match 88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 3 QKLVPFA 9

RESULT 19
US-09-580-018-22
; Sequence 22, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-22

Query Match 88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 2 QKLVPFA 8

RESULT 20
US-09-580-018-23
; Sequence 23, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-23

Query Match 88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 1 QKLVPFA 7

RESULT 21
US-09-724-551-20
; Sequence 20, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid

```
; OTHER INFORMATION: peptide)
US-09-724-551-20

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 4 QKLVPFA 10

RESULT 22
US-09-724-551-21
; Sequence 21, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-21

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 3 QKLVPFA 9

RESULT 23
US-09-724-551-22
; Sequence 22, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-22

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 1 QKLVPFA 7

RESULT 24
US-09-724-551-23
; Sequence 23, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-23

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
   :|||||
Db 1 QKLVPFA 7

RESULT 25
US-09-724-940-20
; Sequence 20, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
```

; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-20

Query Match 88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db :|||||
4 QKLVPFA 10

RESULT 26

US-09-724-940-21
; Sequence 21, Application US/09724940
; Patent No. 6905686

; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki

; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940

; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015

; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430

; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810

; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970

; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740

; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-21

Query Match 88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db :|||||
3 QKLVPFA 9

RESULT 27

US-09-724-940-22

; Sequence 22, Application US/09724940
; Patent No. 6905686

; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940

; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015

; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430

; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810

; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970

; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740

; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-22

Query Match 88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db :|||||
2 QKLVPFA 8

RESULT 28

US-09-724-940-23

; Sequence 23, Application US/09724940
; Patent No. 6905686

; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki

; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940

; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015

; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430

; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810

; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970

; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740

; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence

```
/ ; FEATURE:
/ ; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
/ ; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
/ ; OTHER INFORMATION: peptide)
US-09-724-940-23

Query Match      88.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
Db      1 QKLVPFA 7

RESULT 29
US-08-630-645-14
/ ; Sequence 14, Application US/08630645
/ ; Patent No. 5948763
/ ; GENERAL INFORMATION:
/ ; APPLICANT: SOTO-JARA, Claudio
/ ; APPLICANT: BAUMANN, Marc
/ ; APPLICANT: FRANGIONE, Blas
/ ; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
/ ; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
/ ; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
/ ; NUMBER OF SEQUENCES: 26
/ ; CORRESPONDENCE ADDRESS:
/ ; ADDRESSEE: BROWDY AND NEIMARK
/ ; STREET: 419 Seventh Street, N.W., Suite 400
/ ; CITY: Washington
/ ; STATE: D.C.
/ ; COUNTRY: USA
/ ; ZIP: 20004
/ ; COMPUTER READABLE FORM:
/ ; MEDIUM TYPE: Floppy disk
/ ; COMPUTER: IBM PC compatible
/ ; OPERATING SYSTEM: PC-DOS/MS-DOS
/ ; SOFTWARE: PatentIn Release #1.0, Version #1.30
/ ; CURRENT APPLICATION DATA:
/ ; APPLICATION NUMBER: US/08/630,645
/ ; FILING DATE:
/ ; CLASSIFICATION: 530
/ ; PRIOR APPLICATION DATA:
/ ; APPLICATION NUMBER: US 08/478,326
/ ; FILING DATE: 06-JUN-1995
/ ; ATTORNEY/AGENT INFORMATION:
/ ; NAME: YUN, Allen C.
/ ; REGISTRATION NUMBER: 37,971
/ ; REFERENCE/DOCKET NUMBER: SOTO-JARA=1
/ ; TELECOMMUNICATION INFORMATION:
/ ; TELEPHONE: 202-628-5197
/ ; TELEFAX: 202-737-3528
/ ; INFORMATION FOR SEQ ID NO: 14:
/ ; SEQUENCE CHARACTERISTICS:
/ ; LENGTH: 11 amino acids
/ ; TYPE: amino acid
/ ; STRANDEDNESS: single
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: peptide
US-08-630-645-14

Query Match      88.2%; Score 30; DB 1; Length 11;
Best Local Similarity 85.7%; Pred. No. 5.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
Db      1 QKLVPFA 7

RESULT 30
US-08-766-596A-14
```

```
/ ; Sequence 14, Application US/08766596A
/ ; Patent No. 6462171
/ ; GENERAL INFORMATION:
/ ; APPLICANT: SOTO-JARA, Claudio
/ ; APPLICANT: BAUMANN, Marc
/ ; APPLICANT: FRANGIONE, Blas
/ ; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
/ ; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
/ ; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
/ ; TITLE OF INVENTION: DEPOSITS
/ ; NUMBER OF SEQUENCES: 69
/ ; CORRESPONDENCE ADDRESS:
/ ; ADDRESSEE: BROWDY AND NEIMARK
/ ; STREET: 419 Seventh Street, N.W., Suite 400
/ ; CITY: Washington
/ ; STATE: D.C.
/ ; COUNTRY: USA
/ ; ZIP: 20004
/ ; COMPUTER READABLE FORM:
/ ; MEDIUM TYPE: Floppy disk
/ ; COMPUTER: IBM PC compatible
/ ; OPERATING SYSTEM: PC-DOS/MS-DOS
/ ; SOFTWARE: PatentIn Release #1.0, Version #1.30
/ ; CURRENT APPLICATION DATA:
/ ; APPLICATION NUMBER: US/08/766,596A
/ ; FILING DATE:
/ ; CLASSIFICATION: 435
/ ; PRIOR APPLICATION DATA:
/ ; APPLICATION NUMBER: US 08/630,645
/ ; FILING DATE: 10-APR-1996
/ ; PRIOR APPLICATION NUMBER:
/ ; APPLICATION NUMBER: US 08/478,326
/ ; FILING DATE: 06-JUN-1995
/ ; ATTORNEY/AGENT INFORMATION:
/ ; NAME: YUN, Allen C.
/ ; REGISTRATION NUMBER: 37,971
/ ; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
/ ; TELECOMMUNICATION INFORMATION:
/ ; TELEPHONE: 202-628-5197
/ ; TELEFAX: 202-737-3528
/ ; INFORMATION FOR SEQ ID NO: 14:
/ ; SEQUENCE CHARACTERISTICS:
/ ; LENGTH: 11 amino acids
/ ; TYPE: amino acid
/ ; STRANDEDNESS: single
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: peptide
US-08-766-596A-14

Query Match      88.2%; Score 30; DB 2; Length 11;
Best Local Similarity 85.7%; Pred. No. 5.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
Db      1 QKLVPFA 7

RESULT 31
US-09-988-842-9
/ ; Sequence 9, Application US/09988842
/ ; Patent No. 6716589
/ ; GENERAL INFORMATION:
/ ; APPLICANT: Johansson, Jan
/ ; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
/ ; TITLE OF INVENTION: OF AMYLOID FORMATION
/ ; FILE REFERENCE: 12125-002001
/ ; CURRENT APPLICATION NUMBER: US/09/988,842
/ ; CURRENT FILING DATE: 2001-11-19
/ ; PRIOR APPLICATION NUMBER: US 60/251,662
/ ; PRIOR FILING DATE: 2000-12-06
/ ; PRIOR APPLICATION NUMBER: US 60/253,695
/ ; PRIOR FILING DATE: 2000-11-20
```

```
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

Query Match      88.2%; Score 30; DB 2; Length 11;
Best Local Similarity 85.7%; Pred. No. 5.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 1 QKLVPFA 7

RESULT 32
US-09-988-842-25
; Sequence 25, Application US/09988842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johanson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

Query Match      88.2%; Score 30; DB 2; Length 11;
Best Local Similarity 85.7%; Pred. No. 5.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 1 QKLVPFA 7

RESULT 33
PCT-US96-10220-14
; Sequence 14, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEROP FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

Query Match      88.2%; Score 30; DB 2; Length 11;
Best Local Similarity 85.7%; Pred. No. 5.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 1 QKLVPFA 7

RESULT 34
US-09-594-366-5
; Sequence 5, Application US/09594366
; Patent No. 6582945
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2004
; CURRENT APPLICATION NUMBER: US/09/594,366
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-594-366-5

Query Match      88.2%; Score 30; DB 2; Length 14;
Best Local Similarity 85.7%; Pred. No. 6.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 3 QKLVPFA 9

RESULT 35
US-09-992-800-5
; Sequence 5, Application US/09992800
; Patent No. 6872554
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2006
; CURRENT APPLICATION NUMBER: US/09/992,800
```

; CURRENT FILING DATE: 2001-11-06
 ; PRIOR APPLICATION NUMBER: 09/594,366
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/139,408
 ; PRIOR FILING DATE: 1999-06-16
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-992-800-5

Query Match 88.2%; Score 30; DB 2; Length 14;
 Best Local Similarity 85.7%; Pred. No. 6.8;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
 Db 3 QKLVFFA 9

RESULT 36
 US-08-612-785B-37
 ; Sequence 37, Application US/08612785B
 ; Patent No. 5854204
 ; GENERAL INFORMATION:
 ; APPLICANT: Findeis, Mark A. et al.
 ; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
 ; NUMBER OF INVENTIONS: Aggregation
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 28 State Street, Suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION NUMBER: US/08/612,785B
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: USSN 08/404,831
 ; FILING DATE: 14-MAR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: USSN 08/475,579
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: USSN 08/548,998
 ; FILING DATE: 27-OCT-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DeConti, Giulio A.
 ; REGISTRATION NUMBER: 31,503
 ; REFERENCE/DOCKET NUMBER: PPI-002CP3
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214
 ; INFORMATION FOR SEQ ID NO: 37:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 US-08-612-785B-37

Query Match 88.2%; Score 30; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 7.3;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVFFA 7
 Db 5 QKLVFFA 11
 RESULT 37
 US-08-766-596A-56
 ; Sequence 56, Application US/08766596A
 ; Patent No. 6462171
 ; GENERAL INFORMATION:
 ; APPLICANT: SOTO-JARA, Claudio
 ; APPLICANT: BAUMANN, Marc
 ; APPLICANT: FRANGIONE, Blas
 ; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
 ; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
 ; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 400
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/766,596A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/630,645
 ; FILING DATE: 10-APR-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/478,326
 ; FILING DATE: 06-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: YUN, Allen C.
 ; REGISTRATION NUMBER: 37,971
 ; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-766-596A-56

Query Match 88.2%; Score 30; DB 2; Length 15;
 Best Local Similarity 85.7%; Pred. No. 7.3;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
 Db 4 QKLVFFA 10

RESULT 38
 US-08-766-596A-57
 ; Sequence 57, Application US/08766596A
 ; Patent No. 6462171
 ; GENERAL INFORMATION:

APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/766,596A
FILING DATE: 10-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-57

Query Match 88.2%; Score 30; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 7.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 4 QKLVPFA 10

RESULT 39
US-08-766-596A-60
Sequence 60, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-60

Query Match 88.2%; Score 30; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 7.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 4 QKLVPFA 10

RESULT 40
US-08-766-596A-61
Sequence 61, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645

;; FILING DATE: 10-APR-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/478,326
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: YUN, Allen C.
;; REGISTRATION NUMBER: 37,971
;; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 61:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-766-596A-61

Query Match 88.2%; Score 30; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 7.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 4 QKLVPFA 10

RESULT 41
US-08-766-596A-63
; Sequence 63, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-766-596A-63

Query Match 88.2%; Score 30; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 7.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 4 QKLVPFA 10

RESULT 42
US-08-766-596A-65
; Sequence 65, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-65

Query Match 88.2%; Score 30; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 7.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 4 QKLVPFA 10

Db 4 QKLVFFA 10

RESULT 43

US-09-264-709A-2
; Sequence 2, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
; APPLICANT: Roberts, Eugene
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
; TITLE OF INVENTION: Improve the Quality of Life
; FILE REFERENCE: 2124-310
; CURRENT APPLICATION NUMBER: US/09/264,709A
; CURRENT FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 08/797,782
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-264-709A-2

Query Match 88.2%; Score 30; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
:|||||
Db 4 QKLVFFA 10

RESULT 44

US-09-594-366-3
; Sequence 3, Application US/09594366
; Patent No. 6582945
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2004
; CURRENT APPLICATION NUMBER: US/09/594,366
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-594-366-3

Query Match 88.2%; Score 30; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
:|||||
Db 7 QKLVFFA 13

RESULT 45

US-09-623-548A-950
; Sequence 950, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen

; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 950
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-950

Query Match 88.2%; Score 30; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
:|||||
Db 4 QKLVFFA 10

RESULT 46

US-09-623-548A-983
; Sequence 983, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 983
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-983

Query Match 88.2%; Score 30; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
:|||||
Db 4 QKLVFFA 10

```
RESULT 47
US-09-992-800-3
; Sequence 3, Application US/09992800
; Patent No. 6872554
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2006
; CURRENT APPLICATION NUMBER: US/09/992,800
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-800-3

Query Match      88.2%; Score 30; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFA 7
DB      7 QKLVEFA 13

RESULT 48
US-09-657-276-950
; Sequence 950, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjugchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 950
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-950

Query Match      88.2%; Score 30; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFA 7
DB      7 QKLVEFA 13

RESULT 49
US-09-657-276-983
; Sequence 983, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjugchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 983
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-983

Query Match      88.2%; Score 30; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFA 7
DB      4 QKLVEFA 10

RESULT 50
US-08-970-833-11
; Sequence 11, Application US/08970833
; Patent No. 6022859
; GENERAL INFORMATION:
; APPLICANT: Kiessling, Laura L.
; APPLICANT: Murphy, Regina M.
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,833
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
```

```

; OTHER INFORMATION: inserted and two added Gly residues
;
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)_
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-724-552-5

Query Match      88.2%  Score 30;  DB 2;  Length 19;
Best Local Similarity 85.7%  Pred. No. 9;
Matches 6;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1  KKLVFFA 7
      : |||||

```

Db 3 QKLVFFA 9

RESULT 54

US-09-580-018-75
; Sequence 75, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Beta 13-28
; OTHER INFORMATION: peptide with two Gly residues added and inserted
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = N-acetyl His
US-09-580-018-75

Query Match 88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
:|||||
Db 3 QKLVFFA 9

RESULT 55

US-09-723-927-5
; Sequence 5, Application US/09723927
; Patent No. 6787138
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/723,927
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-723-927-5

Query Match 88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
:|||||
Db 3 QKLVFFA 9

Query Match 88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
:|||||
Db 3 QKLVFFA 9

RESULT 56

US-09-724-489-5
; Sequence 5, Application US/09724489
; Patent No. 6787140
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/724,489
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-724-489-5

Query Match 88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
:|||||
Db 3 QKLVFFA 9

RESULT 57

US-09-724-477-5
; Sequence 5, Application US/09724477
; Patent No. 6787143
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/724,477
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT

Query Match 88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFFA 7
:|||||
Db 3 QKLVFFA 9

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-724-477-5

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
Db 3 QKLVFPA 9

RESULT 58
US-09-723-762-5
; Sequence 5, Application US/09723762
; Patent No. 6787144
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/723,762
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-723-762-5

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
Db 3 QKLVFPA 9

RESULT 59
US-09-201-430-5
; Sequence 5, Application US/09201430
; Patent No. 6787523
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/09/201,430
; CURRENT FILING DATE: 1998-11-30

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-09-723-762-5

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
Db 3 QKLVFPA 9

RESULT 60
US-09-724-551-75
; Sequence 75, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta 13-28
; OTHER INFORMATION: peptide with two Gly residues added and inserted
; OTHER INFORMATION: Cys residue
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = N-acetyl His
US-09-724-551-75

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFPA 7
Db 3 QKLVFPA 9

RESULT 61
US-10-815-353-5
; Sequence 5, Application US/10815353
; Patent No. 6808712
```

```
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/10/815,353
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-815-353-5

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
       :|||||
DB      3 QKLVPFA 9

RESULT 62
US-10-816-529-5
; Sequence 5, Application US/10816529
; Patent No. 6818218
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/10/816,529
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-816-529-5

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
       :|||||
DB      3 QKLVPFA 9

US-10-816-529-5
; Sequence 5, Application US/10816529
; Patent No. 6818218
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/10/816,529
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-816-529-5

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
       :|||||
DB      3 QKLVPFA 9

RESULT 63
US-10-815-391-5
; Sequence 5, Application US/10815391
; Patent No. 6866849
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/10/815,391
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-815-391-5

Query Match      88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFA 7
       :|||||
DB      3 QKLVPFA 9

RESULT 64
US-10-816-022-5
; Sequence 5, Application US/10816022
; Patent No. 6866850
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/10/816,022
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```


; OTHER INFORMATION: Description of Artificial Sequence:Abetal3-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-816-022-5

Query Match 88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
:|||||
Db 3 QKLVPFA 9

RESULT 65

US-09-724-940-75
; Sequence 75, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 75
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta 13-28
; OTHER INFORMATION: peptide with two Gly residues added and inserted
; OTHER INFORMATION: Cys residue
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = N-acetyl His
US-09-724-940-75

Query Match 88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
:|||||
Db 3 QKLVPFA 9

RESULT 66

US-10-934-609-5
; Sequence 5, Application US/10934609
; Patent No. 6946135
; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/10/934,609
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abetal3-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-609-5

Query Match 88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
:|||||
Db 3 QKLVPFA 9

RESULT 67

US-10-884-892-5
; Sequence 5, Application US/10884892
; Patent No. 6962707
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004720US
; CURRENT APPLICATION NUMBER: US/10/884,892
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abetal3-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-884-892-5

Query Match 88.2%; Score 30; DB 2; Length 19;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 KKLVEFA 7
      :|||||
Db      3 QKLVEFA 9

RESULT 68
US-08-970-833-10
; Sequence 10, Application US/08970833
; Patent No. 6022859
; GENERAL INFORMATION:
; APPLICANT: Klessling, Laura L.
; APPLICANT: Murphy, Regina M.
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,833
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 960296.94291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 13..14
; OTHER INFORMATION: /note= "amino caproate should
; OTHER INFORMATION: appear between residues 13 and 14."
US-08-970-833-10

Query Match      88.2%; Score 30; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 9.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFA 7
      :|||||
Db      2 QKLVEFA 8

RESULT 69
US-09-724-953-33
; Sequence 33, Application US/09724953
; Patent No. 6875434
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Elan Pharmaceuticals
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Diseases
; FILE REFERENCE: 015270-005913US
; CURRENT APPLICATION NUMBER: US/09/724,953
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/585,817

; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/137,010
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta 13-28
; OTHER INFORMATION: peptide with Cys added
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl-asparagine
US-09-724-567-33

Query Match      88.2%; Score 30; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 9.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVEFA 7
      :|||||
Db      4 QKLVEFA 10

RESULT 71
US-09-979-952-33
; Sequence 33, Application US/09979952
; Patent No. 6913745
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Elan Pharmaceuticals

```

```
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-0059150S
; CURRENT APPLICATION NUMBER: US/09/979,952
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: WO PCT/US00/25239
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/137,010
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Abeta 13-28
; OTHER INFORMATION: peptide with Cys added
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl-asparagine
US-09-979-952-33

Query Match      88.2%; Score 30; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 9.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKLVPFA 7
Db      4 QKLVPFA 10

RESULT 72
US-09-585-817-33
; Sequence 33, Application US/09585817
; Patent No. 6923964
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Diseases
; FILE REFERENCE: 015270-005910US
; CURRENT APPLICATION NUMBER: US/09/585,817
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: WO PCT/US00/25239
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/137,010
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Abeta 13-28
; OTHER INFORMATION: peptide with Cys added
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl-asparagine
US-09-585-817-33

Query Match      88.2%; Score 30; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 9.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKLVPFA 7
Db      4 QKLVPFA 10

RESULT 73
US-08-304-585-7
; Sequence 7, Application US/08304585
; Patent No. 5721166
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,585
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: .peptide
US-08-304-585-7

Query Match      88.2%; Score 30; DB 1; Length 26;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KKLVPFA 7
Db      6 QKLVPFA 12

RESULT 74
US-08-346-849-4
; Sequence 4, Application US/08346849
; Patent No. 5670483
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshin, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-346-849-4

Query Match 88.2%; Score 30; DB 1; Length 28;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 15 QKLVPFA 21

RESULT 75
US-08-302-808-7
Sequence 7, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uhiro
APPLICANT: OAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SRP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235

REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-7

Query Match 88.2%; Score 30; DB 1; Length 28;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
:|||||
Db 15 QKLVPFA 21

Search completed: December 29, 2005, 17:52:32
Job time : 24.471 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 91.2258 Seconds
(without alignments)
54.137 Million cell updates/sec

Title: US-10-009-122-2
Perfect score: 34
Sequence: 1 KKLFFFA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	137	2 QUPRI_RHOBA	Qupri rhodopirell
2	34	100.0	493	2 Q5K4D5_9POTV	Q5k4d5 soybean mos
3	33	97.1	284	2 Q4ZX22_PSESY	Q4zx22 pseudomonas
4	32	94.1	387	2 Q81FHS_BACCR	Q81fhs bacillus ce
5	31	91.2	51	2 Q72A51_DESVH	Q72a51 desulfovibr
6	31	91.2	137	2 Q74E04_GEOSL	Q74e04 geobacter s
7	31	91.2	176	2 Q4QLX3_HAB18	Q4qlx3 haemophilus
8	31	91.2	183	2 Q9RQ09_BACTIN	Q9rq09 bacteroides
9	31	91.2	314	2 Q8PUW1_METWA	Q8puw1 methanosaar
10	31	91.2	362	2 Q4HSJ7_CAMUP	Q4hsj7 campylobact
11	31	91.2	387	2 Q8K110_BACCE	Q8k110 bacillus ce
12	31	91.2	387	2 Q4MT39_BACCE	Q4mt39 bacillus ce
13	31	91.2	387	2 Q63D04_BACZ	Q63dd4 bacillus ce
14	31	91.2	387	2 Q6HKU6_BACHK	Q6hku6 bacillus th
15	31	91.2	387	2 Q73AP3_BACCI1	Q73ap3 bacillus ce
16	31	91.2	387	2 Q81SK9_BACAN	Q81sk9 bacillus an
17	31	91.2	447	2 Q59243_PYRHO	Q59243 pyrococcus
18	31	91.2	488	2 Q37931_POTV	Q37931 ceratobium
19	31	91.2	488	2 Q37932_POTV	Q37932 ceratobium
20	31	91.2	488	2 Q37933_POTV	Q37933 ceratobium
21	31	91.2	488	2 Q37934_POTV	Q37934 ceratobium
22	31	91.2	697	2 Q5AU77_EMENI	Q5au77 aspergillus
23	31	91.2	3222	2 Q563A1_BCMVN	Q563a1 peanut stri
24	30	88.2	33	2 Q9UC33_HUMAN	Q9uc33 homo sapien
25	30	88.2	34	2 Q9XQR5_PEA	Q9xqr5 pisum sativ
26	30	88.2	42	2 Q56JJ6_GRAGR	Q56jj6 grampus gri
27	30	88.2	42	2 Q56JJ7_TURTR	Q56jj7 turslops tr
28	30	88.2	42	2 Q7M088_CAVPO	Q7m088 cavia porce
29	30	88.2	52	2 Q8WZ99_HUMAN	Q8wz99 homo sapien
30	30	88.2	57	1 A4_URSWA	Q29149 u alzheimer
31	30	88.2	58	1 A4_CANFA	Q28280 c alzheimer

32	30	88.2	58	1 A4_RABIT	Q28748 o alzheimer
33	30	88.2	58	1 A4_SHEEP	Q28757 o alzheimer
34	30	88.2	59	1 A4_BOVIN	Q28053 b alzheimer
35	30	88.2	79	2 Q35463_CRIGR	Q35463 cricetus
36	30	88.2	94	2 Q5XD67_STRP6	Q5xd67 streptococc
37	30	88.2	94	2 Q9A0W1_STRPY	Q9a0w1 streptococc
38	30	88.2	94	2 Q7CNF7_STRP8	Q7cnf7 streptococc
39	30	88.2	94	2 Q8PIX8_STRP3	Q8pix8 streptococc
40	30	88.2	113	2 Q8JH58_CHESE	Q8jh58 chelydra se
41	30	88.2	125	2 Q5TUI4_ANOGA	Q5tui4 anopheles g
42	30	88.2	150	1 FAB2_DESPS	Q6aj07 desulfofatale
43	30	88.2	165	2 Q6CX11_KLULA	Q6cx11 kluyveromyc
44	30	88.2	187	2 Q4TUZ7_MAIZE	Q4tuz7 ze mays (m
45	30	88.2	214	2 Q64NE8_BACFR	Q64me8 bacteroides
46	30	88.2	218	2 Q8BPV5_MOUSE	Q8bpv5 mus musculu
47	30	88.2	228	2 Q64MC9_BACFR	Q64mc9 bacteroides
48	30	88.2	270	2 Q7MV75_PORGI	Q7mv75 porphyromon
49	30	88.2	336	2 Q74HY9_LACJO	Q74hy9 lactobacill
50	30	88.2	346	2 Q9PMW9_CAMJE	Q9pmw9 campylobact
51	30	88.2	357	2 Q8UUI8_BRARE	Q8uii8 brachydanio
52	30	88.2	359	1 MLTA_BUCAI	P57531 buchnera ap
53	30	88.2	380	2 Q67225_AQUAB	Q67225 aquifex aeo
54	30	88.2	384	2 Q8BPC7_MOUSE	Q8bpc7 mus musculu
55	30	88.2	426	2 Q83DX9_COXBU	Q83dx9 coxiella bu
56	30	88.2	472	2 Q8UUS0_BRARE	Q8uus0 brachydanio
57	30	88.2	479	2 Q9XI52_ARATH	Q9xi52 arabidopsis
58	30	88.2	481	2 Q8L731_ARATH	Q8l731 arabidopsis
59	30	88.2	493	2 Q5K4D4_9POTV	Q5k4d4 soybean mos
60	30	88.2	534	2 Q93296_CHICK	Q93296 gallus gall
61	30	88.2	569	2 Q9PVL1_CHICK	Q9pvl1 gallus gall
62	30	88.2	572	2 Q75JL6_DICDI	Q75jl6 dictyosteli
63	30	88.2	586	1 RPOCI_EUGGR	P23580 euglena gra
64	30	88.2	612	2 Q919E7_BRARE	Q919e7 brachydanio
65	30	88.2	639	2 Q8LD58_ARATH	Q8ld58 arabidopsis
66	30	88.2	645	2 Q9ZT08_ARATH	Q9zt08 arabidopsis
67	30	88.2	647	2 Q9LV16_ARATH	Q9lv16 arabidopsis
68	30	88.2	655	2 Q9LP77_ARATH	Q9lp77 arabidopsis
69	30	88.2	678	2 Q7ZT11_BRARE	Q7zt11 brachydanio
70	30	88.2	693	2 Q98SG0_XENLA	Q98sg0 xenopus lae
71	30	88.2	694	2 Q6Y2W9_MAIZE	Q6y2w9 ze mays (m
72	30	88.2	695	2 Q5R477_PONPY	Q5r477 pongo pygma
73	30	88.2	695	2 Q6RH29_CANFA	Q6rh29 canis fami
74	30	88.2	695	2 Q56JK3_CANFA	Q56jk3 canis fami
75	30	88.2	695	2 Q6GR78_MOUSE	Q6gr78 mus musculu
76	30	88.2	695	2 Q9DGJ8_CHICK	Q9dgj8 gallus gall
77	30	88.2	695	2 Q98SF9_XENLA	Q98sf9 xenopus lae
78	30	88.2	695	2 Q7ZXQ0_XENLA	Q7zxq0 xenopus lae
79	30	88.2	702	2 Q4WT56_ASPFU	Q4wt56 aspergillus
80	30	88.2	714	2 Q56JK4_CANFA	Q56jk4 canis fami
81	30	88.2	733	2 Q6PQ05_RAT	Q6pq05 rattus norv
82	30	88.2	737	1 A4_FUGRU	Q93279 fugu rubrip
83	30	88.2	738	2 Q6NUZ1_BRARE	Q6nuz1 brachydanio
84	30	88.2	738	2 Q90W28_BRARE	Q90w28 brachydanio
85	30	88.2	747	2 Q91963_9PIPI	Q91963 xenopus. ap
86	30	88.2	749	2 Q56JK2_STECO	Q56jk2 stenella co
87	30	88.2	749	2 Q6NRR1_XENLA	Q6nrri xenopus lae
88	30	88.2	750	2 Q6DJB6_XENTR	Q6djb6 xenopus tro
89	30	88.2	751	1 A4_SAISC	Q95241 s amyloid b
90	30	88.2	751	2 Q6GSC0_HUMAN	Q6gsc0 homo sapien
91	30	88.2	751	2 Q6RH28_CANFA	Q6rh28 canis fami
92	30	88.2	751	2 Q56JK5_CANFA	Q56jk5 canis fami
93	30	88.2	751	2 Q4R4R8_MACFA	Q4r4r8 macaca fasc
94	30	88.2	751	2 Q9DGJ7_CHICK	Q9dgj7 gallus gall
95	30	88.2	754	2 Q4RY33_TETNG	Q4ry33 tetraodon n
96	30	88.2	759	2 Q4S0J4_TETNG	Q4s0j4 tetraodon n
97	30	88.2	770	1 A4_CAVFO	Q4s0j4 tetraodon n
98	30	88.2	770	1 A4_HUMAN	Q60495 c amyloid b
99	30	88.2	770	1 A4_MACFA	P05067 h amyloid b
100	30	88.2	770	1 A4_MOUSE	P53601 m amyloid b
101	30	88.2	770	1 A4_PANTR	P12023 m amyloid b
102	30	88.2	770	1 A4_PIG	Q5i880 p amyloid b
103	30	88.2	770	1 A4_RAT	P79307 s amyloid b
104	30	88.2	770	2 Q6RH30_CANFA	P08592 r amyloid b

105	30	88.2	770	2	Q56JK6_CANFA	Q56JK6 canis famil	178	29	85.3	809	2	Q9N3K6_CABEL	Q9N3K6 caenothabdi
106	30	88.2	770	2	Q53ZT3_MOUSE	Q53ZT3 mus musculus	179	29	85.3	866	2	Q4YAT8_PLABE	Q4YAT8 plasmodium
107	30	88.2	770	2	Q547B7_RAT	Q547B7 rattus norv	180	29	85.3	911	2	Q6MUF5_MYCMS	Q6MUF5 mycoplasma
108	30	88.2	780	1	A4_TETFL	Q736B3 tetraodon f	181	29	85.3	962	2	Q4NTK2_9DELT	Q4NTK2 anceromyxob
109	30	88.2	955	2	Q80RZ2_9POTV	Q80RZ2 calla lily	182	29	85.3	970	2	Q758X5_ASHGO	Q758X5 ashbya goss
110	30	88.2	1678	2	Q6BUD9_DEBHA	Q6BUD9 debaryomyce	183	29	85.3	1016	2	Q05912_9POTV	Q05912 zucchini ye
111	30	88.2	3105	2	Q70XR2_9POTV	Q70XR2 soybean mos	184	29	85.3	1056	2	Q6FKH6_CANGA	Q6FKH6 candida gia
112	30	88.2	4664	2	Q4QFY9_LEIMA	Q4QFY9 leishmania	185	29	85.3	1293	2	Q55A32_DFCYD	Q55A32 dictyosteli
113	30	88.2	5808	2	Q4UFB3_THEAN	Q4UFB3 theileria a	186	29	85.3	1492	2	Q83Y21_PEWBP	Q83Y21 peanut wic
114	29	85.3	34	2	Q8GJC8_CAMJE	Q8GJC8 campylobact	187	29	85.3	1916	2	Q8OKU4_9POTV	Q8OKU4 zucchini ye
115	29	85.3	45	2	Q4XF00_PLACH	Q4XF00 plasmodium	188	29	85.3	3080	1	POLG_ZYMVS	POLG_ZYMVS z genome po
116	29	85.3	96	1	IFIC_TOBAC	IFIC_TOBAC nicotiana t	189	29	85.3	3080	2	Q6WN47_9POTV	Q6WN47 zucchini ye
117	29	85.3	104	2	Q9G8Z7_OCHDN	Q9G8Z7 ochromonas	190	29	85.3	3080	2	Q6WN48_9POTV	Q6WN48 zucchini ye
118	29	85.3	109	2	Q9X292_THEMEA	Q9X292 thermotoga	191	29	85.3	3080	2	Q6WN49_9POTV	Q6WN49 zucchini ye
119	29	85.3	127	2	Q4XF83_PLACH	Q4XF83 plasmodium	192	29	85.3	3080	2	Q6Y2U7_9POTV	Q6Y2U7 zucchini ye
120	29	85.3	149	2	Q6AIF8_DESPS	Q6AIF8 desulfotale	193	29	85.3	3080	2	Q7T908_9POTV	Q7T908 zucchini ye
121	29	85.3	152	2	Q9STZ9_ARATH	Q9STZ9 arabidopsis	194	29	85.3	3080	2	Q7T914_9POTV	Q7T914 zucchini ye
122	29	85.3	158	2	Q4FPG2_9RICK	Q4FPG2 candidatus	195	29	85.3	3083	1	POLG_ZYMVS	POLG_ZYMVS z genome po
123	29	85.3	176	1	NRFX_HABIN	NRFX_HABIN haemophilus	196	28	82.4	26	2	Q4XGPI_PLACH	Q4XGPI plasmodium
124	29	85.3	177	2	Q5LD66_BACFN	Q5LD66 bacteroides	197	28	82.4	46	2	Q4Y2T9_PLABE	Q4Y2T9 leptospira
125	29	85.3	177	2	Q64U86_BACFR	Q64U86 bacteroides	198	28	82.4	46	2	Q8EXM4_LBPIN	Q8EXM4 leptospira
126	29	85.3	229	2	Q8VY56_ARATH	Q8VY56 arabidopsis	199	28	82.4	51	2	Q7RF81_PLAYO	Q7RF81 plasmodium
127	29	85.3	230	2	Q7RDM9_PLAYO	Q7RDM9 plasmodium	200	28	82.4	66	2	Q7Z8F0_DESVH	Q7Z8F0 desulfovibr
128	29	85.3	231	2	Q9SV79_ARATH	Q9SV79 arabidopsis	201	28	82.4	72	2	Q4HSS4_CAMUP	Q4HSS4 campylobact
129	29	85.3	258	2	Q65K48_BACLD	Q65K48 bacillus li	202	28	82.4	79	2	Q8FAZ7_ECOL6	Q8FAZ7 escherichia
130	29	85.3	268	2	Q6YPU1_ONYPE	Q6YPU1 onion yello	203	28	82.4	88	2	Q4LB08_SODGL	Q4LB08 sodalis glo
131	29	85.3	275	2	Q55E89_DICDI	Q55E89 dictyosteli	204	28	82.4	105	2	Q64CV5_9ARCH	Q64CV5 uncultured
132	29	85.3	283	2	Q7R9D9_PLAYO	Q7R9D9 plasmodium	205	28	82.4	109	2	Q8XQ19_RALSO	Q8XQ19 ralstonia s
133	29	85.3	294	2	Q4XEU4_PLACH	Q4XEU4 plasmodium	206	28	82.4	118	2	Q5ZDN6_ORYSA	Q5ZDN6 oryza sativ
134	29	85.3	296	2	Q5NQG3_ZYMNO	Q5NQG3 zymomonas m	207	28	82.4	118	2	Q8Y1S2_RALSO	Q8Y1S2 ralstonia s
135	29	85.3	296	2	Q8F385_LEPIN	Q8F385 leptospira	208	28	82.4	123	2	Q8Y1W1_SULSO	Q8Y1W1 sulfolobus
136	29	85.3	296	2	Q7ZSD7_LEPIC	Q7ZSD7 leptospira	209	28	82.4	130	1	Y613_PASMU	Y613 pasteurella
137	29	85.3	316	2	Q8Y985_LISMO	Q8Y985 listeria mo	210	28	82.4	133	2	Q8KKC9_HELPY	Q8KKC9 helicobacte
138	29	85.3	316	2	Q92E10_LISIN	Q92E10 listeria in	211	28	82.4	141	2	Q5LGT9_BACFN	Q5LGT9 bacteroides
139	29	85.3	316	2	Q722Q1_LISMP	Q722Q1 listeria mo	212	28	82.4	141	2	Q84XPI_BACFR	Q84XPI bacteroides
140	29	85.3	324	2	Q4Y0J6_PLACH	Q4Y0J6 plasmodium	213	28	82.4	143	2	Q8EMC6_OCEIH	Q8EMC6 oceanobacil
141	29	85.3	352	2	Q9XGY6_SIMCH	Q9XGY6 simmondsia	214	28	82.4	144	2	Q67K60_SYMTH	Q67K60 symbiodin
142	29	85.3	357	2	Q8U460_PYRFU	Q8U460 pyrococcus	215	28	82.4	165	2	Q5NX98_AZOSE	Q5NX98 azoarcus sp
143	29	85.3	366	2	Q8PPL1_XELANP	Q8PPL1 xanthomonas	216	28	82.4	176	2	Q6AM23_DESPS	Q6AM23 desulfotale
144	29	85.3	380	2	Q7VJCI_HELHP	Q7VJCI helicobacte	217	28	82.4	182	2	Q5OY54_ENTHI	Q5OY54 entamoeba h
145	29	85.3	386	2	Q5L1A8_GEOKA	Q5L1A8 geobacillus	218	28	82.4	182	2	Q5NSY6_ENTHI	Q5NSY6 entamoeba h
146	29	85.3	386	2	Q627Y5_CABER	Q627Y5 caenothabdi	219	28	82.4	196	2	Q7RCT7_PLAYO	Q7RCT7 campylobact
147	29	85.3	386	2	Q45308_BACME	Q45308 bacillus me	220	28	82.4	207	2	Q4HDT2_CAMCO	Q4HDT2 campylobact
148	29	85.3	391	2	Q4NSU7_THERPA	Q4NSU7 theileria p	221	28	82.4	214	2	Q9LZV2_ARATH	Q9LZV2 arabidopsis
149	29	85.3	403	2	Q5L117_GEOKA	Q5L117 geobacillus	222	28	82.4	218	2	Q9WZ39_THEMEA	Q9WZ39 thermotoga
150	29	85.3	404	2	Q4UY55_XANCP	Q4UY55 xanthomonas	223	28	82.4	220	2	Q79A00_STRPY	Q79A00 streptococc
151	29	85.3	404	2	Q8P597_XANCP	Q8P597 xanthomonas	224	28	82.4	236	2	P97163_STRPY	P97163 streptococc
152	29	85.3	421	2	Q9LH60_ARATH	Q9LH60 arabidopsis	225	28	82.4	236	2	Q54779_STRPY	Q54779 streptococc
153	29	85.3	421	2	Q9PNU9_CAMJE	Q9PNU9 campylobact	226	28	82.4	236	2	Q57453_STRPY	Q57453 streptococc
154	29	85.3	421	2	Q5HUH1_CAMJR	Q5HUH1 campylobact	227	28	82.4	243	2	Q4V613_DROME	Q4V613 drosophila
155	29	85.3	423	2	Q59MK9_CANAL	Q59MK9 candida alb	228	28	82.4	244	2	Q9VQ40_DROME	Q9VQ40 drosophila
156	29	85.3	428	2	Q9M1Q8_ARATH	Q9M1Q8 arabidopsis	229	28	82.4	245	1	VITO_BACSU	VITO_BACSU geobacillus su
157	29	85.3	461	2	Q89329_9POTV	Q89329 zucchini ye	230	28	82.4	248	2	Q5L384_GROKA	Q5L384 geobacillus su
158	29	85.3	470	2	Q7T910_9POTV	Q7T910 zucchini ye	231	28	82.4	251	1	SPEA_STRPY	SPEA_STRPY streptococc
159	29	85.3	484	1	Y1062_METUA	Y1062 methanococ	232	28	82.4	251	1	SPEA_STRPY	SPEA_STRPY streptococc
160	29	85.3	485	2	Q4F982_9POTV	Q4F982 siratino 2 v	233	28	82.4	251	2	Q9YWB3_MSEPV	Q9YWB3 melanoplus
161	29	85.3	488	2	Q52NV6_9POTV	Q52NV6 zucchini ye	234	28	82.4	254	2	Q9YWB3_MSEPV	Q9YWB3 melanoplus
162	29	85.3	490	2	Q7T911_9POTV	Q7T911 zucchini ye	235	28	82.4	266	2	Q6FY12_BARQU	Q6FY12 bartonella
163	29	85.3	490	2	Q7T912_9POTV	Q7T912 zucchini ye	236	28	82.4	273	2	Q4L2R4_BARQU	Q4L2R4 bartonella
164	29	85.3	502	2	Q5LUS5_GEOKA	Q5LUS5 geobacillus	237	28	82.4	273	2	Q4HSP7_CAMUP	Q4HSP7 campylobact
165	29	85.3	508	2	Q5GVS5_XANOR	Q5GVS5 xanthomonas	238	28	82.4	275	2	Q7SDV7_NEUCR	Q7SDV7 neurospora
166	29	85.3	533	2	Q975B3_SULTO	Q975B3 sulfolobus	239	28	82.4	275	2	Q5K2M1_BACLI	Q5K2M1 bacillus li
167	29	85.3	610	2	Q21604_CABEL	Q21604 caenothabdi	240	28	82.4	275	2	Q5WTR1_LSGPL	Q5WTR1 legionella
168	29	85.3	615	2	Q50285_ENTHI	Q50285 entamoeba h	241	28	82.4	275	2	Q5X1Y6_LEGPA	Q5X1Y6 legionella
169	29	85.3	636	2	Q6CHB2_YARLI	Q6CHB2 yarrowia li	242	28	82.4	276	2	Q7QS35_GIALA	Q7QS35 giardia lam
170	29	85.3	638	2	Q5B2V4_EMENI	Q5B2V4 aspergillus	243	28	82.4	276	2	Q5E2G2_VIBF1	Q5E2G2 vibrio fisc
171	29	85.3	675	2	Q8H811_ORYSA	Q8H811 oryza sativ	244	28	82.4	276	2	Q9KT31_VIBCH	Q9KT31 vibrio chol
172	29	85.3	686	2	Q7ARUQ7_ORYSA	Q7ARUQ7 oryza sativ	245	28	82.4	293	1	Q5ZSH6_LRGPH	Q5ZSH6 legionella
173	29	85.3	716	2	Q7RB60_PLAYO	Q7RB60 plasmodium	246	28	82.4	293	1	Y844_ARCFU	Y844 archaeoglob
174	29	85.3	743	2	Q6BM34_DEBHA	Q6BM34 debaryomyce	247	28	82.4	294	2	Q97XW2_SULSO	Q97XW2 sulfolobus
175	29	85.3	763	2	Q9CH71_LACLA	Q9CH71 lactococcus	248	28	82.4	301	2	Q8EB34_SHEON	Q8EB34 shewanella
176	29	85.3	774	2	Q64777_ARATH	Q64777 arabidopsis	249	28	82.4	306	2	Q4YZW0_PLABE	Q4YZW0 plasmodium
177	29	85.3	804	2	Q64770_ARATH	Q64770 arabidopsis	250	28	82.4	310	2	Q6R7D4_9HERP	Q6R7D4 ostreid her

251 28 82.4 315 2 065532 AQUAE
 252 28 82.4 320 2 Q59DR9 drosophila
 253 28 82.4 321 1 Y189 RICPR
 254 28 82.4 326 2 Q627D1 CAEBR
 255 28 82.4 327 2 Q7Q914 ANOGEA
 256 28 82.4 330 2 Q8ZU32 PYRAE
 257 28 82.4 333 2 P72489 STRPN
 258 28 82.4 333 2 Q72SK3 STRPN
 259 28 82.4 334 2 Q81KN3 PLAF7
 260 28 82.4 339 2 Q5FNR0 GLUOX
 261 28 82.4 343 2 Q5V531 DROSOPHILA
 262 28 82.4 355 2 Q8DR72 STRR6
 263 28 82.4 367 2 Q4PRF7 9GAMM
 264 28 82.4 370 2 Q5SSJ1 MANSM
 265 28 82.4 371 2 Q6C6Q0 YARLI
 266 28 82.4 372 2 Q6D7U3 ERWCT
 267 28 82.4 383 2 Q8YYZ5 ANASP
 268 28 82.4 403 2 Q5CTP3 CRYPV
 269 28 82.4 423 2 Q6C1K6 YARLI
 270 28 82.4 434 2 Q89YS3 BACTN
 271 28 82.4 463 2 Q8ESN1 OCEIH
 272 28 82.4 464 2 Q4S4T5 TETNG
 273 28 82.4 465 2 Q82YV5 ENTTPA
 274 28 82.4 469 2 Q4Y318 PLACH
 275 28 82.4 473 2 Q5UPQ3 MIMIV
 276 28 82.4 479 2 Q9QDU5 9POTV
 277 28 82.4 479 2 Q4F979 9POTV
 278 28 82.4 480 2 Q4N8N8 THEPA
 279 28 82.4 488 2 Q52NV7 9POTV
 280 28 82.4 496 2 Q5K4D0 9POTV
 281 28 82.4 504 2 Q4H3G7 CIOIN
 282 28 82.4 505 2 Q47G0 GEOSL
 283 28 82.4 528 2 Q9P7P2 SCHPO
 284 28 82.4 542 2 Q9P7N7 CANGA
 285 28 82.4 542 2 Q8X0Z5 CANGA
 286 28 82.4 557 2 Q4UG24 THEAN
 287 28 82.4 559 2 Q4XZR3 PLACH
 288 28 82.4 562 2 Q7NNW2 CHRVO
 289 28 82.4 605 2 Q9TYX2 CABEL
 290 28 82.4 605 2 Q6MP23 BDEBA
 291 28 82.4 606 2 Q1V1V5 MOUSE
 292 28 82.4 614 2 Q7P291 ANOGEA
 293 28 82.4 624 2 Q7SD58 NEUCR
 294 28 82.4 648 2 Q6C0N6 YARLI
 295 28 82.4 652 2 Q9F531 ECOLI
 296 28 82.4 655 2 Q7R9H2 PLAYO
 297 28 82.4 663 2 Q6RUU2 MOUSE
 298 28 82.4 685 1 M0L1 CANAL
 299 28 82.4 685 2 Q2A951 CANAL
 300 28 82.4 704 2 Q65J18 BACILLUS LI

ALIGNMENTS

RESULT 1
 Q7UPR1_RHOBA PRELIMINARY; PRT; 137 AA.
 ID Q7UPR1_RHOBA PRELIMINARY;
 AC Q7UPR1_RHOBA PRELIMINARY;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=RB6777;
 OS Rhodospirillum rubrum
 OC Bacteria; Planctomycetacia; Planctomycetaciales;
 OC Planctomycetacia; Pirellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,

RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schleiner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
 DR EMBL; BX294144; CAD75000.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 137 AA; 15530 MW; 5DCCL33B06CC5FC0 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 137;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
 Db 84 KKLVPFA 90

RESULT 2

Q5K4D5_9POTV PRELIMINARY; PRT; 493 AA.
 ID Q5K4D5_9POTV PRELIMINARY;
 AC Q5K4D5_9POTV PRELIMINARY;
 DT 10-MAY-2005 (TRENBLrel. 30, Created)
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
 DE Polyprotein (Fragment).
 OS Soybean mosaic virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 OX NCBI_TaxID=12222;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=P;
 RX PubMed=15449140; DOI=10.1007/s00705-004-0390-z;
 RA Shi Y.H., Hong X.Y., Chen J., Adams M.J., Zheng H.Y., Lin L.,
 RA Qing B.X., Chen J.;
 RT "Further molecular characterisation of potyviruses infecting aroid
 plants for medicinal use in China.";
 RL Arch. Virol. 150:135-135 (2005).
 DR EMBL; AJ628751; CAF32241.1; -; Genomic RNA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0003968; P:RNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0019079; P:Viral genome replication; IEA.
 DR InterPro; IPR001592; Poty coat.
 DR InterPro; IPR001205; RNA_pol_P3D.
 DR Pfam; PF00767; Poty coat; 1.
 DR Pfam; PF00680; RdRP_1; 1.
 KW Capsid protein; Polyprotein. Nib protein.
 FT CHAIN <1 211 coat protein.
 FT NON TER 1 1
 SQ SEQUENCE 493 AA; 55866 MW; 6D50976B5C7DF5F3 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 493;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
 Db 37 KKLVPFA 43

RESULT 3

Q4ZXZ2_PSESY PRELIMINARY; PRT; 284 AA.
 ID Q4ZXZ2_PSESY PRELIMINARY;
 AC Q4ZXZ2_PSESY PRELIMINARY;
 DT 13-SEP-2005 (TRENBLrel. 31, Created)
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
 DE Glycosyl transferase, family 2 precursor.
 GN ORFNames=Psyr_0922;
 OS Pseudomonas syringae pv. syringae B728a.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=205918;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B728a;
 RG DOE Joint Genome Institute;
 RA Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Trong S.,
 RA Nolan M., Goltsman E., Thiel J., Malfatti S., Lapidus A., Dettler J.C.,
 RA Land M., Richardson P.M., Kyrpides N.C., Ivanova N.;
 RT "Comparison of two complete genome sequences of Pseudomonas syringae
 RT pv. syringae B728a and pv. tomato DC3000.";
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B728a;
 RA Loper J.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B728a;
 RA Feil H., Feil W.S., Lindow S.E.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CF000075; AY35980.1; -; Genomic DNA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 KW Signal; Transferase.
 FT SIGNAL 284 284 Potential.
 SQ SEQUENCE 284 AA; 30871 MW; 37921A81C4BB728D CRC64;
 Query Match 97.1%; Score 33; DB 2; Length 284;
 Best Local Similarity 85.7%; Pred. No. 37;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVPFA 7
 Db |||:|
 2 KKLIFPA 8
 RESULT 4
 ID Q81FH5_BACCR PRELIMINARY; PRT; 387 AA.
 AC Q81FH5;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Na+/H+ antiporter Napa (inosine-dependent germination).
 GN OrderedLocNames=BC1612;
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=226900;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,
 RA Kapral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
 RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
 RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
 RA Overbeek R., Kyrpides N.C.;
 RT "Genome sequence of Bacillus cereus and comparative analysis with
 RT Bacillus anthracis.";
 RL Nature 423:87-91(2003).
 RL EMBL; AB017003; AAP08591.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008324; F:cation transporter activity; IEA.
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006885; P:regulation of pH; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR004771; K eff.
 DR InterPro; IPR006153; Na/H porter.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 DR TIGRPFAM; TIGR00932; 2a37; 1.

KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 387 AA; 41037 MW; 907C03E6BA150B4A CRC64;
 Query Match 94.1%; Score 32; DB 2; Length 387;
 Best Local Similarity 85.7%; Pred. No. 84;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVPFA 7
 Db |||:|
 183 KKLVPFA 189
 RESULT 5
 ID Q72A51_DESVH PRELIMINARY; PRT; 51 AA.
 AC Q72A51;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocNames=DVU2146;
 OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
 OS 8303).
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 OX NCBI_TaxID=882;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15077118; DOI=10.1038/nbt959;
 RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
 RA Kotonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
 RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
 RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
 RA Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
 RA Dimitrov G., Hance W., Tran K., Khouri H.M., Gill J., Utterback T.R.,
 RA Firdlyum T.V., Wall J.D., Voordouw G., Frazer C.M.;
 RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
 RT Desulfovibrio vulgaris Hildenborough.";
 RL Nat. Biotechnol. 22:554-559(2004).
 DR EMBL; AE017316; AAS96619.1; -; Genomic DNA.
 DR TIGR; DVU2146; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 51 AA; 6205 MW; E7F69C0D8432B7F5 CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 51;
 Best Local Similarity 85.7%; Pred. No. 24;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVPFA 7
 Db |||:|
 17 KKLVPFA 23
 RESULT 6
 ID Q74E04_GEOSL PRELIMINARY; PRT; 137 AA.
 AC Q74E04;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocNames=GSU1160;
 OS Geobacter sulfurreducens.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteraceae; Geobacter.
 OX NCBI_TaxID=35554;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PCA / ATCC 51573;
 RX PubMed=14671304; DOI=10.1126/science.1088727;
 RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
 RA Heidelberg J.F., Wu D., Ward N.L., Beanan M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,

RA Gwinn M.L., Kolonay J.P., Sullivan S.A., Haft D.H., Selengut J.,
RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Khouri H.M., Feldblum T.V., Utterback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments";
RL Science 302:1967-1969(2003).
DR EMBL; AB017180; AAR34536.1; -; Genomic_DNA.
DR TIGR; GSU1160; -;
DR GO; GO:0042597; C:periplasmic space; IEA.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA;
DR GO; GO:0006118; P:electron transport; IEA;
KW Complete proteome; Copper; Hypothetical protein; Metal-binding;
KW Oxidoreductase; Periplasmic.
SQ SEQUENCE 137 AA; 15272 MW; 3C3F00FFDD6B2FC7 CRC64;
Query Match 91.2%; Score 31; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKLVPFA 7
Db 116 KKLFFFA 122
|||:||||
|||:||||
RESULT 7
Q4QLX3 HAE18
ID Q4QLX3 HAE18 PRELIMINARY; PRT; 176 AA.
AC Q4QLX3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Probable thiol:disulfide interchange protein Debe.
GN Name=debe2; OrderedLocNames=NT11106;
OS Haemophilus influenzae (strain 86-028NP).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=281310;
[1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
RA Harrison A., Dyer D.W., Gillespy A., Ray W.C., Mungur R., Carson M.B.,
RA Zhong H., Gipson J., Johnson L.S., Lewis L., Bakaletz L.O.,
RA Munson R.S. Jr.;
RT "Genomic sequence of an otitis media isolate of nontypeable
RT Haemophilus influenzae: comparative study with H. influenzae serotype
RT d, strain KW20.";
RL J. Bacteriol. 187:4627-4636(2005).
CC -1- FUNCTION: Involved in disulfide bond formation. Catalyzes a late,
CC reductive step in the assembly of periplasmic c-type cytochromes,
CC probably the reduction of disulfide bonds of the apocytochrome c
CC to allow covalent linkage with the heme. Possible subunit of a
CC heme lyase (By similarity).
CC -1- SUBCELLULAR LOCATION: Mostly periplasmic; anchored in the inner
CC membrane (By similarity).
DR EMBL; CP000057; AAX87974.1; -; Genomic_DNA.
DR InterPro; IPR004799; DabE.
DR InterPro; IPR006662; Thioired.
DR InterPro; IPR006663; Thioiredox dom2.
DR InterPro; IPR012336; Thioiredoxin-like.
DR InterPro; IPR011594; Thioiredoxin_like.
DR PRINTS; PR00421; THIOREDOXIN.
DR PRODOM; PD003679; Thioiredoxin_like; 1.
DR TIGRFAMs; TIGR00385; dabe; 1.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN 1.
KW Complete proteome; Cytochrome c-type biogenesis; Inner membrane;
KW Membrane; Redox-active center; Transmembrane.
SQ SEQUENCE 176 AA; 19783 MW; 19A38F868C161582 CRC64;
Query Match 91.2%; Score 31; DB 2; Length 176;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 3 KKLFFFA 9
|||:||||
|||:||||
RESULT 8
Q9RQ09 BACTN
ID Q9RQ09 BACTN PRELIMINARY; PRT; 183 AA.
AC Q9RQ09; Q7C422;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE RNA polymerase sigma factor SigZ-like protein (RNA polymerase ECF-type
DE sigma factor).
DE sigma factor).
GN Names=sigZ; OrderedLocNames=Btl1278;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482;
RX MEDLINE=99380605; PubMed=10449780; DOI=10.1073/pnas.96.17.9833;
RA Hooper L.V., Xu J., Palk P.G., Midtvedt T., Gordon J.I.;
RT "A molecular sensor that allows a gut commensal to control its
RT nutrient foundation in a competitive ecosystem.";
RT Proc. Natl. Acad. Sci. U.S.A. 96:9833-9838(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RT Science 299:2074-2076(2003).
DR EMBL; AF137263; AAF01488.1; -; Genomic DNA.
DR EMBL; AB016931; AAO76385.1; -; Genomic DNA.
DR GO; GO:0016987; P:sigma factor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006352; P:transcription initiation; IEA.
DR InterPro; IPR007627; Sigma70 r2.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF04542; Sigma70 r2; 1.
KW Complete proteome; DNA-binding; DNA-directed RNA polymerase;
KW Nucleotidyltransferase; Sigma factor; Transcription;
KW Transcription regulation; Transferase.
SQ SEQUENCE 183 AA; 22042 MW; 5B24DABC99EBC643 CRC64;
Query Match 91.2%; Score 31; DB 2; Length 183;
Best Local Similarity 71.4%; Pred. No. 74;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKLVPFA 7
Db 171 KKLFFFA 177
|||:||||
|||:||||
RESULT 9
Q8PUW1 METWA
ID Q8PUW1 METWA PRELIMINARY; PRT; 314 AA.
AC Q8PUW1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Conserved protein.
DE OrderedLocNames=MW2217;
GN Methanosarcina mazei (Methanosarcina frisia).
OS Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

RC STRAIN=Coel / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINS=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wiezer A., Baumer S., Jacobi C.,
RA Bruggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Mechanosarcina mazel: evidence for lateral gene
RT transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AS013463; AM31913.1; -: Genomic DNA.
DR GO; GO:0005794; C:Golgi apparatus; IEA.
DR InterPro; IPR001173; Glyco_transf_2; 1.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Complete proteome.
SQ SEQUENCE 314 AA; 36354 MW; A8BAB274A44808B7 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 314;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
Db 158 KKLVPFS 164
|||||:

RESULT 10
Q4HSJ7 CAMUP
ID Q4HSJ7_CAMUP PRELIMINARY; PRT; 362 AA.
AC Q4HSJ7_
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hydrogenase expression/formation protein Hypd.
GN Name-hypd; ORFNames=CUP0294;
OS Campylobacter upsaliensis RM3195.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=306264;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RM3195;
RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
RA Nelson K.E.;
RT "Major structural and novel potential virulence mechanisms from the
RT genomes of multiple Campylobacter species.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFJ0100002; FAL5713.1; -: Genomic DNA.
SQ SEQUENCE 362 AA; 40365 MW; 15B0A8B12B60C8AD CRC64;

Query Match 91.2%; Score 31; DB 2; Length 362;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
Db 131 KKIIFPA 137
|||||:

RESULT 11
Q9K110_BACCE
ID Q9K110_BACCE PRELIMINARY; PRT; 387 AA.
AC Q9K110;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GerN.

```

```

GN Name=gerN;
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1396;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC10876;
RX MEDLINE=20576148; PubMed=11133940; DOI=10.1128/JB.183.2.476-482.2001;
RA "GerN, an antiporter homologue important in germination of Bacillus
RA cereus endospores.";
RL J. Bacteriol. 183:476-482(2001).
DR EMBL; AF246294; AAF91326.1; -: Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41093 MW; 40DE45B71B715D01 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 387;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
Db 183 KKVFFFA 189
|||||:

RESULT 12
Q4MT39_BACCE
ID Q4MT39_BACCE PRELIMINARY; PRT; 387 AA.
AC Q4MT39;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Na+/H+ antiporter.
GN ORFNames=BCE_G9241_1647;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Malden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Ralstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAEX0100008; FAL15336.1; -: Genomic DNA.
SQ SEQUENCE 387 AA; 41122 MW; 15CC136E9B12C38 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 387;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7
Db 183 KKVFFFA 189
|||||:

```

Db 183 KKVFFFA 189

RESULT 13

ID Q63DD4_BACCCZ
AC Q63DD4_BACCCZ PRELIMINARY; PRT; 387 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Na+/H+ exchanger family protein.
GN Name=gerN;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
[1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; A018770.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41090 MW; DBA5991F6DD63F33 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 387;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7

Db 183 KKVFFFA 189

RESULT 14

ID Q6HKU6_BACHK
AC Q6HKU6_BACHK PRELIMINARY; PRT; 387 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN; OrderedLocusNames=Br9727_1493;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
[1]

NUCLEOTIDE SEQUENCE.

RP STRAIN=97-27;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; A017355; AAT63168.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.

DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41076 MW; DFPECAD90985F951 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 387;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7

Db 183 KKVFFFA 189

RESULT 15

ID Q73AP3_BACCI PRELIMINARY; PRT; 387 AA.
AC Q73AP3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Germination protein gerN.
GN OrderedLocusNames=BCEI729;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=22523;
[1]

NUCLEOTIDE SEQUENCE.

RP PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXOI.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017269; AAS40658.1; -; Genomic_DNA.
DR TIGR; BCEI729; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41104 MW; DC7CD48C609FEBA3 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 387;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVFPA 7

Db 183 KKVFFFA 189

RESULT 16

ID Q81SK9_BACAN
AC Q81SK9_BACAN PRELIMINARY; PRT; 387 AA.
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Germination protein gerN.
GN OrderedLocusNames=BAI639, BAS1521, GBAA1639;
OS Bacillus anthracis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=1392;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ames / isolate Porton;
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Touts N.J., Baillie L.W., Paulsen I.T.,
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Kolczapple E.K., Oksad O.A., Helgason E., Rilstone J., Wu M.,
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Knouri H.M., Radune D.,
 RA Benson J.L., Mahamoud Y.J., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Niedman W.C.,
 RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
 RA Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
 RA "The genome sequence of *Bacillus anthracis* Ames and comparison to
 RT closely related bacteria.";
 RT Nature 423:81-86(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ames / isolate 0581;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RA "Bacillus anthracis comparative genomics.";
 RT Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Sterner;
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RA "Complete genome sequence of *Bacillus anthracis* Sterne.";
 RT Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AS017029; AAP25572.1; -; Genomic DNA.
 DR EMBL; AS017334; AAT30749.1; -; Genomic DNA.
 DR EMBL; AR017225; AAT53839.1; -; Genomic DNA.
 DR TIGR; BA1639; -;
 DR TIGR; GAA1639; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008324; F:cation transporter activity; IEA.
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006885; P:regulation of pH; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR004771; K_eff.
 DR InterPro; IPR006153; Na_H_porter.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 DR TIGRFAMs; TIGR00932; 2a37; 1.
 KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 387 AA; 40932 MW; D59F6A08A283BCA3 CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 387;
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVEFA 7
 Db 183 KKLVEFA 189
 RESULT 17
 OS9243 PYRHO
 ID O59243_PYRHO PRELIMINARY; PRT; 447 AA.
 AC O59243;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein PH1606.
 GN Ordered locus names=PH1606;

OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=53953;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RA "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, *Pyrococcus horikoshii* OT3.";
 RL DNA Res. 5:55-76(1998).
 DR EMBL; BA000001; BAA30718.1; -; Genomic DNA.
 DR FIR; F71039; F71039.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005355; F:glucose transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000803; Gluc transporter.
 DR PRINTS; PR00172; GLUCTRNSPORT.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 447 AA; 51173 MW; 509F45A302D3B059 CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 447;
 Best Local Similarity 71.4%; Pred. No. 1.6e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLVEFA 7
 Db 206 KKLVEFA 212
 RESULT 18
 OS37931_9POTV
 ID O37931_9POTV PRELIMINARY; PRT; 488 AA.
 AC O37931;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Polypeptide (Fragment).
 GN Name=N1b/CP;
 OS Ceratobium mosaic potyvirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 OX NCBI_TaxID=66702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CerMV-13;
 RX MEDLINE=98309067; PubMed=9645197; DOI=10.1007/s007050050341;
 RA Mackenzie A.M., Nolan M., Wei K.J., Clements M.A., Gowanlock D.,
 RA Wallace B.J., Gibbs A.J.;
 RA "Ceratobium mosaic potyvirus: another virus from orchids.";
 RT Arch. Virol. 143:903-914(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CerMV-13;
 RA Gibbs A., Mackenzie A., Blanchfield A., Cross P., Wilson C.,
 RA Kitajima E., Nightingale M., Clements M.;
 RT "Viruses of orchids in Australia: their identification, biology and
 RT control.";
 RL Aust. Orchid Rev. 65:10-21(2000).
 DR EMBL; AF022442; AAC59610.1; -; Genomic DNA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0004386; F:helicase activity; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR GO; GO:0019079; P:viral genome replication; IEA.


```

OX NCBI_TaxID=66702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CerMV-18;
RX MEDLINE=98309067; PubMed=9645197; DOI=10.1007/s007050050341;
RA Mackenzie A.M., Nolan M., Wei K.J., Clements M.A., Gowanlock D.,
RA Wallace B.J., Gibbs A.J.;
RT "Ceratobium mosaic potyvirus: another virus from orchids.";
RL Arch. Virol. 143:903-914(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CerMV-19;
RA Gibbs A., Mackenzie A., Blanchfield A., Cross P., Wilson C.,
RA Kitajima E., Nightingale M., Clements M.;
RT "Viruses of orchids in Australia: their identification, biology and
RT control.";
RL Aust. Orchid Rev. 65:10-21(2000).
DR EMBL: AF022445; AAC59613.1; -; Genomic_DNA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0004386; F:helicase activity; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006350; P:transcription; IEA.
DR GO: GO:0019079; P:viral genome replication; IEA.
DR InterPro: IPR001592; Poty coat.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR007094; RNA_pol_P5vir.
DR Pfam: PF00767; Poty coat; 1.
DR Pfam: PF00680; RdRP_1; 1.
KW Polyprotein.
FT CHAIN <1 211 Nib polymerase.
FT CHAIN 212 488 coat protein.
FT NON_TER 1 1
SQ SEQUENCE 488 AA; 55976 MW; 1DCAEF91D1813C8 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 488;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 37 KRLVPFA 43

RESULT 22
QSAU77 EMENI PRELIMINARY; PRT; 697 AA.
AC QSAU77;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AN8153.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepl Y., Collamore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gierke S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt T., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,

```

```

RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rhee C., Rogov P.,
RA Ronan J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome Sequence of Aspergillus nidulans.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AAC001000141; EAA59175.1; -; Genomic_DNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR InterPro: IPR003593; AAA_ATPase_cent.
DR InterPro: IPR003959; AAA_ATPase_cent.
DR Pfam: PF00004; AAA; 1.
DR SMART: SM00382; AAA; 1.
KW ATP-binding; Hypothetical protein; Nucleotide-binding.
SQ SEQUENCE 697 AA; 78657 MW; DED32691DDD5754A CRC64;

Query Match 91.2%; Score 31; DB 2; Length 697;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 123 KKLVPFA 129

RESULT 23
Q563A1 BCMVN PRELIMINARY; PRT; 3222 AA.
AC Q563A1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Polyprotein.
OS Peanut stripe virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=28353;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang H.L., Chang Y.Y.;
RT "Molecular sequencing and analysis of the viral genome of Peanut
RT stripe virus Ts strain.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY968604; AAX82171.1; -; Genomic_RNA.
KW Polyprotein.
FT CHAIN 1 443 P1 protein.
FT CHAIN 444 900 HC-Pro protein.
FT CHAIN 901 1247 P3 protein.
FT CHAIN 1248 1299 6K1 protein.
FT CHAIN 1934 1986 6K2 protein.
FT CHAIN 1987 2176 VPg protein.
FT CHAIN 2177 2419 NIa protein.
FT CHAIN 2420 2935 NIb protein.
FT CHAIN 2936 3222 coat protein.
SQ SEQUENCE 3222 AA; 365455 MW; AC20BF2371EC338 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 3222;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 2761 KRLVPFA 2767

RESULT 24

```

Q9UC33_HUMAN
ID Q9UC33_HUMAN PRELIMINARY; PRT; 33 AA.
AC Q9UC33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RA MEDLINE=3024877; PubMed=1406936; DOI=10.1038/359325a0;
RX Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.,
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids".
RL Nature 359:325-327(1992).
DR HSPP; Q16019; 1BA4.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
SQ SEQUENCE 33 AA; 3674 MW; B1DEFE2F4167ABD0 CRC64;
Query Match 88.2%; Score 30; DB 2; Length 33;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLVPFA 7
DB 15 QKLVPFA 21

RESULT 25
Q9XQR5_PEA
ID Q9XQR5_PEA PRELIMINARY; PRT; 34 AA.
AC Q9XQR5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Pium sativum (Garden pea).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lehmbeck J., Stummann B.M., Henningsen K.W.;
RT "Nucleotide sequence of the 5.6 kbp psbB operon of pea chloroplast
RT DNA".
RL Physiol. Plantarum 76:57-64(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lehmbeck J., Stummann B.M., Henningsen K.W.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF153442; AA041885.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009539; C:photosystem II reaction center; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
DR InterPro; IPR001743; PSII_PsbT.
DR Pfam; PF01405; PsbT; 1.
DR ProDom; PD004453; PSII_PsbT; 1.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 34 AA; 4005 MW; F99C563A18BD170 CRC64;
Query Match 88.2%; Score 30; DB 2; Length 34;

Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLVPFA 7
DB 13 KKLVPFA 19

RESULT 26
Q56J36_GRAGR
ID Q56J36_GRAGR PRELIMINARY; PRT; 42 AA.
AC Q56J36;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Grampus griseus (Risso's dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Grampus.
OX NCBI_TaxID=83653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin".
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926589; AAX81918.1; -; mRNA.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;
Query Match 88.2%; Score 30; DB 2; Length 42;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLVPFA 7
DB 15 QKLVPFA 21

RESULT 27
Q56J37_TURTR
ID Q56J37_TURTR PRELIMINARY; PRT; 42 AA.
AC Q56J37;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Tursiops.
OX NCBI_TaxID=9739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin".
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926588; AAX81917.1; -; mRNA.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;
Query Match 88.2%; Score 30; DB 2; Length 42;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLVPFA 7
DB 15 QKLVPFA 21

RESULT 28

```

Q7M088_CAVPO
ID Q7M088_CAVPO PRELIMINARY; PRT; 42 AA.
AC Q7M088;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid protein (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93290653; PubMed=7685598;
RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,
RA Kamiya H., Ohno M.;
RT "Receptor-mediated specific biological activity of a beta-amyloid
RT protein fragment for NK-1 substance p receptors.";
RL Biochem. Biophys. Res. Commun. 193:624-630(1993).
DR PIR; P0512; P0512.
DR HSSP; Q16019; 11YT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR NON_TER 1
DR NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 42;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 15 QKLVPFA 21

RESULT 29
ID Q8WZ99_HUMAN PRELIMINARY; PRT; 52 AA.
AC Q8WZ99;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Amyloid protein (Fragment).
GN Name=APP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15201367; DOI=10.1136/jnnp.2003.010611;
RA Wakutani Y., Watanabe K., Adachi Y., Wada-Isoe K., Urakami K.,
RA Ninomiya H., Saido TC., Haebimoto T., Iwatsubo T., Nakashima K.;
RT "Novel amyloid precursor protein gene missense mutation (D678N) in
RT probable familial Alzheimer's disease.";
RL J. Neurol. Neurosurg. Psychiatr. 75:1039-1042(2004).
DR EMBL; AB066441; BAB71958.2; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR NON_TER 1
DR NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 5597 MW; 3F0E8E9EC18011AD CRC64;

Query Match 88.2%; Score 30; DB 2; Length 52;
Best Local Similarity 85.7%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 15 QKLVPFA 21

RESULT 30
ID A4_URSMA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Ursidae;
OC Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X56128; CAA39593.1; -; mRNA.
DR PIR; B60045; B60045.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >57 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >57 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >57 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT NON_TER 1
FT NON_TER 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 88.2%; Score 30; DB 1; Length 57;
Best Local Similarity 85.7%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```



```

Qy 1 KKLVEFA 7
Db 20 QKLVEFA 26

RESULT 31
A4_CANFA STANDARD; PRT; 58 AA.
ID_A4_CANFA
AC Q2820;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G1O (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X56125; CAA39590.1; -; mRNA.
CC HSP; P08592; INMJ.
CC Ensembl; ENSCAG00000008557; Canis familiaris.
CC InterPro; IPR008155; A4_APP.
CC InterPro; IPR001255; Beta-APP.
CC PANTHER; PTHR10083:SF6; Beta-APP; 1.
CC Pfam; PF03494; Beta-APP; 1.
CC PRINTS; PR00204; BETAAPPYLOID.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Amyloid; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2B12DFA CRC64;

Query Match 88.2%; Score 30; DB 1; Length 58;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVEFA 7
Db 20 QKLVEFA 26

RESULT 32
A4_RABIT STANDARD; PRT; 58 AA.
ID_A4_RABIT
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G1O (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X56129; CAA39594.1; -; mRNA.
CC HSP; P08592; INMJ.
CC InterPro; IPR008155; A4_APP.
CC InterPro; IPR001255; Beta-APP.
CC PANTHER; PTHR10083:SF6; Beta-APP; 1.
CC Pfam; PF03494; Beta-APP; 1.
CC PRINTS; PR00204; BETAAPPYLOID.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 88.2%; Score 30; DB 1; Length 58;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVEFA 7
Db 20 QKLVEFA 26

```

RESULT 33				RESULT 34					
ID	A4 SHEEP	STANDARD;	PRT;	58 AA.	ID	A4 BOVIN	STANDARD;	PRT;	59 AA.
AC	Q28757;				AC	Q28053;			
DT	01-NOV-1997 (Rel. 35, Created)				DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)				DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DE	Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-				DE	Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-			
DE	Beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);				DE	Beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);			
DE	Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase				DE	Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase			
DE	C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal				DE	C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal			
DE	fragment 57)] (Fragment).				DE	fragment 57)] (Fragment).			
GN	Name=APP;				GN	Name=APP;			
OS	Ovis aries (Sheep).				OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;				OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;			
OC	Pecora; Bovidae; Caprinae; Ovis.				OC	Pecora; Bovidae; Caprinae; Ovis.			
OX	NCBI_TaxID=9940;				OX	NCBI_TaxID=9913;			
RN	[1]				RN	[1]			
RP	NUCLEOTIDE SEQUENCE.				RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Heart;				RC	TISSUE=Brain;			
RC	MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;				RC	MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;			
RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;				RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;			
RT	"Conservation of the sequence of the Alzheimer's disease amyloid				RT	"Conservation of the sequence of the Alzheimer's disease amyloid			
RT	peptide in dog, polar bear and five other mammals by cross-species				RT	peptide in dog, polar bear and five other mammals by cross-species			
RT	polymerase chain reaction analysis.";				RT	polymerase chain reaction analysis.";			
RL	Brain Res. Mol. Brain Res. 10:299-305(1991).				RL	Brain Res. Mol. Brain Res. 10:299-305(1991).			
CC	-1- FUNCTION: Functional neuronal receptor which couples to				CC	-1- FUNCTION: Functional neuronal receptor which couples to			
CC	intracellular signaling pathway through the GTP-binding protein				CC	intracellular signaling pathway through the GTP-binding protein			
CC	G(O) (By similarity).				CC	G(O) (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: Belongs to the APP family.				CC	-1- SIMILARITY: Belongs to the APP family.			
CC	-----				CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration				CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its				CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not				CC	use as long as its content is in no way modified and this statement is not			
CC	removed.				CC	removed.			
DR	EMBL; X56130; CAA39595.1; -; mRNA.				DR	EMBL; X56124; CAA39589.1; -; mRNA.			
DR	HSSP; P08592; INMU.				DR	HSSP; P08592; INMU.			
DR	InterPro; IPR008155; A4 APP.				DR	InterPro; IPR008155; A4 APP.			
DR	InterPro; IPR001255; Beta-APP.				DR	InterPro; IPR001255; Beta-APP.			
DR	PANTHER; PTHR10083.SF6; Beta-APP; 1.				DR	PANTHER; PTHR10083.SF6; Beta-APP; 1.			
DR	Pfam; PF03494; Beta-APP; 1.				DR	Pfam; PF03494; Beta-APP; 1.			
DR	PRINTS; PR00204; BETAAMYLOID.				DR	PRINTS; PR00204; BETAAMYLOID.			
DR	PROSITE; PS00319; A4 EXTRA; PARTIAL.				DR	PROSITE; PS00319; A4 EXTRA; PARTIAL.			
DR	PROSITE; PS00320; A4 INTRA; PARTIAL.				DR	PROSITE; PS00320; A4 INTRA; PARTIAL.			
KW	Amyloid; Transmembrane.								

035463_CRIGR	035463_CRIGR PRELIMINARY;	PRT;	79 AA.
ID	Q35463		
AC	Q35463		
DT	01-JAN-1998 (TrEMBLrel. 05, Created)		
DT	01-JAN-1998 (TrEMBLrel. 05, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Alzheimer's amyloid beta protein (Fragment).		
GN	Name-beta APP;		
OS	Cricetulus griseus (Chinese hamster).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Cricetinae; Cricetulus.		
OX	NCBI_TaxID=10029;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	Sambamurti K., Pinnix I., Gandhi S.;		
RL	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF030413; AAB86608.1; -; mRNA.		
DR	HSP; P08592; INM3.		
DR	GO; GO:0016021; C: integral to membrane; IEA.		
DR	GO; GO:0005488; F: binding; IEA.		
DR	InterPro; IPR001255; Beta-APP.		
DR	Pfam; PF03494; Beta-APP; 1.		
DR	PRINTS; PR00204; BETAAMYLOID.		
FT	NON_TER 1		
FT	NON_TER 79		
FT	SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;		
Query Match	88.2%;	Score 30; DB 2; Length 79;	
Best Local Similarity	85.7%;	Pred. No. 60;	
Matches	6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 KKLVPFA 7		
Db	35 QKLVPFA 41		
RESULT 36			
Q5XD67_STRP6	Q5XD67_STRP6 PRELIMINARY;	PRT;	94 AA.
ID	Q5XD67		
AC	Q5XD67		
DT	25-OCT-2004 (TrEMBLrel. 28, Created)		
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)		
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)		
DE	Hypothetical protein.		
GN	OrderedLocuNames=M6_Spy0511;		
OS	Streptococcus pyogenes (serotype M6).		
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		
OC	Streptococcus.		
OX	NCBI_TaxID=301450;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=MGAS103394;		
RX	PubMed=15272401; DOI=10.1086/422697;		
RA	Banks D.J., Porcella S.F., Barbican K.D., Beres S.B., Phillips L.E.,		
RA	Voyich J.M., DeLeo P.R., Martin J.M., Somerville G.A., Musser J.M.;		
RT	"Progress toward characterization of the group A Streptococcus		
RT	metagenome: complete genome sequence of a macrolide-resistant serotype		
RT	M6 strain";		
RL	J. Infect. Dis. 190:727-738 (2004).		
RL	EMBL; CP000003; AAT86646.1; -; Genomic DNA.		
KW	Complete proteome; Hypothetical protein.		
SQ	SEQUENCE 94 AA; 10579 MW; FE5064A8B849FED0 CRC64;		
Query Match	88.2%;	Score 30; DB 2; Length 94;	
Best Local Similarity	85.7%;	Pred. No. 70;	
Matches	6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 KKLVPFA 7		
Db	38 KKLVPFA 44		
RESULT 37			
Q9A0W1_STRPY	Q9A0W1_STRPY PRELIMINARY;	PRT;	94 AA.
ID	Q9A0W1		
AC	Q9A0W1		
DT	01-JUN-2001 (TrEMBLrel. 17, Created)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	Hypothetical protein SPY0589.		
GN	OrderedLocuNames=SPY0589;		
OS	Streptococcus pyogenes.		
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		
OC	Streptococcus.		
OX	NCBI_TaxID=13114;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=SF370 / ATCC 700294 / Serotype M1;		
RX	MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;		
RA	Ferrretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,		
RA	Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,		
RA	Qian Y., Jia H.G., Najjar P.Z., Ren Q., Zhu H., Song L., White J.,		
RA	Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;		
RT	"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).		
DR	EMBL; AE006514; AAK33570.1; -; Genomic DNA.		
KW	Complete proteome; Hypothetical protein.		
SQ	SEQUENCE 94 AA; 10613 MW; FE58C6A8B849FED0 CRC64;		
Query Match	88.2%;	Score 30; DB 2; Length 94;	
Best Local Similarity	85.7%;	Pred. No. 70;	
Matches	6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 KKLVPFA 7		
Db	38 KKLVPFA 44		
RESULT 38			
Q7CNF7_STRP8	Q7CNF7_STRP8 PRELIMINARY;	PRT;	94 AA.
ID	Q7CNF7		
AC	Q7CNF7		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Hypothetical protein spym18		

```
RESULT 39
QBPI1X8 STRP3 PRELIMINARY; PRT; 94 AA.
AC QBPI1X8_07CF33;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Hypothetical protein SPa1439 (Hypothetical protein SpyM3_0416).
GN OrderedLocusNames=SPa1439, SpyM3_0416;
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=301448;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSI-1 / Serotype M3;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution.";
RL Genome Res. 13:1042-1055(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RA Berges S.B., Sylva G.B., Barbian K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
DR EMBL; BA000034; BAC64534.1; -; Genomic DNA.
DR EMBL; AF014144; AM79023.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 94 AA; 10579 MW; FE50648B849FED0 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 94;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 38 KKLVPFA 44
|:|||||

RESULT 40
QBH58 CHESE PRELIMINARY; PRT; 113 AA.
AC QBH58;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Chelydra serpentina serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX NCBI_TaxID=134619;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21876906; PubMed=11882478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT "Ocylphenol (OP) alters the expression of members of the amyloid
RT protein family in the hypothalamus of the snapping turtle, Chelydra
RT serpentina serpentina.";
RL Environ. Health Perspect. 110:269-275(2002).
DR EMBL; AF541917; RAN04908.1; -; mRNA.
DR HSSP; Q16019; IIYT.
```

```
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR InterPro; IPR008155; A4 APP.
DR Pfam; PF03494; Beta-APP.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00204; BETAAMYLOID.
FT NON TER 1
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 113;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 29 KKLVPFA 35
|:|||||

RESULT 41
QSTUI4 ANOGA PRELIMINARY; PRT; 125 AA.
AC QSTUI4;
DT 01-FEB-2005 (TReMBLrel. 29, Created)
DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE ENGANGP0000025864 (Fragment).
GN Name=CTL2; ORFNames=ENGANGG00000022826;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA801008848; EAL41080.1; -; Genomic DNA.
DR GO; GO:0005529; F: sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C_1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
FT NON TER 1
FT NON TER 125
SQ SEQUENCE 125 AA; 14081 MW; F4BC758D6262EA7F CRC64;

Query Match 88.2%; Score 30; DB 2; Length 125;
Best Local Similarity 85.7%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
DB 7 KKLVPFA 13
|:|||||

RESULT 42
FABZ DESPS STANDARD; PRT; 150 AA.
ID FABZ DESPS
AC Q6AJ07;
DT 10-MAY-2005 (Rel. 47, Created)
```

DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE (3R)-hydroxymyristoyl-(acyl carrier protein) dehydratase (BC 4.2.1.-)
DE (3R)-hydroxymyristoyl ACP dehydratase)
GN Name=fabZ; OrderedLocusNames=DP2944;
OS Desulfotalea psychrophila
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobulbaceae; Desulfotalea
OX NCBI_TaxID=84980;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=LSV54 / DSM 12343;
RX PubMed=15305914; DOI=10.1101/1462-2920.2004.00665.x;
RA Ruben R., Ruepp A., Frickey T., Rattei T., Partmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:987-902(2004).
CC -!- FUNCTION: Involved in saturated fatty acids biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the thioester dehydratase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; CR522870; CAG37673.1; -, Genomic_DNA.
DR HAMAP; MP 00406; -, 1.
DR InterPro; IPR010084; FabZ.
DR TIGRPFAMs; TIGR01750; fabZ; 1.
KW Complete proteome; Lipid A biosynthesis; Lipid synthesis; Lyase.
FT ACT_SITE 56 56 By similarity
SQ SEQUENCE 150 AA; 16687 MW; 37FA4FC716389219 CRC64;

Query Match 88.2%; Score 30; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKLVPFA 7
Db 90 KKLAPFA 96
||| |||
||| |||

RESULT 43
Q6CKLI_KLUJA
ID Q6CKLI_KLUJA PRELIMINARY; PRT; 165 AA.
AC Q6CKLI;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|Q12322 Saccharomyces cerevisiae YOL114c singleton.
GN OrderedLocusNames=KLLA0A073819;
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durieux P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talia E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barney S., Bianchini S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisarame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye P., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-P., Straub M.-L., Suleau A.,

RA Swennen D., Tekai F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudion B., Scarpetti C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR382121; CAH02916.1; -, Genomic DNA.
DR GO; GO:0003747; P:translation release factor activity; IEA.
DR GO; GO:0006415; P:translational termination; IEA.
DR InterPro; IPR000352; Pep_rel_factor_1.
DR Pfam; PF00472; RF-1; 1.
KW Complete proteome.
SQ SEQUENCE 165 AA; 19350 MW; EEDF94B5004EFD93 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPF 6
Db 117 KKLVPF 122
||| |||
||| |||

RESULT 44
Q4TUZ7_MAIZE
ID Q4TUZ7_MAIZE PRELIMINARY; PRT; 187 AA.
AC Q4TUZ7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Atypical receptor-like kinase MARK (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ohtsu K., Hake S.C., Schnable P.S.;
RT "SAM control genes.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ056240; AAY57565.1; -, mRNA.
KW Kinase; Receptor.
FT NON_TER 1 1
FT NON_TER 187 187
SQ SEQUENCE 187 AA; 18072 MW; E5291DD1F65F8FB8 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVPF 6
Db 152 KKLVPF 157
||| |||
||| |||

RESULT 45
Q64ME8_BACFR
ID Q64ME8_BACFR PRELIMINARY; PRT; 214 AA.
AC Q64ME8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BFP0012;
OS Bacteroides fragilis.
OS Plasmid pBF46.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YCH46;

```

RX PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kubara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RL inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924 (2004).
DR EMBL; AF006842; BAD51339.1; -; Genomic DNA.
SQ Complete proteome; Hypothetical protein; Plasmid.
KW SEQUENCE 214 AA; 25216 MW; CESD86CD4212ADC8 CRC64;

Query Match      88.2%; Score 30; DB 2; Length 214;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7
DB 2 KKLIFFS 8

RESULT 46
QBPPV5 MOUSE
ID Q8BPV5 MOUSE PRELIMINARY; PRT; 218 AA.
AC Q8BPV5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
DE library, clone: D430025B14 product: amyloid beta (A4) protein, full
DE insert sequence. (Fragment).
GN Name=App;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Mateu Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga M., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald W., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";

```

```

RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Katsuka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Harada A.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Kashiwagi K.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kurihara K., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tomaru A., Toyata T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK052448; BAC34997.1; -; mRNA.
DR HSP; P08592; 1NMJ.
DR MGI; MGI:88059; App.
DR GO; GO:0016021; C: integral to membrane; IDA.
DR GO; GO:0016020; C: membrane; TAS.
DR GO; GO:0005515; P: protein binding; IPI.
DR GO; GO:0030198; P: extracellular matrix organization and bioge. .; IGI.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 218 AA; 24118 MW; 95B55AFDAE1D0EF5 CRC64;

Query Match      88.2%; Score 30; DB 2; Length 218;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFFA 7
DB 134 KKLVEFFA 140

RESULT 47
QB4MC9 BACFR PRELIMINARY; PRT; 228 AA.
ID Q64MC9;
AC Q64MC9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BFP0031;

```

```

OS Bacteroides fragilis.
OG Plasmid pBFY46.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
ON NCBI_TaxID=817;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YCH46;
RX PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayaishi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924 (2004).
DR EMBL; AP006842; BAD51358.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 228 AA; 25837 MW; 2A53B2BB05742631 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 228;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
DB 2 KKLIFPS 8

RESULT 48
Q7MV75_PORGI
ID Q7MV75_PORGI PRELIMINARY; PRT; 270 AA.
AC Q7MV75;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Lipoprotein protein, putative.
GN OrderedLocusNames=FG1215;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
ON NCBI_TaxID=837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601 (2003).
DR EMBL; AB017176; AAQ66305.1; -; Genomic_DNA.
DR TIGR; FG1215; -
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like helical.
KW Complete proteome; Lipoprotein.
SQ SEQUENCE 270 AA; 31551 MW; DA058B9B99FF6A5D CRC64;

Query Match 98.2%; Score 30; DB 2; Length 270;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFA 7
DB 4 KKLIFFA 10

RESULT 49
Q74HY9_LACJO
ID Q74HY9_LACJO PRELIMINARY; PRT; 336 AA.
AC Q74HY9;

```

```

DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=LJ0670;
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
ON NCBI_TaxID=33959;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCC 533;
RX PubMed=14983040; DOI=10.1073/pnas.0307327101;
RA Pridmore R.D., Berger B., Desiere P., Vilanova D., Barretto C.,
RA Pittet A.-C., Zwaehler M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
RT Lactobacillus johnsonii NCC 533.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517 (2004).
DR EMBL; AS017205; AAS09551.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 336 AA; 37650 MW; F97C983851FBF1CC CRC64;

Query Match 88.2%; Score 30; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFF 6
DB 258 KKLVEFF 263

RESULT 50
Q9PMW9_CAMJE
ID Q9PMW9_CAMJE PRELIMINARY; PRT; 346 AA.
AC Q9PMW9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Putative fucose synthetase.
GN Names=fcl; OrderedLocusNames=Cj1428c;
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
ON NCBI_TaxID=197;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
RA Parkhill J., Wren B.W., Mungall K.L., Kettle J.M., Churcher C.M.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtwell S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668 (2000).
DR EMBL; AL139078; CAB73852.1; -; Genomic_DNA.
DR PIR; D81288; D81288.
DR HSP; P32055; IE6U.
DR InterPro; IPR001509; Epimerase_Dh.
DR Pfam; PF01370; Epimerase; 1.
KW Complete proteome.
SQ SEQUENCE 346 AA; 39431 MW; DF7D95EB5630FC3 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFF 6
DB 100 KKLVEFF 105

```

```

RESULT 51
Q8UUI8 BRARE PRELIMINARY; PRT; 357 AA.
AC Q8UUI8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative membrane protein (Fragment).
GN Name=appa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole embryo;
RX PubMed=11862463; DOI=10.1007/s00427-001-0189-9;
RA Musa A., Lehrach H., Russo V.E.A.;
RT "Distinct expression patterns of two zebrafish homologues of the human
RT APP gene during embryonic development.";
RL Dev. Genes Evol. 211:563-567(2001).
DR EMBL; AJ315637; CAC85734.1; -; mRNA.
DR HSSP; Q16019; 1HZ3.
DR SMR; Q8UUI8; 62-170.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005488; F:Binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta_APP.
DR Pfam; PF03494; Beta_APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 357 AA; 40962 MW; 07D99BEF6C55B2D8 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 357;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 273 QKLVPFA 279

RESULT 52
MLTA_BUCAI STANDARD; PRT; 359 AA.
AC P57531;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Membrane-bound lytic murein transglycosylase A homolog (EC 3.2.1.-)
DE (Murein hydrolase A).
GN Name=mlta; OrderedLocNames=BU458;
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
NCBI_TaxID=118099;
RX [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077; DOI=10.1038/35024074;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -!- FUNCTION: Murein-degrading enzyme. May play a role in recycling of
CC muropeptides during cell elongation and/or cell division (By
CC similarity).

```

```

CC -!- CATALYTIC ACTIVITY: Cleavage of the beta-1,4-glycosidic bond
CC between N-acetylmuramic acid and N-acetylglucosamine residues,
CC thereby conserving the energy in a newly synthesized 1,6-
CC anhydrobond in the muramic acid residue.
CC -!- SUBCELLULAR LOCATION: In closeley related bacteria this protein is
CC attached to the outer membrane by a lipid anchor. This is
CC apparently not the case here.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BA000003; BAB13155.1; -; Genomic_DNA.
CC InterPro; IPR010611; 3D.
CC InterPro; IPR005300; MltA.
CC Pfam; PF06725; 3D; 1.
CC Pfam; PF03562; MltA; 1.
CC Cell wall; Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 359 AA; 41773 MW; 24E12A2778D351AB CRC64;

Query Match 88.2%; Score 30; DB 1; Length 359;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 196 KKLIFPS 202

RESULT 53
O67225 AQUAE PRELIMINARY; PRT; 380 AA.
AC O67225;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hydrogenase expression/formation protein HypD.
GN Name=hypD; OrderedLocNames=AQ_1157;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OC NCBI_TaxID=63363;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
DR EMBL; AE000726; AAC07185.1; -; Genomic_DNA.
DR PIR; F70399; F70399.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR PIRSF; PIRSF005622; Hydrgn_mat_hypD; 1.
DR TIGRFAMs; TIGR00075; hypD; 1.
KW Complete proteome.
SQ SEQUENCE 380 AA; 42791 MW; 49C0E52BA655A5F5 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 380;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 140 KKVIFPA 146

RESULT 54
Q8BPC7_MOUSE

```


ID QBPC7_MOUSE PRELIMINARY; PRT; 384 AA.
AC QBPC7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
DE library, clone:483432109 product:amylod beta (A4) protein, full
DE insert sequence. (Fragment).
GN Name=App;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa;
OC Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Nishikawa K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Schenwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Haegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:689-690(2001).
[3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayata N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RX Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Orawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.

RT *RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka T.,
RA Tomaru A., Tova T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK076506; BAC36369.1; -, mRNA.
DR HSSP; P08592; INMJ.
DR SMR; Q8BPC7; 74-183.
DR MGI; MGI:88059; App.
DR GO; GO:0016021; C:integral to membrane; IDA.
DR GO; GO:0016020; C:membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0030198; P:extracellular matrix organization and bioge. .; IGI.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR0203; AMYLOIDA4.
DR PRINTS; PR0204; BETAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 384 AA; 43990 MW; A81B1AD8AE683173 CRC64;
Query Match 88.2%; Score 30; DB 2; Length 384;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLVPFA 7
:|||||
DB 300 QKLVPFA 306
RESULT 55
Q83DX9 COXBU
ID Q83DX9 COXBU PRELIMINARY; PRT; 426 AA.
AC Q83DX9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=CBU0562;
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coxiellaceae; Coxiella.
OC NCBI_TaxID=777;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Nine Mile phase I / RSA 493;
RC MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
RX Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
RA Nelson W.C., Ward N.L., Tettelin H., Daviden T.M., Beanan K.J.,
RA DeBoy R.T., Dougherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
RA Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
RT "Complete genome sequence of the Q-fever pathogen, Coxiella
RT burnetii.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
DR EMBL; AE016961; AA090106.1; -, Genomic_DNA.
DR TIGR; CBU0562; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 426 AA; 49687 MW; 0BA2844C7E052CB2 CRC64;

```

Query Match      88.2%; Score 30; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFF 6
DB      237 KKLVPFF 242

RESULT 56
Q8U50_BRARE
ID Q8U50_BRARE PRELIMINARY; PRT; 472 AA.
AC Q8U50;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative membrane protein (Fragment).
GN Name=appa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX PubMed=11862463; DOI=10.1007/s00427-001-0189-9;
RA Musa A., Lehrach H., Russo V.E.A.;
RT "Distinct expression patterns of two zebrafish homologues of the human
  APP gene during embryonic development.";
RL Dev. Genes Evol. 211:563-567(2001).
DR EMBL; AJ315636; CAC85733.1; -; mRNA.
DR HSP; Q16019; 1H23.
DR SMR; Q8U50; 177-285.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; ANYLOIDA4.
DR PRINTS; PR00204; BETAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 472 AA; 53787 MW; 24F7128BE3356550 CRC64;

Query Match      88.2%; Score 30; DB 2; Length 472;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFF 7
DB      388 KKLVPFF 394

RESULT 57
Q9X152_ARATH
ID Q9X152_ARATH PRELIMINARY; PRT; 479 AA.
AC Q9X152;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE F9L1.11 protein.
GN Name=F9L1.11;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,

```

```

RA Lee J., Liu A., Li J., Kremenetskaia I., Luros J., Gonzalez A.,
RA Altafi H., Araujo R., Brooks S., Buehler E., Chao Q., Conn L.,
RA Conway A.B., Dunn P., Hansen N., Huizar L., Khan S., Kim C., Palm C.,
RA Rowley D., Shinn P., Walker M., Davis R.W., Ecker J.R.,
RA Pederspiel N.A., Theologis A.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007591; AAD39644.1; -; Genomic_DNA.
DR PIR; F86285; F86285.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; F:antipporter activity; IEA.
DR GO; GO:0015238; F:drug transporter activity; IEA.
DR GO; GO:0006855; F:multidrug transport; IEA.
DR InterPro; IPR002528; MatE.
DR Pfam; PF01554; MatE; 2.
DR TIGRFAMs; TIGR00797; matE; 1.
SQ SEQUENCE 479 AA; 52123 MW; 05D2044C9331806B CRC64;

Query Match      88.2%; Score 30; DB 2; Length 479;
Best Local Similarity 71.4%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKLVPFF 7
DB      36 KKLIPFF 42

RESULT 58
Q8L731_ARATH
ID Q8L731_ARATH PRELIMINARY; PRT; 481 AA.
AC Q8L731;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein Atg15170.
GN Name=Atg15170;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Palm C.J., Davis R.W.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,
RA Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY139985; AAM39128.1; -; mRNA.
DR EMBL; BT006616; AAP31960.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; F:antipporter activity; IEA.
DR GO; GO:0015238; F:drug transporter activity; IEA.
DR GO; GO:0006855; F:multidrug transport; IEA.
DR InterPro; IPR002528; MatE.
DR Pfam; PF01554; MatE; 2.
DR TIGRFAMs; TIGR00797; matE; 1.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52188 MW; 47876B51B57CE760 CRC64;

```

Query Match 88.2%; Score 30; DB 2; Length 481;
 Best Local Similarity 71.4%; Pred. No. 3e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 Db 36 KRLIFFA 42

RESULT 59
 Q5K4D4_9POTV PRELIMINARY; PRT; 493 AA.
 AC Q5K4D4;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Polypeptide (Fragment).
 OS Soybean mosaic virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 OC NCBI_TaxID=12222;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=P;
 RX PubMed=15449140; DOI=10.1007/s00705-004-0390-z;
 RA Shi Y.H., Hong X.Y., Chen J., Adams M.J., Zheng H.Y., Lin L.,
 RA Qing B.X., Chen J.;
 RT "Further molecular characterisation of potyviruses infecting aroid
 RT plants for medicinal use in China.";
 RL Arch. Virol. 150:125-135(2005).
 DR EMBL; AJ628752; C: viral capsid; IEA.
 DR GO; GO:0019028; C: viral capsid; IEA.
 DR GO; GO:0003968; F: RNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0019079; F: viral genome replication; IEA.
 DR InterPro; IPR001592; Poty. coat.
 DR InterPro; IPR001205; RNA_Pol_P3D.
 DR InterPro; IPR007094; RNA_Pol_P3D.
 DR Pfam; PF00676; Poty. coat; 1.
 DR Pfam; PF00680; RdRP_1; 1.
 KW Capsid protein; Polyprotein.
 FT CHAIN <1 211
 FT CHAIN 212 493 coat protein.
 FT NON TER 1
 SQ SEQUENCE 493 AA; 55921 MW; 0898559BD4C19F6F CRC64;

Query Match 88.2%; Score 30; DB 2; Length 493;
 Best Local Similarity 85.7%; Pred. No. 3.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 Db 37 EKLVPFA 43

RESULT 60
 O93296_CHICK PRELIMINARY; PRT; 534 AA.
 AC O93296;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Amyloid protein (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98337885; PubMed=9671674;
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
 RA Milligan C.E.;

RT "Increased production of amyloid precursor protein provides a
 RT substrate for caspase-3 in dying motoneurons.";
 RL J. Neurosci. 18:5869-5880(1998).
 DR EMBL; AF042098; AAC25052.1; -; mRNA.
 DR HSP; Q16019; IYT.
 DR SNR; O93296; 224-333.
 DR Ensembl; ENSGALG0000015770; Gallus gallus.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0005488; F: binding; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00204; BETAMYLOID.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 FT NON TER 1
 SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 534;
 Best Local Similarity 85.7%; Pred. No. 3.3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
 Db 450 QKLVPFA 456

RESULT 61
 Q9PVL1_CHICK PRELIMINARY; PRT; 569 AA.
 AC Q9PVL1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Amyloid protein (Fragment).
 GN Name=APP;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA Coulson E.J., Palla K., Beyreuther K., Masters C.L.;
 RT "What the evolution of the amyloid protein precursor superegene family
 RT tells us about its function.";
 RL Neurochem. Int. 0:0-0(2000).
 DR EMBL; AF030341; AAF12698.1; -; mRNA.
 DR HSP; Q16019; IYT.
 DR SNR; Q9PVL1; 1-64, 260-369.
 DR Ensembl; ENSGALG0000015770; Gallus gallus.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0005488; F: binding; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00204; BETAMYLOID.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 FT NON TER 1
 SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;

Query Match 88.2%; Score 30; DB 2; Length 569;
 Best Local Similarity 85.7%; Pred. No. 3.5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 486 OKLVFFA 492

RESULT 62

Q75JL6_DICDI
ID Q75JL6_DICDI PRELIMINARY; PRT; 572 AA.
AC Q75JL6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Similar to Leishmania major. Lail.4 (Hypothetical protein).
GN ORFNames=DD0169466;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J.A.,
RA Bankier A.T., Dear P.H., Lehmann R., Baugart C., Parra G.,
RA Abril J.F., Guigo R., Kumpf K., Tungal B., Cox E., Quail M.A.,
RA Platzter M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."
RL Nature 418:79-85(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX Baugart C.;
RN Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RX Sugang R., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Tungal B., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Pey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren B., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsey R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulsegged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzter M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuapa A.;
RT "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 0:0-0(2005).
RL Nucleotide sequence of the genome of Dictyostelium discoideum.
DR EMBL; AC116979; AAS38717.1; -; Genomic DNA.
DR EMBL; AAF10100032; BAL69334.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 572 AA; 63642 MW; 7B9158ADA5020D1 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 572;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 3 KKLIFFS 9

RESULT 63

RPOC1_EUGR
ID RPOC1_EUGR STANDARD; PRT; 586 AA.
AC P23580;

DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (PEP) (Plastid-
DE encoded RNA polymerase beta' subunit) (RNA polymerase beta' subunit).
GN Name=rpoC1;
OS Euglena gracilis.
OC Chloroplast.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID=3039;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Z / UTEX 753;
RX MEDLINE=90245579; PubMed=2110656;
RA Yeliz-Plascencia G.M., Radebaugh C.A., Hallick R.B.;
RT "The Euglena gracilis chloroplast rpoB gene. Novel gene organization
RT and transcription of the RNA polymerase subunit operon."
RL Nucleic Acids Res. 18:1869-1878(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Z / UTEX 753;
RX MEDLINE=93347989; PubMed=8346031;
RA Hallick R.B., Hong L., Drager R.G., Favreau M.R., Monfort A.,
RA Orsat B., Spieemann A., Stutz E.;
RT "Complete sequence of Euglena gracilis chloroplast DNA."
RL Nucleic Acids Res. 21:3537-3544(1993).
CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC of DNA into RNA using the four ribonucleoside triphosphates as
CC substrates.
CC -!- CATALYTIC ACTIVITY: Nucleoside triphosphate + RNA(n) = diphosphate
CC + RNA(n+1).
CC -!- SUBUNIT: In plastids the minimal PEP RNA polymerase catalytic core
CC is composed of four subunits: alpha, beta, beta', and beta''. When
CC a (nuclear-encoded) sigma factor is associated with the core the
CC holoenzyme is formed, which can initiate transcription (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC -!- SIMILARITY: Belongs to the RNA polymerase beta' chain family.
CC RpoC1 subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X17191; CAA35053.1; -; Genomic DNA.
CC EMBL; X70810; CAA50137.1; -; Genomic DNA.
CC PIR; S19258; RNEGB1.
CC HSSP; Q9KWU6; 1HQW.
CC HAMAP; MF_01323; -; 1.
CC InterPro; IPR000722; RNA_pol_A.
CC InterPro; IPR007080; RNA_pol_Rpb1_1.
CC InterPro; IPR006592; RNA_pol_N.
CC Pfam; PF04997; RNA_pol_Rpb1_1; 1.
CC Pfam; PF00623; RNA_pol_Rpb1_2; 1.
CC SMART; SM00663; RPOA_N; 1.
CC Chloroplast; DNA-directed RNA polymerase; Nucleotidyltransferase;
KW Transcription; Transferase.
SQ SEQUENCE 586 AA; 68142 MW; D346474567910763 CRC64;

Query Match 88.2%; Score 30; DB 1; Length 586;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFF 6
Db 564 KKLVPFF 569

RESULT 64

Q919E7_BRARE
ID Q919E7_BRARE PRELIMINARY; PRT; 612 AA.

AC Q919B7; 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Amyloid protein (Fragment).
 GN Name: appa;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Slavov D.B., Gardiner K.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF257742; AAF71748.1; -, mRNA.
 DR HSP; Q16019; 1HZ3.
 DR SMR; Q919B7; 1-56, 317-425.
 DR ZFIN; ZDB-GENE-000616-13; appa.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0005488; F: binding; IEA.
 DR InterPro; IPR008155; A4 APP.
 DR InterPro; IPR008154; A4 extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4-EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00319; A4 EXTRA; 1.
 DR PROSITE; PS00320; A4-INTRA; 1.
 FT NON TER 1
 SQ SEQUENCE 612 AA; 69710 MW; 59A9ACBDP9C59EPF CRC64;
 Query Match 88.2%; Score 30; DB 2; Length 612;
 Best Local Similarity 85.7%; Pred. No. 3.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KKLVFFA 7
 Db 528 QKLVFFA 534
 RESULT 65
 Q8LD58 ARATH PRELIMINARY; PRT; 639 AA.
 ID Q8LD58 ARATH PRELIMINARY; PRT; 639 AA.
 AC Q8LD58;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Receptor kinase, putative.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 annotation.";
 RL Genome Biol. 3: RESEARCH0029-RESEARCH0029 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY086189; AAM64268.1; -, mRNA.
 DR GO; GO:0005524; F: ATP binding; IEA.
 DR GO; GO:0004672; F: protein kinase activity; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0006468; P: protein amino acid phosphorylation; IEA.

DR InterPro; IPR000560; HisAc_phosphatase.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007090; LRR_plant.
 DR InterPro; IPR000719; Prot_kinase.
 DR Pfam; PF00560; LRR_1; 4.
 DR Pfam; PF00069; PKinase; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 KW Kinase; Receptor.
 SQ SEQUENCE 639 AA; 69564 MW; E0A5FEB857D8DB80 CRC64;
 Query Match 88.2%; Score 30; DB 2; Length 639;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KKLVFF 6
 Db 338 KKLVFF 343
 RESULT 66
 Q9ZT08 ARATH PRELIMINARY; PRT; 645 AA.
 ID Q9ZT08 ARATH PRELIMINARY; PRT; 645 AA.
 AC Q9ZT08;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Receptor-like protein kinase.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=20550477; PubMed=11100776; DOI=10.1093/pcp/pcd028;
 RA Ontake Y., Takahashi T., Komeda Y.;
 RT "Salicylic acid induces the expression of a number of receptor-like
 kinase genes in Arabidopsis thaliana.";
 RL Plant Cell Physiol. 41:1038-1044 (2000).
 DR EMBL; AF084034; AAC95351.1; -, Genomic DNA.
 DR GO; GO:0005524; F: ATP binding; IEA.
 DR GO; GO:0004672; F: protein kinase activity; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0006468; P: protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000560; HisAc_phosphatase.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007090; LRR_plant.
 DR Pfam; PF00560; LRR_1; 5.
 DR PRINTS; PR00019; LEURICHRPT.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 KW Kinase; Receptor.
 SQ SEQUENCE 645 AA; 69917 MW; 7769E17D5A1600E CRC64;
 Query Match 88.2%; Score 30; DB 2; Length 645;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KKLVFF 6
 Db 342 KKLVFF 347
 RESULT 67
 Q9LV16 ARATH

ID Q9LV16 ARATH PRELIMINARY; PRT; 647 AA.
 AC Q9LV16;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Probable receptor-like protein kinase protein (AT3917840/NEBS_6).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eucosids II; Brassicales; Brassicaceae; Arabidopses.
 OC NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20277480; PubMed=10819329;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
 RT clones."; DNA Res. 7:131-135 (2000).
 RL [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.B., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Quach H.B., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
 RA Toriumi M., Wallender E.K., Wong C., Wu H.C., Yamada K., Yu G.,
 RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB019230; BAB02707.1; -; Genomic_DNA.
 DR EMBL; AY095994; RAN19950.1; -; mRNA.
 DR EMBL; BT002283; RAN72294.1; -; mRNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004672; F:protein kinase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000560; HisAc_phsphtse.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007090; LRR_plant.
 DR InterPro; IPR000719; Prot_kinase.
 DR Pfam; PF00560; LRR_1; 4.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Kinase; Receptor.
 SQ SEQUENCE 647 AA; 70406 MW; 1FF91B013B75A1DA CRC64;

Query Match 88.2%; Score 30; DB 2; Length 647;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFF 6
 Db 346 KKLVEFF 351

RESULT 68
 Q9LP77 ARATH PRELIMINARY; PRT; 655 AA.
 AC Q9LP77;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE T1N15.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eucosids II; Brassicales; Brassicaceae; Arabidopses.
 OC NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
 RA Shinn P., Altafi H., Bei Q., Chin C., Chioi J., Choi B., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharasy N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chioi J., Choi B.,
 RA Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharasy N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RA Theologis A., Ecker J.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC020889; AAF79696.1; -; Genomic_DNA.
 DR FIR; G96524; G96524.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004672; F:protein kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000560; HisAc_phsphtse.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007090; LRR_plant.
 DR InterPro; IPR000719; Prot_kinase.
 DR Pfam; PF00560; LRR_1; 5.
 DR PRINTS; PR00019; LEURICHRPT.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 SQ SEQUENCE 655 AA; 71131 MW; 734B4A7D2E956456 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 655;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVEFF 6
 Db 352 KKLVEFF 357

RESULT 69
 Q7ZT1 BRARE PRELIMINARY; PRT; 678 AA.
 AC Q7ZT1;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Amyloid protein a variant 2.
 GN Name=appa;

OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Cypriniformes;
 OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Groth C., Lardelli M.,
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RE EMBL; AY271746; AAP22958.1; -, mRNA.
RS HSP; Q16019; 1H23.
DR SMR; Q7221; 29-124, 393-491.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SMO0006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 678 AA; 76755 MW; 94163778444FD0BC CRC64;

Query Match 88.2%; Score 30; DB 2; Length 678;
Best Local Similarity 85.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLVPFA 7

Db 594 QKLVPFA 600

RESULT 70

ID Q98SG0 XENLA PRELIMINARY; PRT; 693 AA.
AC Q98SG0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DR Beta-amyloid precursor protein A.
GN Name=app;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=83355;
RN [1]
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=2161008; PubMed=11744158; DOI=10.1016/S0169-328X(01)00279-0;
RA Van den Hurk W.H., Bloemen M., Martens G.J.M.;
RT "Expression of the gene encoding the beta-amyloid precursor protein
APP in *Xenopus laevis*.";
RL Brain Res. Mol. Brain Res. 97:13-20(2001).
RN [2]

RN NUCLEOTIDE SEQUENCE.

RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences, University of
NL Nijmegen, Nijmegen, Netherlands.
RL EMBL; AJ298150; CAC37193.1; -, mRNA.
RS HSP; Q16019; 1H23.
DR SMR; Q98SG0; 27-122, 393-492.

DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0005488; F: binding; IEA.

DR InterPro; IPR008155; A4 APP.

DR InterPro; IPR008154; A4 APP.

DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF02177; A4_EXTRA; 1.

DR Pfam; PF03494; Beta-APP; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00204; BETAAMYLOID.

DR SMART; SMO0006; A4_EXTRA; 1.

DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.

KW Signal.

FT SIGNAL 1 19 Potential.
SQ SEQUENCE 693 AA; 78567 MW; CAF1DF655CIAB653 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 693;

Best Local Similarity 85.7%; Pred. No. 4.1e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLVPFA 7

Db 609 QKLVPFA 615

RESULT 71

Q6Y2W9 MAIZE
ID Q6Y2W9 MAIZE PRELIMINARY; PRT; 694 AA.
AC Q6Y2W9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DR Atypical receptor-like kinase MARK.
GN Name=ark;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22995821; PubMed=12966093; DOI=10.1074/jbc.M307482200;
RA Llompart B., Castells E., Rio A., Roca R., Ferrando A., Stiefel V.,
RA Puigdomenech P., Casacuberta J.M.;
RT "The direct activation of MKK, a germinal center kinase (GCK)-like
kinase, by MARK, a maize atypical receptor kinase, suggests a new
mechanism for signaling through kinase-dead receptors.";
RL J. Biol. Chem. 278:48105-48111(2003).
DR EMBL; AY188755; AA083390.1; -, mRNA.
DR Gramene; Q6Y2W9; -.
DR GO; GO:0005524; F: ATP binding; IEA.
DR GO; GO:0004674; F: protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F: protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0006468; P: protein amino acid phosphorylation; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR002016; Peroxidase.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00560; LRR_1; 4.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc_1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Kinase; Receptor.

SQ SEQUENCE 694 AA; 71924 MW; 49883823202B6B5 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 694;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLVPFA 6

Db 373 KKLVPFA 378

RESULT 72

Q5R477_PONPY

ID Q5R477_PONPY PRELIMINARY; PRT; 695 AA.

```

AC QSR477;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp459D212.
GN Name=DKFZp459D212;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR861380; CAH93439.1; -; mRNA.
DR SMR; QSR477; 28-123, 124-189, 385-494.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR012282; Cytochrome_c_r.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Hypothetical protein.
SQ SEQUENCE 695 AA; 78626 MW; 0BF5DD9BA2213E49 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 695;
Best Local Similarity 85.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 611 QKLVPFA 617

RESULT 73
QGRH29_CANFA
ID Q6RH29_CANFA PRELIMINARY; PRT; 695 AA.
AC Q6RH29;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta amyloid protein isoform APP695.
GN Name=beta APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY498707; IBA4.
DR HSP; Q6019; IBA4.
DR SMR; Q6RH29; 28-123, 124-189, 385-494.
DR Ensembl; ENSCAF0000008557; Canis familiaris.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.

```

```

DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78649 MW; 718CA42A9F9B6C10 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 695;
Best Local Similarity 85.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 611 QKLVPFA 617

RESULT 74
Q56JK3_CANFA
ID Q56JK3_CANFA PRELIMINARY; PRT; 695 AA.
AC Q56JK3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Beta-amyloid protein 695.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926582; AAX81911.1; -; mRNA.
SQ SEQUENCE 695 AA; 78748 MW; 5A253E0DB677875A CRC64;

Query Match 88.2%; Score 30; DB 2; Length 695;
Best Local Similarity 85.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLVPFA 7
Db 611 QKLVPFA 617

RESULT 75
Q6GR78_MOUSE
ID Q6GR78_MOUSE PRELIMINARY; PRT; 695 AA.
AC Q6GR78;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amyloid beta (A4) protein.
GN Name=App;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

```


RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Mazra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC070409; AAH70409.1; -; mRNA.
 SQ SEQUENCE 695 AA; 78442 MW; 0DE93FA56FEB20F3A CRC64;

Query Match 88.2%; Score 30; DB 2; Length 695;
 Best Local Similarity 85.7%; Pred. No. 4.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLVFFA 7
 :|||||
 Db 611 QKLVFFA 617

Search completed: December 29, 2005, 17:46:58
 Job time : 99.2258 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds
(without alignments)
24.763 Million cell updates/sec

Title: US-10-009-122-7

Perfect score: 29

Sequence: 1 KAVFPA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	2	US-09-747-408-7
2	29	100.0	6	2	US-09-747-408-15
3	29	100.0	74	2	US-09-194-468A-19
4	29	100.0	74	2	US-09-194-468A-25
5	29	100.0	108	2	US-09-194-468A-20
6	29	100.0	108	2	US-09-194-468A-26
7	29	100.0	193	2	US-09-194-468A-18
8	29	100.0	193	2	US-09-194-468A-24
9	29	100.0	222	2	US-09-194-468A-17
10	29	100.0	428	2	US-09-194-468A-23
11	29	100.0	429	2	US-09-194-468A-45
12	29	100.0	631	2	US-09-448-489-17
13	29	100.0	631	2	US-09-689-730-17
14	29	100.0	660	2	US-08-704-711A-18
15	29	100.0	660	2	US-08-521-220-18
16	29	100.0	660	2	US-09-391-104-19
17	29	100.0	660	2	US-09-917-254-89
18	29	100.0	660	2	US-09-949-016-6512
19	29	100.0	660	2	US-09-949-016-7937
20	29	100.0	660	2	US-10-153-185-14
21	29	100.0	663	2	US-09-194-468A-30
22	26	89.7	65	2	US-09-471-276-1595
23	26	89.7	128	2	US-09-540-236-2808
24	26	89.7	295	2	US-09-248-796A-18333
25	26	89.7	334	2	US-09-205-258-348
26	26	89.7	334	2	US-10-004-860-348
27	26	89.7	494	2	US-09-328-352-7729

28	89.7	535	2	US-09-902-540-10002	Sequence 10002, A
29	89.7	1507	2	US-08-929-329-5	Sequence 5, Appli
30	86.2	5	2	US-09-095-106A-40	Sequence 40, Appli
31	86.2	6	2	US-09-747-408-9	Sequence 9, Appli
32	86.2	6	2	US-09-747-408-17	Sequence 17, Appli
33	86.2	28	1	US-08-461-216-4	Sequence 4, Appli
34	86.2	77	2	US-09-513-999C-6921	Sequence 6921, Ap
35	86.2	80	2	US-09-248-796A-27785	Sequence 27785, A
36	86.2	142	2	US-09-270-767-33756	Sequence 33756, A
37	86.2	142	2	US-09-270-767-43456	Sequence 43456, A
38	86.2	261	2	US-09-270-767-43456	Sequence 43456, A
39	86.2	281	2	US-09-252-991A-29199	Sequence 29199, A
40	86.2	282	2	US-09-845-713A-2	Sequence 2, Appli
41	86.2	306	2	US-09-303-518D-676	Sequence 676, App
42	86.2	306	2	US-09-303-518D-678	Sequence 678, App
43	86.2	307	2	US-09-303-518D-680	Sequence 680, App
44	86.2	322	2	US-09-495-406-34	Sequence 34, Appl
45	86.2	322	2	US-09-816-028A-48	Sequence 48, Appl
46	86.2	322	2	US-10-303-162-48	Sequence 48, Appl
47	86.2	322	2	US-10-303-134-48	Sequence 48, Appl
48	86.2	322	2	US-10-303-118-48	Sequence 48, Appl
49	86.2	322	2	US-10-303-128-48	Sequence 48, Appl
50	86.2	334	2	US-09-270-767-43522	Sequence 43522, A
51	86.2	337	2	US-09-438-185A-960	Sequence 960, App
52	86.2	347	2	US-08-749-816-3	Sequence 3, Appli
53	86.2	347	2	US-09-144-914-6	Sequence 6, Appli
54	86.2	375	2	US-09-489-039A-11261	Sequence 11261, A
55	86.2	421	2	US-09-543-681A-5731	Sequence 5731, Ap
56	86.2	430	2	US-09-272-960-2	Sequence 2, Appli
57	86.2	430	2	US-10-058-636-2	Sequence 2, Appli
58	86.2	462	2	US-09-583-110-3587	Sequence 3587, Ap
59	86.2	473	2	US-09-107-433-3273	Sequence 3273, Ap
60	86.2	474	2	US-09-489-039A-13140	Sequence 13140, A
61	86.2	532	1	US-08-288-405A-10	Sequence 10, Appl
62	86.2	532	2	US-10-162-012-13	Sequence 13, Appl
63	86.2	547	2	US-09-605-703B-2398	Sequence 2398, Ap
64	86.2	560	1	US-08-594-031-90	Sequence 90, Appl
65	86.2	560	2	US-09-643-597-225	Sequence 225, App
66	86.2	560	2	US-09-480-884A-225	Sequence 225, App
67	86.2	560	2	US-09-542-615A-225	Sequence 225, App
68	86.2	560	2	US-09-606-421B-225	Sequence 225, App
69	86.2	560	2	US-09-476-496A-225	Sequence 225, App
70	86.2	560	2	US-09-630-940B-225	Sequence 225, App
71	86.2	560	2	US-09-943-075A-6	Sequence 6, Appli
72	86.2	560	2	US-10-039-272A-2	Sequence 2, Appli
73	86.2	560	2	US-10-007-700-225	Sequence 225, App
74	86.2	560	5	US-09-985-799-90	Sequence 90, Appl
75	86.2	560	5	US-09-977-371-90	Sequence 90, Appl
76	86.2	591	2	US-09-489-039A-12837	Sequence 12837, A
77	86.2	605	2	US-08-693-214-8	Sequence 8, Appli
78	86.2	945	2	US-09-198-452A-1030	Sequence 1030, Ap
79	86.2	1144	1	US-08-147-812-5	Sequence 5, Appli
80	86.2	1144	1	US-08-319-866-12	Sequence 12, Appl
81	86.2	1144	2	US-09-123-708-2	Sequence 2, Appli
82	86.2	1144	2	US-09-123-624-2	Sequence 2, Appli
83	86.2	1144	2	US-09-661-258-5	Sequence 5, Appli
84	86.2	1144	2	US-08-809-917-12	Sequence 12, Appl
85	86.2	1144	2	US-09-419-371-12	Sequence 12, Appl
86	86.2	2343	2	US-09-324-867-2	Sequence 2, Appli
87	82.8	5	1	US-08-612-785B-25	Sequence 25, Appl
88	82.8	5	2	US-08-703-675C-38	Sequence 38, Appl
89	82.8	5	2	US-08-617-267C-25	Sequence 25, Appl
90	82.8	6	1	US-08-612-785B-9	Sequence 9, Appli
91	82.8	6	2	US-08-703-675C-32	Sequence 32, Appl
92	82.8	6	2	US-08-617-267C-9	Sequence 9, Appli
93	82.8	6	2	US-09-747-408-1	Sequence 1, Appli
94	82.8	6	2	US-09-747-408-3	Sequence 3, Appli
95	82.8	6	2	US-09-747-408-10	Sequence 10, Appl
96	82.8	6	2	US-09-747-408-11	Sequence 11, Appl
97	82.8	7	1	US-08-127-904-14	Sequence 14, Appl
98	82.8	7	1	US-08-612-785B-7	Sequence 7, Appli
99	82.8	7	2	US-08-703-675C-30	Sequence 30, Appl
100	82.8	7	2	US-08-617-267C-7	Sequence 7, Appli

101	24	82.8	7	2	US-09-264-709A-13	Sequence 13, Appl	174	24	82.8	19	2	US-10-815-353-5	Sequence 5, Appl
102	24	82.8	7	2	US-09-747-408-2	Sequence 2, Appl	175	24	82.8	19	2	US-10-816-529-5	Sequence 5, Appl
103	24	82.8	7	2	US-09-747-408-18	Sequence 18, Appl	176	24	82.8	19	2	US-10-815-391-5	Sequence 5, Appl
104	24	82.8	7	2	US-09-747-408-19	Sequence 19, Appl	177	24	82.8	19	2	US-10-816-022-5	Sequence 5, Appl
105	24	82.8	7	4	PCT-US94-10475-14	Sequence 14, Appl	178	24	82.8	19	2	US-09-724-940-75	Sequence 75, Appl
106	24	82.8	8	1	US-08-612-785B-5	Sequence 5, Appl	179	24	82.8	19	2	US-10-934-609-5	Sequence 5, Appl
107	24	82.8	8	1	US-08-630-645-1	Sequence 1, Appl	180	24	82.8	19	2	US-10-884-892-5	Sequence 5, Appl
108	24	82.8	8	2	US-08-703-675C-28	Sequence 28, Appl	181	24	82.8	20	2	US-08-970-833-10	Sequence 10, Appl
109	24	82.8	8	2	US-08-617-267C-5	Sequence 5, Appl	182	24	82.8	20	2	US-09-724-953-33	Sequence 33, Appl
110	24	82.8	8	2	US-09-095-106A-44	Sequence 44, Appl	183	24	82.8	20	2	US-09-724-567-33	Sequence 33, Appl
111	24	82.8	8	2	US-08-766-596A-1	Sequence 1, Appl	184	24	82.8	20	2	US-09-979-952-33	Sequence 33, Appl
112	24	82.8	8	2	US-08-766-596A-1	Sequence 73, Appl	185	24	82.8	20	2	US-09-585-817-33	Sequence 33, Appl
113	24	82.8	8	4	PCT-US96-10220-1	Sequence 1, Appl	186	24	82.8	26	1	US-08-304-585-7	Sequence 7, Appl
114	24	82.8	9	2	US-08-766-596A-50	Sequence 50, Appl	187	24	82.8	28	1	US-08-346-849-4	Sequence 4, Appl
115	24	82.8	9	2	US-08-766-596A-64	Sequence 64, Appl	188	24	82.8	28	1	US-08-302-808-7	Sequence 7, Appl
116	24	82.8	9	2	US-09-747-408-20	Sequence 20, Appl	189	24	82.8	28	1	US-08-603-090-2	Sequence 2, Appl
117	24	82.8	9	2	US-10-014-658-15	Sequence 15, Appl	190	24	82.8	28	1	US-08-986-948-7	Sequence 7, Appl
118	24	82.8	10	2	US-08-970-833-3	Sequence 3, Appl	191	24	82.8	28	1	US-08-293-284A-4	Sequence 4, Appl
119	24	82.8	10	2	US-09-724-961-20	Sequence 20, Appl	192	24	82.8	28	1	US-08-461-216-2	Sequence 2, Appl
120	24	82.8	10	2	US-09-724-961-21	Sequence 21, Appl	193	24	82.8	28	2	US-09-388-890-2	Sequence 2, Appl
121	24	82.8	10	2	US-09-724-961-22	Sequence 22, Appl	194	24	82.8	28	2	US-09-388-890-3	Sequence 3, Appl
122	24	82.8	10	2	US-09-724-961-23	Sequence 23, Appl	195	24	82.8	28	2	US-09-388-890-4	Sequence 4, Appl
123	24	82.8	10	2	US-09-724-961-24	Sequence 24, Appl	196	24	82.8	28	2	US-09-388-890-5	Sequence 5, Appl
124	24	82.8	10	2	US-09-580-018-20	Sequence 20, Appl	197	24	82.8	28	2	US-09-388-890-6	Sequence 6, Appl
125	24	82.8	10	2	US-09-580-018-21	Sequence 21, Appl	198	24	82.8	28	2	US-09-388-890-7	Sequence 7, Appl
126	24	82.8	10	2	US-09-580-018-22	Sequence 22, Appl	199	24	82.8	28	2	US-09-388-890-8	Sequence 8, Appl
127	24	82.8	10	2	US-09-580-018-23	Sequence 23, Appl	200	24	82.8	28	2	US-09-388-890-9	Sequence 9, Appl
128	24	82.8	10	2	US-09-580-018-24	Sequence 24, Appl	201	24	82.8	28	2	US-09-388-890-10	Sequence 10, Appl
129	24	82.8	10	2	US-09-724-551-20	Sequence 20, Appl	202	24	82.8	28	2	US-09-388-890-12	Sequence 12, Appl
130	24	82.8	10	2	US-09-724-551-21	Sequence 21, Appl	203	24	82.8	28	2	US-09-388-890-13	Sequence 13, Appl
131	24	82.8	10	2	US-09-724-551-22	Sequence 22, Appl	204	24	82.8	28	2	US-09-388-890-14	Sequence 14, Appl
132	24	82.8	10	2	US-09-724-551-23	Sequence 23, Appl	205	24	82.8	28	2	US-09-264-709A-1	Sequence 1, Appl
133	24	82.8	10	2	US-09-724-551-24	Sequence 24, Appl	206	24	82.8	28	2	US-08-723-661B-2	Sequence 2, Appl
134	24	82.8	10	2	US-09-724-940-20	Sequence 20, Appl	207	24	82.8	28	2	US-09-660-954-2	Sequence 2, Appl
135	24	82.8	10	2	US-09-724-940-21	Sequence 21, Appl	208	24	82.8	28	2	US-09-660-954-3	Sequence 3, Appl
136	24	82.8	10	2	US-09-724-940-22	Sequence 22, Appl	209	24	82.8	28	2	US-09-660-954-4	Sequence 4, Appl
137	24	82.8	10	2	US-09-724-940-23	Sequence 23, Appl	210	24	82.8	28	2	US-09-660-954-5	Sequence 5, Appl
138	24	82.8	10	2	US-09-724-940-24	Sequence 24, Appl	211	24	82.8	28	2	US-09-660-954-6	Sequence 6, Appl
139	24	82.8	11	1	US-08-630-645-14	Sequence 14, Appl	212	24	82.8	28	2	US-09-660-954-7	Sequence 7, Appl
140	24	82.8	11	2	US-08-766-596A-14	Sequence 14, Appl	213	24	82.8	28	2	US-09-660-954-8	Sequence 8, Appl
141	24	82.8	11	2	US-09-988-842-9	Sequence 9, Appl	214	24	82.8	28	2	US-09-660-954-9	Sequence 9, Appl
142	24	82.8	11	4	PCT-US96-10220-14	Sequence 14, Appl	215	24	82.8	28	2	US-09-660-954-10	Sequence 10, Appl
143	24	82.8	11	2	US-09-594-366-5	Sequence 5, Appl	216	24	82.8	28	2	US-09-660-954-12	Sequence 12, Appl
144	24	82.8	14	2	US-09-992-800-5	Sequence 5, Appl	217	24	82.8	28	2	US-09-660-954-13	Sequence 13, Appl
145	24	82.8	14	2	US-09-992-800-5	Sequence 5, Appl	218	24	82.8	28	2	US-09-660-954-14	Sequence 14, Appl
146	24	82.8	15	1	US-08-612-785B-14	Sequence 14, Appl	219	24	82.8	28	2	US-08-898-300-4	Sequence 4, Appl
147	24	82.8	15	1	US-08-612-785B-37	Sequence 37, Appl	220	24	82.8	28	2	US-08-824-513-4	Sequence 4, Appl
148	24	82.8	15	2	US-08-617-267C-14	Sequence 14, Appl	221	24	82.8	28	2	US-09-623-548A-959	Sequence 959, App
149	24	82.8	15	2	US-08-766-596A-56	Sequence 56, Appl	222	24	82.8	28	2	US-09-623-548A-965	Sequence 965, App
150	24	82.8	15	2	US-08-766-596A-57	Sequence 57, Appl	223	24	82.8	28	2	US-09-623-548A-976	Sequence 976, App
151	24	82.8	15	2	US-08-766-596A-58	Sequence 58, Appl	224	24	82.8	28	2	US-09-623-548A-992	Sequence 992, App
152	24	82.8	15	2	US-08-766-596A-60	Sequence 60, Appl	225	24	82.8	28	2	US-09-623-548A-1003	Sequence 1003, App
153	24	82.8	15	2	US-08-766-596A-61	Sequence 61, Appl	226	24	82.8	28	2	US-09-657-276-959	Sequence 959, App
154	24	82.8	15	2	US-08-766-596A-63	Sequence 63, Appl	227	24	82.8	28	2	US-09-657-276-965	Sequence 965, App
155	24	82.8	15	2	US-08-766-596A-65	Sequence 65, Appl	228	24	82.8	28	2	US-09-657-276-976	Sequence 976, App
156	24	82.8	17	2	US-09-264-709A-2	Sequence 2, Appl	229	24	82.8	28	2	US-09-657-276-992	Sequence 992, App
157	24	82.8	17	2	US-09-594-366-3	Sequence 3, Appl	230	24	82.8	28	2	US-09-657-276-1003	Sequence 1003, App
158	24	82.8	17	2	US-09-623-548A-950	Sequence 950, App	231	24	82.8	28	2	US-09-865-294A-66	Sequence 66, Appl
159	24	82.8	17	2	US-09-623-548A-983	Sequence 983, App	232	24	82.8	30	1	US-08-609-090-3	Sequence 3, Appl
160	24	82.8	17	2	US-09-992-800-3	Sequence 3, Appl	233	24	82.8	30	1	US-09-861-847A-1	Sequence 1, Appl
161	24	82.8	17	2	US-09-657-276-950	Sequence 950, App	234	24	82.8	33	1	US-08-609-090-4	Sequence 4, Appl
162	24	82.8	17	2	US-09-657-276-983	Sequence 983, App	235	24	82.8	34	1	US-08-475-579A-4	Sequence 4, Appl
163	24	82.8	19	2	US-08-970-833-11	Sequence 11, Appl	236	24	82.8	35	1	US-08-304-585-6	Sequence 6, Appl
164	24	82.8	19	2	US-09-723-384-5	Sequence 5, Appl	237	24	82.8	35	1	US-08-612-785B-16	Sequence 16, Appl
165	24	82.8	19	2	US-09-724-961-75	Sequence 75, Appl	238	24	82.8	35	1	US-08-612-785B-36	Sequence 36, Appl
166	24	82.8	19	2	US-09-724-552-5	Sequence 5, Appl	239	24	82.8	35	1	US-08-612-785B-38	Sequence 38, Appl
167	24	82.8	19	2	US-09-580-018-75	Sequence 75, Appl	240	24	82.8	35	1	US-08-612-785B-40	Sequence 40, Appl
168	24	82.8	19	2	US-09-723-927-5	Sequence 5, Appl	241	24	82.8	35	2	US-08-617-267C-16	Sequence 16, Appl
169	24	82.8	19	2	US-09-724-489-5	Sequence 5, Appl	242	24	82.8	35	2	US-09-623-548A-979	Sequence 979, App
170	24	82.8	19	2	US-09-724-477-5	Sequence 5, Appl	243	24	82.8	35	2	US-09-623-548A-1006	Sequence 1006, App
171	24	82.8	19	2	US-09-723-762-5	Sequence 5, Appl	244	24	82.8	35	2	US-09-657-276-979	Sequence 979, App
172	24	82.8	19	2	US-09-201-430-5	Sequence 5, Appl	245	24	82.8	35	2	US-09-657-276-1006	Sequence 1006, App
173	24	82.8	19	2	US-09-724-551-75	Sequence 75, Appl	246	24	82.8	36	1	US-08-609-090-6	Sequence 6, Appl

```
247 24 82.8 36 2 US-09-861-847A-6
248 24 82.8 36 2 US-09-861-847A-11
249 24 82.8 38 1 US-08-302-808-1
250 24 82.8 38 1 US-07-737-371E-68
251 24 82.8 38 1 US-08-986-948-1
252 24 82.8 38 2 US-09-623-548A-975
253 24 82.8 38 2 US-09-623-548A-1002
254 24 82.8 38 2 US-09-657-276-975
255 24 82.8 38 2 US-09-657-276-1002
256 24 82.8 39 1 US-08-304-585-5
257 24 82.8 39 1 US-08-302-808-2
258 24 82.8 39 1 US-08-609-090-7
259 24 82.8 39 1 US-08-682-245A-1
260 24 82.8 39 1 US-08-986-948-2
261 24 82.8 40 1 US-07-744-767A-1
262 24 82.8 40 1 US-08-235-400-2
263 24 82.8 40 1 US-08-476-464A-2
264 24 82.8 40 1 US-08-304-585-1
265 24 82.8 40 1 US-08-304-585-8
266 24 82.8 40 1 US-08-302-808-3
267 24 82.8 40 1 US-08-433-734-1
268 24 82.8 40 1 US-08-609-090-8
269 24 82.8 40 1 US-07-737-371E-69
270 24 82.8 40 1 US-08-682-245A-2
271 24 82.8 40 1 US-08-986-948-3
272 24 82.8 40 1 US-08-461-216-1
273 24 82.8 40 2 US-08-959-148-1
274 24 82.8 40 2 US-09-242-724-22
275 24 82.8 40 2 US-08-723-661B-1
276 24 82.8 40 2 US-09-062-365-3
277 24 82.8 40 2 US-09-133-866-1
278 24 82.8 40 2 US-09-861-847A-7
279 24 82.8 40 2 US-09-861-847A-8
280 24 82.8 40 2 US-09-988-842-3
281 24 82.8 40 2 US-10-455-218-1
282 24 82.8 40 2 US-10-151-614-1
283 24 82.8 40 2 US-09-623-548A-956
284 24 82.8 40 2 US-09-623-548A-962
285 24 82.8 40 2 US-09-623-548A-968
286 24 82.8 40 2 US-09-623-548A-978
287 24 82.8 40 2 US-09-623-548A-989
288 24 82.8 40 2 US-09-623-548A-995
289 24 82.8 40 2 US-09-623-548A-1005
290 24 82.8 40 2 US-09-657-276-956
291 24 82.8 40 2 US-09-657-276-962
292 24 82.8 40 2 US-09-657-276-968
293 24 82.8 40 2 US-09-657-276-978
294 24 82.8 40 2 US-09-657-276-989
295 24 82.8 40 2 US-09-657-276-995
296 24 82.8 40 2 US-09-657-276-1005
297 24 82.8 40 2 US-09-962-955D-36
298 24 82.8 40 4 PCT-US92-06700-1
299 24 82.8 41 1 US-07-819-361-1
300 24 82.8 41 1 US-08-302-808-4
```

ALIGNMENTS

```
RESULT 1
US-09-747-408-7
; Sequence 7, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT FILING DATE: 2000-12-22
; PRIOR FILING DATE: 1999-12-23
```

```
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-7

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 1 KAVFFA 6

RESULT 2
US-09-747-408-15
; Sequence 15, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT FILING DATE: 2000-12-22
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-15

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 1 KAVFFA 6

RESULT 3
US-09-194-468A-19
; Sequence 19, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Chersan, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MERO049S
; CURRENT FILING DATE: 1999-03-23
; PRIOR FILING DATE: 1996-05-31
; PRIOR FILING DATE: 1996-05-31
; PRIOR FILING DATE: 1996-05-31
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 19
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-468A-19
```

Query Match 100.0%; Score 29; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 4
US-09-194-468A-25
; Sequence 25, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; PRIOR FILING DATE: 1999-03-23
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-194-468A-25

Query Match 100.0%; Score 29; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 5
US-09-194-468A-20
; Sequence 20, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; PRIOR FILING DATE: 1999-03-23
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-468A-20

Query Match 100.0%; Score 29; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 38;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 6
US-09-194-468A-26
; Sequence 26, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-194-468A-26

Query Match 100.0%; Score 29; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 7
US-09-194-468A-18
; Sequence 18, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-468A-18

Query Match 100.0%; Score 29; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 64 KAVFFA 69
|||||

RESULT 8
US-09-194-468A-24
; Sequence 24, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-194-468A-24

Query Match 100.0%; Score 29; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||

Db 64 KAVFFA 69

RESULT 9
US-09-194-468A-17
; Sequence 17, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-468A-17

Query Match 100.0%; Score 29; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||

Db 93 KAVFFA 98

RESULT 10

US-09-194-468A-23
; Sequence 23, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-194-468A-23

Query Match 100.0%; Score 29; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||

Db 99 KAVFFA 104

RESULT 11

US-09-194-468A-45
; Sequence 45, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-468A-45

Query Match 100.0%; Score 29; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||

Db 300 KAVFFA 305

RESULT 12

US-08-448-489-17

; Sequence 17, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-17

Query Match 100.0%; Score 29; DB 2; Length 631;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 KAVFFA 6
|||||
Db 502 KAVFFA 507

RESULT 13
US-09-689-730-17
; Sequence 17, Application US/09689730
; Patent No. 6825024
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/09/689,730
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US/08/448,489
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-09-689-730-17

Query Match 100.0%; Score 29; DB 2; Length 631;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||
Db 502 KAVFFA 507

RESULT 14
US-08-704-711A-18
; Sequence 18, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE

; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-18

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||
Db 531 KAVFFA 536

RESULT 15
US-09-521-220-18
; Sequence 18, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/521,220
;; FILING DATE: 08-Mar-2000
;; CLASSIFICATION: <Unknown>
;; 21-OCT-1994
;; 17-MAR-1994
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/704,711
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: DE 4438838.1
;; FILING DATE: 21-OCT-1994
;; APPLICATION NUMBER: DE 4409663.1
;; FILING DATE: 17-MAR-1994
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: GRANADOS, Patricia D.
;; REGISTRATION NUMBER: 33,683
;; REFERENCE/DOCKET NUMBER: 26083/124
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;;
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 660 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-521-220-18

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 531 KAVFFA 536

RESULT 16
US-09-391-104-19
; Sequence 19, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-19

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 531 KAVFFA 536

RESULT 17
US-09-917-254-89
; Sequence 89, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-89

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 531 KAVFFA 536

RESULT 18
US-09-949-016-6512
; Sequence 6512, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6512
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6512

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 531 KAVFFA 536

RESULT 19
US-09-949-016-7937
; Sequence 7937, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7937
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7937

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||
Db 531 KAVFFA 536

RESULT 20
US-10-153-185-14
; Sequence 14, Application US/10153185
; Patent No. 6906036
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-14

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||
Db 531 KAVFFA 536

RESULT 21
US-09-194-468A-30
; Sequence 30, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Chereah, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31

; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-194-468A-30

Query Match 100.0%; Score 29; DB 2; Length 663;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||
Db 534 KAVFFA 539

RESULT 22
US-09-471-276-1595
; Sequence 1595, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: GENSET.025CPI
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 1595
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-276-1595

Query Match 89.7%; Score 26; DB 2; Length 65;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||
Db 54 KAVFFS 59

RESULT 23
US-09-540-236-2808
; Sequence 2808, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2808
; LENGTH: 128
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-2808

Query Match 89.7%; Score 26; DB 2; Length 128;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 55 KAVFYA 60

RESULT 24

US-09-248-796A-18333
; Sequence 18333, Application US/09248796A
; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 18333

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-18333

Query Match 89.7%; Score 26; DB 2; Length 295;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 31 KAVFYA 36

RESULT 25

US-09-205-258-348
; Sequence 348, Application US/09205258
; Patent No. 6525174

; GENERAL INFORMATION:

; APPLICANT: Young et al.

; TITLE OF INVENTION: 207 Human Secreted Proteins

; FILE REFERENCE: P200721

; CURRENT APPLICATION NUMBER: US/09/205,258

; CURRENT FILING DATE: 1998-12-04

; EARLIER APPLICATION NUMBER: PCT/US98/11422

; EARLIER FILING DATE: 1998-06-04

; EARLIER APPLICATION NUMBER: 60/048,885

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,375

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,881

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,880

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,896

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,020

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,876

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,895

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,884

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,894

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,971

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 348
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (288)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (334)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-348

```

Query Match      89.7%; Score 26; DB 2; Length 334;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFPA 6
DB      273 KAVFYA 278

RESULT 26
US-10-004-860-348
; Sequence 348, Application US/10004860
; Patent No. 6914047
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 348
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; FEATURE:
; LOCATION: (288)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (334)
; OTHER INFORMATION: Xaa equals stop translation
US-10-004-860-348

Query Match      89.7%; Score 26; DB 2; Length 334;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFPA 6
DB      273 KAVFYA 278

RESULT 27
US-09-328-352-7729
; Sequence 7729, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7729
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7729

Query Match      89.7%; Score 26; DB 2; Length 494;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFPA 6
DB      79 KSVFFA 84

RESULT 28

```

```

US-09-902-540-10002
; Sequence 10002, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10002
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10002

Query Match      89.7%; Score 26; DB 2; Length 535;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFPA 6
DB      131 KALFFA 136

RESULT 29
US-08-929-329-5
; Sequence 5, Application US/08929329
; Patent No. 6120770
; GENERAL INFORMATION:
; APPLICANT: Adams, John H
; APPLICANT: Dalton, John P
; APPLICANT: Kappe, Stefan
; TITLE OF INVENTION: Plasmodium Proteins Useful for Preparing
; TITLE OF INVENTION: Vaccine Compositions
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Barnes & Thornburg
; STREET: 11 S Meridian
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,329
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Breen, John P
; REGISTRATION NUMBER: 38,833
; REFERENCE/DOCKET NUMBER: 835910-28685
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 231-7745
; TELEFAX: (317) 231-7433
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1507 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

```

; ORIGINAL SOURCE:
; ORGANISM: Plasmodium yoelii
US-08-929-329-5

Query Match 89.7%; Score 26; DB 2; Length 1507;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
| | | | |
Db 1454 KAVTFA 1459

RESULT 30
US-09-095-106A-40
; Sequence 40, Application US/09095106A
; Patent No. 6331440
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TJERNBERG, Lars O.
; APPLICANT: TERENIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 000500-124
; CURRENT APPLICATION NUMBER: US/09/095.106A
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; PRIOR APPLICATION NUMBER: PCT/SB96/01621
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 40
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-095-106A-40

Query Match 86.2%; Score 25; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
| | | | |
Db 1 KAVFF 5

RESULT 31
US-09-747-408-9
; Sequence 9, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-9

Query Match 86.2%; Score 25; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
| | | | |
Db 1 KVVFFA 6

RESULT 32
US-09-747-408-17
; Sequence 17, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-17

Query Match 86.2%; Score 25; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
| | | | |
Db 1 KVVFFA 6

RESULT 33
US-08-461-216-4
; Sequence 4, Application US/08461216
; Patent No. 5958883
; GENERAL INFORMATION:
; APPLICANT: Snow, A.D.
; TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
; COMPUTER: IBM PC/386 Compatible
; OPERATING SYSTEM: MS-DOS 4.01
; SOFTWARE: Word for Windows-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,216
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,734
; FILING DATE: October 23, 1992
; APPLICATION NUMBER: 07/950,417
; FILING DATE: September 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Broderick, Thomas F.
; REGISTRATION NUMBER: 31,332
; REFERENCE/DOCKET NUMBER: UOPW-1-6707
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)
; TELEFAX: 1-206-224-0779

•

; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 43456
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43456

Query Match 86.2%; Score 25; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 184 KAVFF 188

RESULT 39

US-09-252-991A-29199
; Sequence 29199, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29199
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29199

Query Match 86.2%; Score 25; DB 2; Length 281;
Best Local Similarity 83.3%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 6
Db 257 EAVFFA 262

RESULT 40

US-09-845-713A-2
; Sequence 2, Application US/09845713A
; Patent No. 6660476
; GENERAL INFORMATION:
; APPLICANT: MacMurray, James P.
; TITLE OF INVENTION: Polymorphisms in the PMT Gene
; FILE REFERENCE: 1954-327-II
; CURRENT APPLICATION NUMBER: US/09/845,713A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,310
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-713A-2

Query Match 86.2%; Score 25; DB 2; Length 282;
Best Local Similarity 83.3%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 270 KGVFFA 275

RESULT 41

US-09-303-518D-676
; Sequence 676, Application US/09303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Massignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 676
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-303-518D-676

Query Match 86.2%; Score 25; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 155 KAVFF 159

RESULT 42

US-09-303-518D-678
; Sequence 678, Application US/09303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Massignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 678
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (37)..(37)
; OTHER INFORMATION: Xaa= any amino acid
; NAME/KEY: misc_feature
; LOCATION: (67)..(67)
; OTHER INFORMATION: Xaa= any amino acid
; NAME/KEY: misc_feature
; LOCATION: (203)..(203)
; OTHER INFORMATION: Xaa= any amino acid
; NAME/KEY: misc_feature
; LOCATION: (208)..(208)
; OTHER INFORMATION: Xaa= any amino acid

; NAME/KEY: misc feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: Xaa= any amino acid
; NAME/KEY: misc feature
; LOCATION: (269)..(269)
; OTHER INFORMATION: Xaa= any amino acid
US-09-303-518D-678

Query Match 86.2%; Score 25; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
Db 155 KAVFF 159

RESULT 43
US-09-303-518D-680
; Sequence 680, Application US/09303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Massignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 680
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-303-518D-680

Query Match 86.2%; Score 25; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
Db 155 KAVFF 159

RESULT 44
US-09-495-406-34
; Sequence 34, Application US/09495406
; Patent No. 6503744
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000110US
; CURRENT APPLICATION NUMBER: US/09/495,406
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (cstI)
; OTHER INFORMATION: from C. jejuni OH4384
US-09-495-406-34

Query Match 86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
Db 61 KAVFF 65

RESULT 45
US-09-816-028A-48
; Sequence 48, Application US/09816028A
; Patent No. 6699705
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/09/816,028A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-09-816-028A-48

Query Match 86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
Db 61 KAVFF 65

RESULT 46
US-10-303-162-48
; Sequence 48, Application US/10303162
; Patent No. 6723545
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,162
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (cstI)
; OTHER INFORMATION: from C. jejuni OH4384
US-09-495-406-34

; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-162-48

Query Match 86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5
Db 61 KAVPF 65

RESULT 47
US-10-303-134-48
; Sequence 48, Application US/10303134
; Patent No. 6825019
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,134
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-134-48

Query Match 86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5
Db 61 KAVPF 65

RESULT 48
US-10-303-118-48
; Sequence 48, Application US/10303118
; Patent No. 6905867
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,118
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-118-48

Query Match 86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5
Db 61 KAVPF 65

RESULT 49
US-10-303-128-48
; Sequence 48, Application US/10303128
; Patent No. 6911337
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,128
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-128-48

Query Match 86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5
Db 61 KAVPF 65

RESULT 50
US-09-270-767-43522
; Sequence 43522, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43522
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Drosophila melanogaster

US-09-270-767-43522

Query Match 86.2%; Score 25; DB 2; Length 334;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 282 KSIFFA 287

RESULT 51

US-09-438-185A-960
; Sequence 960, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 960
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0958
US-09-438-185A-960

Query Match 86.2%; Score 25; DB 2; Length 337;
Best Local Similarity 66.7%; Pred. No. 7.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 284 RAIFFA 289

RESULT 52

US-08-749-816-3
; Sequence 3, Application US/08749816
; Patent No. 6013470
; GENERAL INFORMATION:
; APPLICANT: Lesage, Florian
; APPLICANT: Guillemare, Eric
; APPLICANT: Fink, Michel
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lazdunski, Michel
; APPLICANT: Romey, Georges
; APPLICANT: Barhanin, Jacques
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
; TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
; TITLE OF INVENTION: OF DRUGS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,816
FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989.6351P
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-816-3

Query Match 86.2%; Score 25; DB 2; Length 347;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 111 KAIFFS 116

RESULT 53

US-09-144-914-6
; Sequence 6, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: TWIK-1 homolog
US-09-144-914-6

Query Match 86.2%; Score 25; DB 2; Length 347;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 111 KAIFFS 116

RESULT 54

US-09-489-039A-11261

; Sequence 11261, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11261
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11261

Query Match 86.2%; Score 25; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5
Db 19 KAVPF 23

RESULT 55
US-09-543-681A-5731
; Sequence 5731, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5731
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5731

Query Match 86.2%; Score 25; DB 2; Length 421;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPFA 6
Db 334 RAIPFA 339

RESULT 56
US-09-272-960-2
; Sequence 2, Application US/09272960
; Patent No. 6689604
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
; TITLE OF INVENTION: Campylobacter jejuni and its Uses
; FILE REFERENCE: 014137-013210US
; CURRENT APPLICATION NUMBER: US/09/272,960
; CURRENT FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: US 60/078,891
; EARLIER FILING DATE: 1998-03-20
; EARLIER APPLICATION NUMBER: US 09/272,960
; EARLIER FILING DATE: 1999-03-18

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-09-272-960-2

Query Match 86.2%; Score 25; DB 2; Length 430;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5
Db 61 KAVPF 65

RESULT 57
US-10-058-636-2
; Sequence 2, Application US/10058636
; Patent No. 6709834
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
; TITLE OF INVENTION: Campylobacter jejuni and its Uses
; FILE REFERENCE: 014137-013210US
; CURRENT APPLICATION NUMBER: US/10/058,636
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/272,960
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/078,891
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/272,960
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-10-058-636-2

Query Match 86.2%; Score 25; DB 2; Length 430;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5
Db 61 KAVPF 65

RESULT 58
US-09-583-110-3587
; Sequence 3587, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3587
; LENGTH: 462

;
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3587

Query Match 86.2%; Score 25; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|||||
Db 4 KAVFF 8

RESULT 59

US-09-107-433-3273
; Sequence 3273, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3273:

SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae

FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...473
SEQUENCE DESCRIPTION: SEQ ID NO: 3273:
US-09-107-433-3273

Query Match 86.2%; Score 25; DB 2; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.1e-03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|||||
Db 15 KAVFF 19

RESULT 60

US-09-489-039A-13140
; Sequence 13140, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13140
LENGTH: 474

TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13140

Query Match 86.2%; Score 25; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|||||
Db 362 KAVFF 366

RESULT 61

US-08-288-405A-10
; Sequence 10, Application US/08288405A
; Patent No. 5559009
; GENERAL INFORMATION:

APPLICANT: Chandy, Kanianthara G.
APPLICANT: Kalman, Katalin
APPLICANT: Chandy, Grischa
APPLICANT: Gutman, George A.
TITLE OF INVENTION: A No. 5559009el Voltage-Gated Potassium Channel
TITLE OF INVENTION: Gene

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert,
ATTN: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/288,405A

FILING DATE: 10-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/207,431

FILING DATE: 04-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-59844-1/WHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 532 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-288-405A-10

Query Match 86.2%; Score 25; DB 1; Length 532;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5
Db 310 KAVPF 314

RESULT 62

US-10-162-012-13
; Sequence 13, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-162-012-13

Query Match 86.2%; Score 25; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5
Db 310 KAVPF 314

RESULT 63

US-09-605-703B-2398
; Sequence 2398, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habethauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 2398
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-2398

Query Match 86.2%; Score 25; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5
Db 454 KAVPF 458

RESULT 64

US-08-594-031-90
; Sequence 90, Application US/08594031
; Patent No. 5783182
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:

; NAME: Remenick, James
 ; REGISTRATION NUMBER: 36,902
 ; REFERENCE/DOCKET NUMBER: 0A146-0110
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-639-7700
 ; TELEFAX: 202-639-7890
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 90:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 560 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; US-08-594-031-90

Query Match 86.2%; Score 25; DB 1; Length 560;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
 Db 537 KAVFF 541

RESULT 65
 US-09-643-597-225
 ; Sequence 225, Application US/09643597
 ; Patent No. 6426072
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: McNeill, Patricia D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.455C11
 ; CURRENT FILING DATE: 2000-08-21
 ; CURRENT APPLICATION NUMBER: US/09/643,597
 ; NUMBER OF SEQ ID NOS: 369
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 225
 ; LENGTH: 560
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-643-597-225

Query Match 86.2%; Score 25; DB 2; Length 560;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
 Db 537 KAVFF 541

RESULT 66
 US-09-480-884A-225
 ; Sequence 225, Application US/09480884A
 ; Patent No. 6482597
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun
 ; APPLICANT: Hosken, Nancy A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
 ; FILE REFERENCE: 210121.455C6
 ; CURRENT APPLICATION NUMBER: US/09/480,884A
 ; CURRENT FILING DATE: 2001-08-27
 ; NUMBER OF SEQ ID NOS: 330
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 225
 ; LENGTH: 560
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-480-884A-225

Query Match 86.2%; Score 25; DB 2; Length 560;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
 Db 537 KAVFF 541

RESULT 67
 US-09-542-615A-225
 ; Sequence 225, Application US/09542615A
 ; Patent No. 6518256
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy A.
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
 ; FILE REFERENCE: 210121.455C8
 ; CURRENT APPLICATION NUMBER: US/09/542,615A
 ; CURRENT FILING DATE: 2000-04-14
 ; NUMBER OF SEQ ID NOS: 350
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 225
 ; LENGTH: 560
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-542-615A-225

Query Match 86.2%; Score 25; DB 2; Length 560;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
 Db 537 KAVFF 541

RESULT 68
 US-09-606-421B-225
 ; Sequence 225, Application US/09606421B
 ; Patent No. 6531315
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-606-421B-225

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFP 5
Db 537 KAVFP 541

RESULT 69

US-09-476-496A-225
; Sequence 225, Application US/09476496A
; Patent No. 6706262
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: LUNG CANCER
; FILE REFERENCE: 210121.455C5
; CURRENT APPLICATION NUMBER: US/09/476.496A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-476-496A-225

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFP 5
Db 537 KAVFP 541

RESULT 70

US-09-630-940B-225
; Sequence 225, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaeir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630.940B

; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-630-940B-225

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFP 5
Db 537 KAVFP 541

RESULT 71

US-09-943-075A-6
; Sequence 6, Application US/09943075A
; Patent No. 6812002
; GENERAL INFORMATION:
; APPLICANT: Popoff, Steven N.
; APPLICANT: Safado, Faysz F.
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Osteoactivin Protein and Nucleic Acids Encoding the Same,
; TITLE OF INVENTION: Compositions and Methods of Stimulating Bone Differentiation
; FILE REFERENCE: 71369.262
; CURRENT APPLICATION NUMBER: US/09/943.075A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,006
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Human
US-09-943-075A-6

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFP 5
Db 537 KAVFP 541

RESULT 72

US-10-039-272A-2
; Sequence 2, Application US/10039272A
; Patent No. 6939955
; GENERAL INFORMATION:
; APPLICANT: RAMESHWAR, Pranela
; TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTOR INDUCIBLE NEUROKININ-TYPE
; FILE REFERENCE: 267/033 (UMD-0055)
; CURRENT APPLICATION NUMBER: US/10/039.272A
; CURRENT FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/241,881
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-272A-2

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

Db 537 KAVFF 541

RESULT 73

US-10-007-700-225

; Sequence 225, Application US/10007700

; Patent No. 6960570

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Li, Samuel X.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Fanger, Neil

; APPLICANT: Retter, Marc W.

; APPLICANT: Durham, Margarita

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Peckman, David W.

; APPLICANT: Cai, Feng

; APPLICANT: Foy, Teresa M.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C17

; CURRENT APPLICATION NUMBER: US/10/007,700

; CURRENT FILING DATE: 2001-11-30

; NUMBER OF SEQ ID NOS: 469

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 225

; LENGTH: 560

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-007-700-225

Query Match 86.2%; Score 25; DB 2; Length 560;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

Db 537 KAVFF 541

RESULT 74

US-985-799-90

; Sequence 90, Application US/09985799

; Patent No. RE38392

; GENERAL INFORMATION:

; APPLICANT: THOMPSON, Timothy C.

; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES

; NUMBER OF SEQUENCES: 175

; CORRESPONDENCE ADDRESS:

ADDRESSEE: BAKER & BOTTS, L.L.P.

STREET: 1299 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20004-2400

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/985,799

; FILING DATE: 06-NO. RE38392-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/594,031

; FILING DATE: 30-JAN-1996

; APPLICATION NUMBER: 60/006,838

; FILING DATE: 16-NOV-1995

; ATTORNEY/AGENT INFORMATION:

NAME: Remenick, James

REGISTRATION NUMBER: 36,902

REFERENCE/DOCKET NUMBER: 0A146-0110

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-639-7700

TELEFAX: 202-639-7890

TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 90:

SEQUENCE CHARACTERISTICS:

LENGTH: 560 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

; SEQUENCE DESCRIPTION: SEQ ID NO: 90:

US-09-985-799-90

Query Match

Best Local Similarity 86.2%; Score 25; DB 5; Length 560;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

Db 537 KAVFF 541

RESULT 75

US-09-977-371-90

; Sequence 90, Application US/09977371

; Patent No. RE38490

; GENERAL INFORMATION:

; APPLICANT: THOMPSON, Timothy C.

; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES

; NUMBER OF SEQUENCES: 175

; CORRESPONDENCE ADDRESS:

ADDRESSEE: BAKER & BOTTS, L.L.P.

STREET: 1299 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20004-2400

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/977,371

FILING DATE: 16-Oct-2001

CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/594,031

FILING DATE: 30-JAN-1996

APPLICATION NUMBER: 60/006,838

FILING DATE: 16-NOV-1995

; ATTORNEY/AGENT INFORMATION:

NAME: Remenick, James

REGISTRATION NUMBER: 36,902

REFERENCE/DOCKET NUMBER: 0A146-0110

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-639-7700

; TELEFAX: 202-639-7890
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 90:
US-09-977-371-90

Query Match 86.2%; Score 25; DB 5; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
|||
Db 537 KAVFF 541

Search completed: December 29, 2005, 17:52:35
Job time : 21.1323 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds
(without alignments)
32.238 Million cell updates/sec

Title: US-10-009-122-7

Perfect score: 29

Sequence: 1 KAVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : A_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	4	AAB48480
2	29	100.0	6	4	AAB48488
3	29	100.0	6	4	AAB82636
4	29	100.0	6	4	AAB82628
5	29	100.0	6	5	AAB96824
6	29	100.0	6	5	AAU96816
7	29	100.0	6	5	AAU11662
8	29	100.0	6	5	AAU11654
9	29	100.0	6	6	AAB35450
10	29	100.0	6	6	AAB35443
11	29	100.0	6	8	AQ37275
12	29	100.0	6	8	AQ37267
13	29	100.0	6	8	AQ37319
14	29	100.0	6	8	AQ37327
15	29	100.0	6	9	ADY37934
16	29	100.0	6	9	ADY37926
17	29	100.0	37	3	AAB05909
18	29	100.0	37	8	ADK34079
19	29	100.0	37	8	ADL70726
20	29	100.0	42	8	ADG17617
21	29	100.0	42	8	ADG17612
22	29	100.0	74	2	AAW41091
23	29	100.0	74	2	AAW41085
24	29	100.0	74	2	AAW41230

25	29	100.0	74	8	ADT05998	Modified
26	29	100.0	74	8	ADT05965	Human mat
27	29	100.0	74	8	ADT05971	Chicken m
28	29	100.0	108	2	AAW41086	Human mat
29	29	100.0	108	2	AAW41092	Chicken m
30	29	100.0	108	2	AAW41231	Alpha-v-b
31	29	100.0	108	2	AAW41237	Alpha-v-b
32	29	100.0	108	8	ADT05972	Chicken m
33	29	100.0	108	8	ADT05966	Human mat
34	29	100.0	108	8	ADT05999	Modified
35	29	100.0	122	2	AAW41238	Alpha-v-b
36	29	100.0	152	2	AAW41232	Alpha-v-b
37	29	100.0	193	2	AAW41090	Chicken m
38	29	100.0	193	2	AAW41084	Human mat
39	29	100.0	193	2	AAW41229	Alpha-v-b
40	29	100.0	193	2	AAW41235	Alpha-v-b
41	29	100.0	193	8	ADT05964	Human mat
42	29	100.0	193	8	ADT05970	Chicken m
43	29	100.0	222	2	AAW41083	Human mat
44	29	100.0	222	2	AAW41228	Alpha-v-b
45	29	100.0	222	8	ADT05963	Human mat
46	29	100.0	228	2	AAW41089	Chicken m
47	29	100.0	228	2	AAW41234	Alpha-v-b
48	29	100.0	228	8	ADT05969	Chicken m
49	29	100.0	261	8	ADT05661	Haemophil
50	29	100.0	429	2	AAW41112	Human mat
51	29	100.0	429	8	ADT05991	Human mat
52	29	100.0	468	4	ABG24001	Novel hum
53	29	100.0	623	8	ABM84057	Human dia
54	29	100.0	626	8	ADG17622	Modified
55	29	100.0	626	8	ADG17627	Modified
56	29	100.0	631	1	AAW96143	Sequence
57	29	100.0	631	1	AAW91139	Human typ
58	29	100.0	631	2	AAW07969	Complete
59	29	100.0	631	2	AAW07350	Human typ
60	29	100.0	631	7	ADM48668	Human mat
61	29	100.0	631	8	ADT05996	Human mat
62	29	100.0	631	8	ADT05997	Mouse mat
63	29	100.0	633	8	ADT05997	Mouse mat
64	29	100.0	644	4	AAW20490	Human mat
65	29	100.0	660	2	AAW06420	Type IV c
66	29	100.0	660	4	AAW84607	Amino aci
67	29	100.0	660	4	AAE10431	Human mat
68	29	100.0	660	5	ABW79413	Human mat
69	29	100.0	660	5	ABW90738	Human mat
70	29	100.0	660	5	AAU84348	Protein M
71	29	100.0	660	6	ABU54445	Human mat
72	29	100.0	660	6	ABP97136	Human mat
73	29	100.0	660	6	AAW16608	Human mat
74	29	100.0	660	6	ABG76322	Human mat
75	29	100.0	660	7	ADD18578	Human dis
76	29	100.0	660	7	ADP65244	Human mat
77	29	100.0	660	8	ADN07697	Human mat
78	29	100.0	660	8	ADQ17097	Human mat
79	29	100.0	660	9	ADV90301	Protease-
80	29	100.0	660	9	ADV68478	Human mat
81	29	100.0	662	7	ADG2857	Rat Prote
82	29	100.0	662	7	ADW46270	Rat Prote
83	29	100.0	663	2	AAW41111	Chicken m
84	29	100.0	663	2	AAW41227	Chicken m
85	29	100.0	663	8	ADT05976	Chicken m
86	29	100.0	663	8	ADT05995	Chicken m
87	29	100.0	708	9	ADP60554	Human con
88	29	100.0	708	9	AEA20970	Novel hum
89	29	100.0	718	8	ADN22220	Bacterial
90	29	100.0	737	8	ADN24980	Bacterial
91	29	100.0	1147	2	AAW02571	Rat induc
92	29	100.0	1330	4	ABG23999	Novel hum
93	28	96.6	383	8	ADN25046	Bacterial
94	28	96.6	383	8	ADN22288	Bacterial
95	26	89.7	65	3	AAW65434	Human 5'
96	26	89.7	65	8	ADU72998	Non-aligna
97	26	89.7	65	9	ADZ73989	Human Com

98	26	89.7	128	8	ADL05122	M. catarr	171	25	86.2	117	4	AAM17468	Aam17468 Peptide #
99	26	89.7	138	4	ABG09090	Novel hum	172	25	86.2	117	4	ABE36488	AbB36488 Peptide #
100	26	89.7	146	9	ABE41486	L. pneumo	173	25	86.2	117	4	AAM29987	Aam29987 Peptide #
101	26	89.7	166	9	AEB38197	L. pneumo	174	25	86.2	117	4	ABB31282	Abb31282 Peptide #
102	26	89.7	208	4	ABG09092	Novel hum	175	25	86.2	117	4	ABB21830	Abb21830 Protein #
103	26	89.7	210	6	ABU33715	Protein e	176	25	86.2	117	4	AAM69653	Aam69653 Human bon
104	26	89.7	238	4	AU31660	Novel hum	177	25	86.2	117	4	AAM57251	Aam57251 Human bra
105	26	89.7	292	4	AAM42075	Human pol	178	25	86.2	117	4	ABG51335	AbG51335 Human liv
106	26	89.7	296	3	AAB43372	Human ORF	179	25	86.2	117	4	AAM05146	Aam05146 Peptide #
107	26	89.7	320	8	ADY08844	Plant ful	180	25	86.2	117	5	ABG39273	AbG39273 Human pep
108	26	89.7	320	8	ADY73944	Plant ful	181	25	86.2	117	5	ABG55307	AbG55307 Human gen
109	26	89.7	322	5	ABBO6658	G protein	182	25	86.2	132	8	ADL06701	AdL06701 Carassius
110	26	89.7	329	4	AAM40289	Human pol	183	25	86.2	141	7	AAD06701	AdA06701 H. pylori
111	26	89.7	334	2	AAM88633	Secreted	184	25	86.2	150	2	AAM20912	Aam20912 Propionib
112	26	89.7	334	6	ABO50400	Human sec	185	25	86.2	160	4	AAM60292	Aam60292 Propionib
113	26	89.7	334	6	ABO44657	Novel hum	186	25	86.2	160	6	ABM56811	AbM56811 Arabidops
114	26	89.7	334	7	ABO26137	Human pro	187	25	86.2	174	3	AGC23502	Aag23502 Arabidops
115	26	89.7	352	8	ADP29738	Human sec	188	25	86.2	174	3	AGC39522	Aag39522 Arabidops
116	26	89.7	358	8	ADQ96208	T cell ac	189	25	86.2	175	4	AAO11219	Aao11219 Human pol
117	26	89.7	358	8	ADQ96210	T cell ac	190	25	86.2	186	7	ADC07962	AdC07962 Rice prot
118	26	89.7	421	4	AGS98352	Escherich	191	25	86.2	186	7	ADC07948	AdC07948 Rice prot
119	26	89.7	421	6	ABU14827	Protein e	192	25	86.2	190	4	AAM83792	Aam83792 Human imm
120	26	89.7	441	3	AY53014	Human sec	193	25	86.2	200	7	ABM89622	Abm89622 Rice abio
121	26	89.7	494	6	ADA36442	Acinetoba	194	25	86.2	201	8	ADY12035	Ady12035 Plant ful
122	26	89.7	535	9	ABM90803	M. xanthu	195	25	86.2	202	8	ADU05630	AdU05630 H. pylori
123	26	89.7	555	4	AAM93388	Human pol	196	25	86.2	206	3	AGC39521	Aag39521 Arabidops
124	26	89.7	555	4	AGG66415	Human maj	197	25	86.2	207	3	AGC23501	Aag23501 Arabidops
125	26	89.7	555	8	ADL30943	Human pro	198	25	86.2	210	6	ABP79894	Abp79894 N. gonorr
126	26	89.7	555	8	ADQ96132	T cell ac	199	25	86.2	210	6	ABU37523	Abu37523 Protein e
127	26	89.7	555	9	ADY07709	Cyclin-de	200	25	86.2	210	6	ABU38175	Abu38175 Protein e
128	26	89.7	556	3	AY87342	Human sig	201	25	86.2	213	3	AGS51077	Ags51077 Arabidops
129	26	89.7	564	4	AAH88362	Human mem	202	25	86.2	239	8	ADN46479	Adn46479 Thermoco
130	26	89.7	564	8	ADQ96212	T cell ac	203	25	86.2	242	3	AGC12759	Aag12759 Arabidops
131	26	89.7	564	9	ADY63089	Human clo	204	25	86.2	243	3	AGC12759	Aag12759 Arabidops
132	26	89.7	715	6	ABU47623	Protein e	205	25	86.2	246	3	AGS51075	Ags51075 Arabidops
133	26	89.7	1042	6	ABU33994	Protein e	206	25	86.2	246	4	ABM58652	Abm58652 Drosophil
134	26	89.7	1172	4	ABG06613	Novel hum	207	25	86.2	247	2	AAW20248	Aaw20248 H. pylori
135	26	89.7	1507	3	ABE24128	Plasmodi	208	25	86.2	249	8	ADS21551	AdS21551 Bacterial
136	25	86.2	5	2	AAW45963	Peptide d	209	25	86.2	254	8	ADS27681	AdS27681 Bacterial
137	25	86.2	6	4	AAW48482	Antifibri	210	25	86.2	255	4	ABM67621	Abm67621 Drosophil
138	25	86.2	6	4	AAW48490	Antifibri	211	25	86.2	255	6	ABM68528	Abm68528 Phototrab
139	25	86.2	6	4	AAH82630	All-D pep	212	25	86.2	268	8	ADS41641	AdS41641 Bacterial
140	25	86.2	6	4	AAH82638	All-D pep	213	25	86.2	272	3	AGC12758	Aag12758 Arabidops
141	25	86.2	6	5	AAU96818	Amyloid t	214	25	86.2	276	3	AGC12757	Aag12757 Arabidops
142	25	86.2	6	5	AAU96818	Amyloid t	215	25	86.2	281	7	ABO80453	AbO80453 Pseudomon
143	25	86.2	6	5	AAU11664	Peptide #	216	25	86.2	282	1	ABP90422	Abp90422 Human phe
144	25	86.2	6	5	AAU11656	Peptide #	217	25	86.2	282	6	ABU09405	Abu09405 Human phe
145	25	86.2	6	6	AAE35452	Beta pep	218	25	86.2	282	8	ADH13186	Adh13186 Human mal
146	25	86.2	6	8	ADQ37277	Vaccine a	219	25	86.2	282	9	AEA15073	Aea15073 Human pol
147	25	86.2	6	8	ADQ37321	Antifibri	220	25	86.2	282	9	AEA08357	Aea08357 Human phe
148	25	86.2	6	9	ADY37329	Amyloid-t	221	25	86.2	285	4	AAM39174	Aam39174 Human pol
149	25	86.2	6	9	ADY37928	Amyloid-t	222	25	86.2	297	8	ADY25262	Ady25262 Plant ful
150	25	86.2	6	9	ADY37936	Amyloid-t	223	25	86.2	303	6	ABR40195	AbR40195 alpha-2.3
151	25	86.2	22	8	ADQ09761	Rice 26kD	224	25	86.2	306	2	AY338837	Ay338837 Neisseria
152	25	86.2	22	8	ADY33984	Rice 26 k	225	25	86.2	306	2	AY338836	Ay338836 Neisseria
153	25	86.2	25	4	ABH03313	Human mus	226	25	86.2	306	4	AGT1923	Aag71923 Human Olf
154	25	86.2	25	6	ABU12607	Novel hum	227	25	86.2	306	9	ABE49486	Aeb49486 N. mening
155	25	86.2	25	8	ADY328633	Human mus	228	25	86.2	306	9	ABE49484	Aeb49484 N. mening
156	25	86.2	28	2	ADY39806	Beta-amyl	229	25	86.2	307	9	AY338838	Ay338838 Neisseria
157	25	86.2	34	7	ADY72404	Human end	230	25	86.2	307	9	ABE49488	Aeb49488 N. gonorr
158	25	86.2	37	3	AAH05910	Mouse ind	231	25	86.2	309	5	ABO66559	AbO66559 G protein
159	25	86.2	37	8	ADK34080	Human rNO	232	25	86.2	314	5	AAU83579	Aau83579 Human nov
160	25	86.2	37	8	ADL70727	Mouse iNO	233	25	86.2	314	7	ADM29640	Adm29640 Novel hum
161	25	86.2	42	3	AGG04347	Arabidops	234	25	86.2	319	7	ABM87620	Abm87620 Rice abio
162	25	86.2	50	3	AGG04346	Arabidops	235	25	86.2	322	5	AAU24642	Aau24642 Human Olf
163	25	86.2	65	3	ABO55025	Human gen	236	25	86.2	322	5	ABM6657	Abm6657 G protein
164	25	86.2	69	8	AGG24897	Arabidops	237	25	86.2	322	5	ABP95886	Abp95886 Human GPC
165	25	86.2	77	3	AGG02840	Human sec	238	25	86.2	322	5	AAU95597	Aau95597 Human Olf
166	25	86.2	80	6	ABO00562	Novel hum	239	25	86.2	322	6	AAU85262	Aau85262 G-coupled
167	25	86.2	83	4	AAM92860	Human dig	240	25	86.2	322	7	ABU11149	Abu11149 Human G-p
168	25	86.2	90	4	AAU47327	Protonib	241	25	86.2	322	7	ADC85681	AdC85681 Human GPC
169	25	86.2	90	6	ABM43846	Protonib	242	25	86.2	322	8	ADG83362	Adg83362 Human Olf
170	25	86.2	105	4	AAO00117	Human pol	243	25	86.2	332	8	ADS44454	AdS44454 Bacterial

XX Chalifour R, Gervais F, Gupta A;
 XX WPI; 2001-031852/04.
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 XX cytoprotection for treating amyloidosis disorders, comprises a peptide,
 XX its isomer or peptidomimetic.
 XX Claim 7; Page 25; 46pp; English.
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 XX for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 XX AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 XX useful for treating amyloidosis disorders such as Alzheimer's disease.
 XX Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 XX binding region and the prot-prot interaction region of the human amyloid
 XX protein.
 XX Sequence 6 AA;
 SQ Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db 1 KAVFFA 6
 RESULT 3
 AAB82636
 ID AAB82636 standard; peptide; 6 AA.
 AC AAB82636;
 XX 02-OCT-2001 (first entry)
 XX All-D peptide used in Alzheimer's disease vaccine.
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 1..6 /note= "all D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT
 XX WO200139796-A2.
 PN 07-JUN-2001.
 XX 29-NOV-2000; 2000WO-CA001413.
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 PA Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 XX disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 XX which elicits production of antibodies to prevent fibrillogenesis and
 XX associated cellular toxicity.
 XX Disclosure; Page 11; 31pp; English.

CC The present sequence is that of an all-D peptide suitable for use in
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC CAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX Sequence 6 AA;
 SQ Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db 1 KAVFFA 6
 RESULT 4
 AAB82628
 ID AAB82628 standard; peptide; 6 AA.
 XX AAB82628;
 AC AAB82628;
 XX 02-OCT-2001 (first entry)
 XX All-D peptide used in Alzheimer's disease vaccine.
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 1..6 /note= "all D-form residues"
 FT
 XX WO200139796-A2.
 PN 07-JUN-2001.
 XX 29-NOV-2000; 2000WO-CA001413.
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 PA Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 XX disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 XX disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 XX

PT which elicits production of antibodies to prevent fibrillogenesis and
 XX associated cellular toxicity.

PS Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis, and
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 1 KAVFFA 6

RESULT 5

AAU96824
 ID AAU96824 standard; peptide; 6 AA.

AC AAU96824;

DT 30-JUL-2002 (first entry)

DE Amyloid targeting peptide #14.

KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..6 /note= "Preferably D-form residue"

FT Modified-site 6 /note= "Ala is amidated"

XX WO200207781-A2.

XX 31-JAN-2002.

XX

PF 25-JUL-2001; 2001WO-CA001071.

XX 25-JUL-2000; 2000US-0220808P.

PR 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

PA Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid

PT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A-t-(A₁n₁k)-z-A₁l₁a₁b (I) where z = 0-1;
 CC A₁t = an amyloid targeting moiety; A₁n₁k = a linker moiety; and A₁l₁a₁b
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (I) to the patient, and ultrasound imaging (I) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC , and a kit for preparing a radiopharmaceutical preparation comprising
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||

Db 1 KAVFFA 6

RESULT 6

AAU96816

ID AAU96816 standard; peptide; 6 AA.

XX AAU96816;

DT 30-JUL-2002 (first entry)

DE Amyloid targeting peptide #6.

KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

FH Key Location/Qualifiers
 FT Misc-difference 1..6
 XX /note= "Preferably D-form residue"
 XX WO200207781-A2.
 PN 31-JAN-2002.
 PD
 XX 25-JUL-2001; 2001WO-CA001071.
 XX 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.
 XX (NEUR-) NEUROCHEM INC.
 XX Gervais F, Kong X, Chalifour R, Migneault D;
 XX WPI; 2002-371447/40.
 DR
 XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 FT plaques and/or for the treatment of amyloidosis disorders.
 XX
 XX Claim 49; Page 21; 57pp; English.
 XX
 CC The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A₁-L₁-K₁-A₂ where z = 0 - 1;
 CC A₁ is an amyloid targeting moiety; L₁ is a linker moiety; and A₁-L₁-K₁-
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (i) to the patient, and ultrasound imaging (i) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (i), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementias), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention
 XX
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFFA 6
 DB 1 KAVFFFA 6
 RESULT 7
 AAU11662
 ID AAU11662 standard; peptide; 6 AA.
 AC AAU11662;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Peptide #15, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
 XX
 KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FT Modified-site 6
 FT /note= "C-terminal amide"
 XX
 PN WO200185093-A2.
 XX 15-NOV-2001.
 PD
 XX 22-DEC-2000; 2000WO-IB002078.
 XX 23-DEC-1999; 99US-0171877P.
 XX (NEUR-) NEUROCHEM INC.
 XX Green AM, Gervais F;
 XX WPI; 2002-075222/10.
 XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 FT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 FT inhibitor.
 XX
 XX Disclosure; Page 10; 68pp; English.
 CC The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11659, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 XX
 XX Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFFA 6
 DB 1 KAVFFFA 6
 RESULT 8
 AAU11654
 ID AAU11654 standard; peptide; 6 AA.
 XX
 AC AAU11654;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Peptide #7, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
 XX
 KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
 XX
 OS Synthetic.
 XX
 XX WO200185093-A2.
 XX 15-NOV-2001.
 PD
 XX 22-DEC-2000; 2000WO-IB002078.
 XX 23-DEC-1999; 99US-0171877P.
 XX

XX PA (NEUR-) NEUROCHEM INC.
 XX PI Green AM, Gervais P;
 XX DR WPI; 2002-075222/10.
 XX PT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 XX PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 XX PT inhibitor.
 XX PS Disclosure; Page 10; 68pp; English.
 XX CC The present invention relates to a new method of inhibiting cerebral
 XX CC amyloid angiopathy. The new method of the invention involves contacting a
 XX CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 XX CC can be used for treating disease states characterised by cerebral amyloid
 XX CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 XX CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 XX CC The present sequence represents one of a group of peptides (AAU11648-
 XX CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 XX CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 XX CC was used in the invention to treat a disease state characterised by
 XX CC cerebral amyloid angiopathy (CAA)
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KAVFFFA 6
 Db 1 KAVFFFA 6
 RESULT 9
 AAE35450
 ID AAE35450 standard; peptide; 6 AA.
 XX AC AAE35450;
 XX DT 17-JUN-2003 (first entry)
 XX DE Abeta peptide #21.
 XX KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 XX KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 XX KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 XX KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 XX KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 XX KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 XX KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 1. .6 /note= "D-form residues"
 XX FT Modified-site 6 /note= "C-terminal amide"
 XX FT
 XX PN WO200296937-A2.
 XX PD 05-DEC-2002.
 XX PF 29-MAY-2002; 2002WO-CA000763.
 XX PR 29-MAY-2001; 2001US-00867847.
 XX PA (NEUR-) NEUROCHEM INC.
 XX FI Gervais P, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.
 XX PT Prevention and/or treatment of an amyloid-related disease e.g.
 XX PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX PS Claim 1; Page 59; 44pp; English.
 XX CC The invention relates to a method for prevention and/or treatment of an
 XX CC amyloid-related disease which comprises administration of an all-D -
 XX CC amyloid-beta peptide. The method is used for preventing and/or treating
 XX CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 XX CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 XX CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 XX CC the mammal; and reducing or inhibiting the formation of plaques. It is
 XX CC also used for treating AA (reactive) amyloid diseases including
 XX CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 XX CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 XX CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 XX CC disease. AA deposits are also produced as a result of chronic microbial
 XX CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 XX CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 XX CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 XX CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 XX CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 XX CC present sequence is an Abeta peptide used to illustrate the method of the
 XX CC invention
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KAVFFFA 6
 Db 1 KAVFFFA 6
 RESULT 10
 AAE35443
 ID AAE35443 standard; peptide; 6 AA.
 XX AC AAE35443;
 XX DT 17-JUN-2003 (first entry)
 XX DE Abeta peptide #14.
 XX KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 XX KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 XX KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 XX KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 XX KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 XX KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 XX KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 1. .6 /note= "D-form residues"
 XX FT
 XX PN WO200296937-A2.
 XX PD 05-DEC-2002.
 XX PF 29-MAY-2002; 2002WO-CA000763.
 XX PR 29-MAY-2001; 2001US-00867847.
 XX PA (NEUR-) NEUROCHEM INC.

PI Gervais F, Hebert L, Challifour RJ, Kong X;
 XX WPI; 2003-201269/19.
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX
 XX Claim 1; Page 59; 44pp; English.
 XX
 XX The invention relates to a method for prevention and/or treatment of an
 XX amyloid-related disease which comprises administration of an all-D -
 XX amyloid-beta peptide. The method is used for preventing and/or treating
 XX Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 XX angiopathy; for altering serum levels of amyloid-beta in a mammal and
 XX favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 XX the mammal; and reducing or inhibiting the formation of plaques. It is
 XX also used for treating AA (reactive) amyloid diseases including
 XX inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 XX arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 XX Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 XX disease. AA deposits are also produced as a result of chronic microbial
 XX infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 XX ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 XX Certain malignant neoplasms can also result in AA fibril amyloid deposits
 XX including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 XX and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 XX present sequence is an A-beta peptide used to illustrate the method of the
 XX invention
 XX Sequence 6 AA;
 XX
 XX Query Match 100.0%; Score 29; DB 6; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFFA 6
 Db |||||
 1 KAVFFFA 6
 RESULT 11
 ADQ37275
 ID ADQ37275 standard; peptide; 6 AA.
 XX AC
 ADQ37275;
 XX DT
 07-OCT-2004 (first entry)
 XX DE Vaccine antigen amyloid-beta related amino acid sequence.
 XX
 XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; nootropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquiliser; uteropathic;
 KW anticonvulsant; anti-Hiv; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 1. .6
 FT /note= "D-form residues"
 FT Modified-site 6
 FT /note= "amidated"

XX WO2004058239-A1.
 XX 15-JUL-2004.
 XX 24-DEC-2003; 2003WO-CA002021.
 XX 24-DEC-2002; 2002US-0436379P.
 XX 23-JUN-2003; 2003US-0482214P.
 XX (NEUR-) NEUROCHEM INT LTD.
 XX Gervais F, Bellini F;
 XX WPI; 2004-543342/52.
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 XX that prevents or treats amyloid-beta related disease and second agent
 XX that is either a peptide or peptidomimetic or an immune system modulator.
 XX Disclosure; Page 67; 143pp; English.
 XX
 XX The present invention describes compositions (C) comprising: (a) a first
 XX agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 XX a second agent (a2) that is: (i) a peptide or peptidomimetic that
 XX modulates amyloid-beta fibril formation or induces a prophylactic or
 XX therapeutic immune response against amyloid-beta fibril formation; or
 XX (ii) an immune system modulator that prevents or inhibits amyloid-beta
 XX fibril formation. Also described is a kit comprising (C). (C) have
 XX nootropic, neuroprotective, cerebroprotective, haemostatic,
 XX ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,
 XX uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 XX neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 XX and can be used as amyloid-beta fibril formation modulators, and as
 XX immune system modulators. (C) can be used for preventing or treating an
 XX amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 XX (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 XX mild-to-moderate cognitive impairment, vascular dementia, cerebral
 XX amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 XX Down's syndrome, inclusion body myositis, age-related macular
 XX degeneration, or a condition associated with Alzheimer's disease
 XX (including hypothyroidism, cerebrovascular disease, cardiovascular
 XX disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 XX aggression, or incontinence), a neurological condition (e.g. Huntington's
 XX disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 XX Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 XX with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 XX field deficits, incoordination, gait disturbance, transient ischaemic
 XX attack or stroke, transient alertness, attention deficit, frequent falls,
 XX syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 XX haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 XX damage), or a psychological condition (e.g. depression, delusions,
 XX illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 XX disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 XX ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 XX excessive guilt)) in a subject e.g. human having a genomic mutation in an
 XX amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 XX having amyloid-beta deposits. The present sequence represents a peptide
 XX that can be used as a vaccine antigen in the exemplification of the
 XX present invention.
 XX Sequence 6 AA;
 XX
 XX Query Match 100.0%; Score 29; DB 8; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFFA 6
 Db |||||
 1 KAVFFFA 6
 RESULT 12

xx Composition for treating e.g. Alzheimer's disease comprises first agent PT
CC (including hypothyroidism, cerebrovascular disease, cardiovascular
CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
CC

PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX Disclosure; Page 69; 143pp; English.
 XX
 XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Mismatches 0; Gaps 0;
 QY 1 KAVFFPA 6
 Db 1 KAVFFPA 6
 RESULT 14
 ADQ37327
 ID ADQ37327 standard; peptide; 6 AA.
 XX
 AC ADQ37327;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Antifibrillogenic amyloidosis inhibiting peptide.
 XX
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; nootropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uteropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;

KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Modified-site 6 /note= "amidated"
 FT WO2004058239-A1.
 XX 15-JUL-2004.
 XX 24-DEC-2003; 2003WO-CA002021.
 XX 24-DEC-2002; 2002US-0436379P.
 XX 23-JUN-2003; 2003US-0482214P.
 XX (NEUR-) NEUROCHEM INT LTD.
 PA Gervais F, Bellini F;
 WIPI; 2004-543342/52.
 PT Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX Disclosure; Page 70; 143pp; English.
 XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KAVFFFA 6
 |||||
 Db 1 KAVFFFA 6

RESULT 15
 ADY37934
 ID ADY37934 standard; peptide; 6 AA.
 XX AC ADY37934;
 XX DT 19-MAY-2005 (first entry)
 XX DE Amyloid-targeting peptide, SEQ ID NO:14, for use in imaging agent.
 XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
 XX KW transmissible spongiform encephalopathy; scrapie; BSE;
 XX KW Alzheimers disease; neurological disease; amyloidosis;
 XX KW non-insulin dependent diabetes; metabolic disorder.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 6 /note= "C-terminal amide"
 FT
 XX US2005048000-A1.
 XX PN 03-MAR-2005.
 XX PD
 XX PF 03-DEC-2003; 2003US-00728028.
 XX PR 25-JUL-2000; 2000US-0220808P.
 XX PR 24-JUL-2001; 2001US-00915092.
 XX PR 29-JAN-2003; 2003US-0443291P.
 XX PA (NEUR-) NEUROCHEM INT LTD.
 XX PI Gervais F, Kong X, Chalifour R, Migneault D;
 XX WPI; 2005-212201/22.
 XX
 PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
 PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.
 XX
 PS Disclosure; SEQ ID NO 14; 34pp; English.
 XX
 CC The invention relates to an amyloid-targeting imaging agent. The imaging
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
 CC a labeling moiety via a linking moiety, and is preferably able to cross
 CC the blood-brain barrier. The invention also relates to a kit for
 CC preparing a radiopharmaceutical preparation from the imaging agent of the
 CC invention, a method for imaging amyloid deposition in a patient and a
 CC method for diagnosing an amyloid-related condition in a patient. The
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
 CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
 CC transmissible cerebral amyloidosis (also known as transmissible virus
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
 CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
 CC mediated diseases, dialysis-related amyloidosis, light chain-related
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
 CC patient. The agent does not exhibit excessive toxicity or irritation,
 CC does not induce an allergic response, and permits an earlier diagnosis of

CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KAVFFFA 6
 |||||
 Db 1 KAVFFFA 6

RESULT 16
 ADY37926
 ID ADY37926 standard; peptide; 6 AA.
 XX AC ADY37926;
 XX DT 19-MAY-2005 (first entry)
 XX DE Amyloid-targeting peptide, SEQ ID NO:6, for use in imaging agent.
 XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
 XX KW transmissible spongiform encephalopathy; scrapie; BSE;
 XX KW Alzheimers disease; neurological disease; amyloidosis;
 XX KW non-insulin dependent diabetes; metabolic disorder.
 XX OS Synthetic.
 XX US2005048000-A1.
 XX PN 03-MAR-2005.
 XX PD
 XX PF 03-DEC-2003; 2003US-00728028.
 XX PR 25-JUL-2000; 2000US-0220808P.
 XX PR 24-JUL-2001; 2001US-00915092.
 XX PR 29-JAN-2003; 2003US-0443291P.
 XX PA (NEUR-) NEUROCHEM INT LTD.
 XX PI Gervais F, Kong X, Chalifour R, Migneault D;
 XX WPI; 2005-212201/22.
 XX
 PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
 PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.
 XX
 PS Disclosure; SEQ ID NO 6; 34pp; English.
 XX
 CC The invention relates to an amyloid-targeting imaging agent. The imaging
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
 CC a labeling moiety via a linking moiety, and is preferably able to cross
 CC the blood-brain barrier. The invention also relates to a kit for
 CC preparing a radiopharmaceutical preparation from the imaging agent of the
 CC invention, a method for imaging amyloid deposition in a patient and a
 CC method for diagnosing an amyloid-related condition in a patient. The
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
 CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
 CC transmissible cerebral amyloidosis (also known as transmissible virus
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
 CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
 CC mediated diseases, dialysis-related amyloidosis, light chain-related
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
 CC patient. The agent does not exhibit excessive toxicity or irritation,
 CC does not induce an allergic response, and permits an earlier diagnosis of

CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 1 KAVFFA 6

RESULT 17
 AAB05909
 ID AAB05909 standard; peptide; 37 AA.

XX AC

XX AAB05909;

XX 16-OCT-2000 (first entry)

DE Rat inducible nitric oxide synthase calmodulin-binding region.

XX Rat; inducible nitric oxide synthase; iNOS;
 KW endothelial nitric oxide synthase; eNOS; vasotropic; hypertensive;
 KW AMP-activated protein kinase; AMPK; calmodulin; CaM;
 KW eNOS phosphorylation; ischaemic heart disease; pulmonary hypertension;
 KW obstructive airways disease.

XX Rattus sp.

XX WO200028076-A1.

XX 18-MAY-2000.

XX 05-NOV-1999; 99WO-AU000968.

XX 06-NOV-1998; 98AU-00006976.

XX (SVIN-) ST VINCENTS INST MEDICAL RES.

XX Stapleton DI, Chen Z, Michell BJ, Kemp BE, Mitchellhill KI;

XX WPI; 2000-376583/32.

XX Identifying modulators of AMP-activated protein kinase-mediated
 PT activation of a nitric oxide synthase (NOS), for use in ischemic heart
 PT disease, comprises testing for the increase or decrease in
 PT phosphorylation of NOS.

XX Example 4; Fig 5; 41pp; English.

XX The present sequence is the calmodulin (CaM)-binding region of rat
 CC inducible nitric oxide synthase (iNOS). iNOS is one of three isoforms of
 CC the enzyme NOS, which synthesises nitric oxide from the amino acid L-
 CC arginine. The sequence is provided for comparison with endothelial nitric
 CC oxide synthase (eNOS). The threonine residue at position 495 of eNOS is
 CC phosphorylated by AMP-activated protein kinase (AMPK) in the absence of
 CC Ca2+-CaM. Phosphorylation results in inhibition of eNOS. In the presence
 CC of Ca2+-CaM, phosphorylation by AMPK occurs predominantly at Ser-1177 and
 CC eNOS is activated. Modulators which activate AMPK may be used in the
 CC treatment of ischaemic heart disease by promoting glucose and fatty acid
 CC metabolism, and improving nutrient and oxygen supply to the myocytes.
 CC They may also be used for the treatment of pulmonary hypertension and
 CC obstructive airways disease

XX Sequence 37 AA;

Query Match 100.0%; Score 29; DB 3; Length 37;
 Best Local Similarity 100.0%; Pred. No. 43;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 |||||
 Db 18 KAVFFA 23

RESULT 18
 ADK34079
 ID ADK34079 standard; peptide; 37 AA.

XX AC ADK34079;

XX 20-MAY-2004 (first entry)

XX Mouse iNOS calmodulin binding domain peptide seqid 6.

XX vasotropic; antiangiogenic; gene therapy; critical limb ischaemia; CLI;
 KW eNOS; endothelial nitric oxide synthase; angiogenesis;
 KW microvascular dysfunction; mouse; calmodulin binding domain;
 KW inducible nitric oxide; iNOS.

XX Mus musculus.

XX WO2004016761-A2.

XX 26-FEB-2004.

XX 15-AUG-2003; 2003WO-US025626.

XX 16-AUG-2002; 2002US-0403637P.

XX (SCHD) SCHERING AG.

XX Dole WP, Kauser K, Qian HS, Rubanyi G;

XX WPI; 2004-203789/19.

XX Treating critical limb ischemia (CLI), or angiogenesis comprises
 PT administering to a patient a polynucleotide encoding a mammalian
 PT endothelial nitric oxide synthase (eNOS) polypeptide.

XX Example 1; SEQ ID NO 6; 82pp; English.

XX The invention describes a method of creating critical limb ischaemia
 CC (CLI) comprising administering to a patient a polynucleotide encoding a
 CC mammalian eNOS (endothelial nitric oxide synthase) polypeptide. Also
 CC described are: a method for treating angiogenesis by administering to a
 CC patient a polynucleotide encoding eNOS; and ameliorating microvascular
 CC dysfunction by administering to the patient the polynucleotide encoding
 CC the eNOS polypeptide. The method is useful for treating critical limb
 CC ischaemia or angiogenesis, or ameliorating a microvascular dysfunction.
 CC This is the amino acid sequence of a mouse inducible nitric synthase
 CC (iNOS) calmodulin binding domain peptide.

XX Sequence 37 AA;

Query Match 100.0%; Score 29; DB 8; Length 37;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 18 KAVFFA 23

RESULT 19
 ADL70726
 ID ADL70726 standard; peptide; 37 AA.

XX AC ADL70726;

XX 20-MAY-2004 (first entry)

XX DE Rat iNOS calmodulin-binding site amino acid sequence SEQ ID NO:6.
 XX KW rat; endothelial nitric oxide synthase; eNOS; enzyme; mutant;
 KW calmodulin-binding domain; vasotropic; antiarteriosclerotic; hypotensive;
 KW antidiabetic; vulnary; antilipemic; anorectic;
 KW reduced calcium dependence; ischaemia; atherosclerosis; hypertension;
 KW diabetes; Raynaud's phenomenon; poor wound healing; hyperlipidaemia;
 KW obesity; iNOS.
 XX OS Rattus rattus.
 XX KW WO2004016764-A2.
 XX PD 26-FEB-2004.
 XX XX 15-AUG-2003; 2003WO-US025745.
 XX XX 16-AUG-2002; 2002US-0403638P.
 XX XX (SCHD) SCHERING AG.
 XX PA Blasko E, Kauser K, Parkinson J;
 XX PI WPI; 2004-203792/19.
 XX XX New isolated endothelial nitric oxide synthase polypeptide mutant, useful
 PT for diagnosing or treating ischemia, atherosclerosis, hypertension,
 PT diabetes, Raynaud's phenomenon, poor wound healing, hyperlipidemia or
 PT obesity.
 XX XX

Example 1; SEQ ID NO 6; 57pp; English.

XX The present sequence represents the calmodulin-binding site of rat iNOS
 CC amino acid sequence. The present invention describes endothelial nitric
 CC oxide synthase (eNOS) mutants having one or more mutations in an amino
 CC acid sequence corresponding to a functional domain of a mammalian eNOS.
 CC At least one of the mutations is at a position corresponding to an amino
 CC acid residue in a calmodulin-binding domain that is phosphorylated in
 CC mammalian cells, and not an amino acid substitution to Ala or Asp. Also
 CC described: (1) an isolated eNOS polypeptide mutant that is substantially
 CC homologous, or has a 95-98% sequence identity to the amino acid sequence
 CC of the novel eNOS polypeptide mutant; (2) an isolated polynucleotide
 CC encoding the polypeptide mutant; (3) a recombinant vector comprising the
 CC polynucleotide operably linked to at least one regulatory sequence; (4) a
 CC pharmaceutical composition comprising the polypeptide mutant or the
 CC polynucleotide; (5) a binding partner of the polypeptide mutant; (6)
 CC modulating eNOS activity in a cell by administering to the cell the
 CC polypeptide mutant; (7) modulating eNOS activity in a cell by
 CC administering the polypeptide mutant or the polynucleotide to the cell,
 CC such that the polypeptide mutant is expressed in the cell; (8) diagnosing
 CC a condition associated with aberrant eNOS activity by contacting a cell
 CC of a patient with the polynucleotide, and detecting a level of eNOS
 CC activity indicative of the medical condition; and (9) prophylactic and
 CC therapeutic methods of treating a condition associated with aberrant eNOS
 CC activity by administering the polypeptide mutant or polynucleotide to the
 CC patient. The eNOS mutant has vasotropic, antiarteriosclerotic,
 CC hypotensive, antidiabetic, vulnary, antilipemic and anorectic
 CC activities, and has reduced calcium dependence and increased activity.
 CC The polypeptide mutant, polynucleotide and methods are useful for
 CC diagnosing or treating a condition associated with aberrant eNOS
 CC activity, e.g. ischaemia, atherosclerosis, hypertension, diabetes,
 CC Raynaud's phenomenon, poor wound healing, hyperlipidaemia or obesity.
 XX XX

Sequence 37 AA;

Query Match 100.0%; Score 29; DB 8; Length 37;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||||
 Db 18 KAVFFA 23

RESULT 20
 ADG17617
 ID ADG17617 standard; protein; 42 AA.
 XX AC ADG17617;
 XX DT 26-FEB-2004 (first entry)
 XX XX Modified amyloid beta precursor protein-related partial protein SeqID8.
 XX KW amyloid beta precursor protein; APP; beta-selectase cleavage;
 KW alpha-selectase cleavage; Alzheimer's disease; dementia.
 XX OS Unidentified.
 XX PN WO2003102177-A1.
 XX PD 11-DEC-2003.
 XX XX 21-MAY-2003; 2003WO-JP006319.
 XX PF 31-MAY-2002; 2002JP-00159472.
 XX PR (SAKA) OTSUKA PHARM CO LTD.
 XX PA Shimabuku A, Ogino K, Taki T, Shin R, Kitamoto T;
 XX PI WPI; 2004-053473/05.
 XX DR Amyloid beta precursor protein cleaved by beta- but not alpha-selectase
 XX PT for screening for treatments for Alzheimers disease.
 XX PS Claim 14; SEQ ID NO 8; 89pp; Japanese.
 XX CC This invention relates to a novel modified amyloid beta precursor protein
 CC (APP) which contains a beta-selectase cleavage site and a modification
 CC for screening for, treating and preventing Alzheimer's disease and
 CC dementia. The present sequence is that of a protein which is related to
 CC the modified amyloid beta precursor proteins of the invention.
 XX SQ Sequence 42 AA;

Query Match 100.0%; Score 29; DB 8; Length 42;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||||
 Db 18 KAVFFA 23

RESULT 21
 ADG17612
 ID ADG17612 standard; protein; 42 AA.
 XX AC ADG17612;
 XX DT 26-FEB-2004 (first entry)
 XX XX Modified amyloid beta precursor protein-related partial protein SeqID3.
 XX KW amyloid beta precursor protein; APP; beta-selectase cleavage;
 KW alpha-selectase cleavage; Alzheimer's disease; dementia.
 XX OS Unidentified.
 XX PN WO2003102177-A1.
 XX PD 11-DEC-2003.

PF 21-MAY-2003; 2003WO-JP006319.
 XX
 PR 31-MAY-2002; 2002JP-00159472.
 XX
 PA (SAKA) OTSUKA PHARM CO LTD.
 XX
 PI Shimabuku A, Ogino K, Taki T, Shin R, Kitamoto T;
 XX
 XX WPI; 2004-053473/05.
 XX
 XX Amyloid beta precursor protein cleaved by beta- but not alpha-selectase
 PT for screening for treatments for Alzheimers disease.
 PT
 XX Claim 13; SEQ ID NO 3; 89pp; Japanese.
 XX
 XX This invention relates to a novel modified amyloid beta precursor protein
 CC (APP) which contains a beta-selectase cleavage site and a modification
 CC which prevents cleavage by alpha-selectase. The invention may be useful
 CC for screening for, treating and preventing Alzheimer's disease and
 CC dementia. The present sequence is that of a protein which is related to
 CC the modified amyloid beta precursor proteins of the invention.
 XX
 XX Sequence 42 AA;
 SQ
 Query Match 100.0%; Score 29; DB 8; Length 42;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFPA 6
 DB 18 KAVFFPA 23
 |||||
 RESULT 22
 AAW41091
 ID AAW41091 standard; protein; 74 AA.
 XX
 AC AAW41091;
 XX
 DT 08-JUN-1998 (first entry)
 XX
 DE Chicken matrix metalloproteinase chMMP-2 (aa445-518).
 XX
 KW Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase; chicken;
 KW angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
 KW diabetic retinopathy; macular degeneration; restenosis; therapy.
 XX
 OS Gallus sp.
 XX
 PN WO9745137-A1.
 XX
 PD 04-DEC-1997.
 XX
 PF 30-MAY-1997; 97WO-US009158.
 XX
 PR 31-MAY-1996; 96US-0015869P.
 XX
 PR 31-MAY-1996; 96US-0018733P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Brooks P, Cheres DA;
 XX
 DR WPI; 1998-032334/03.
 XX
 XX Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.
 PT
 XX Claim 2; Page 159-160; 234pp; English.
 PS
 XX This polypeptide comprises amino acid residues 445-518 of chicken mature
 CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by

CC recombinant methods such as PCR amplification (see AAV12502) of chMMP-2
 CC coding sequence (see AAV03995) and cloning into e.g. pGEX-3X vector for
 CC expression in E. coli as a fusion protein with glutathione-S-transferase.
 CC The invention relates to the discovery that angiogenesis is mediated by
 CC the specific vitronectin receptor alpha-v beta-3, and that inhibition of
 CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of
 CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see
 CC also AAW41098-110), derivatised polypeptides, a monoclonal antibody or
 CC organic mimetic compound. The antagonists are used to inhibit
 CC angiogenesis in: inflamed tissue for treatment of arthritis or
 CC rheumatoid arthritis; solid tumours or metastases, particularly to induce
 CC tumour regression or inhibit growth of tumours; and in ocular disorders
 CC such as diabetic retinopathy or macular degeneration (all claimed). They
 CC can also be used to treat restenosis caused by migration of smooth muscle
 CC cells following angioplasty and to reduce blood supply to selected
 CC tissues (claimed). The new antagonists are highly selective for
 CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature
 CC vessels are unaffected, and the antagonists should be of low toxicity
 XX
 XX Sequence 74 AA;
 SQ
 Query Match 100.0%; Score 29; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFPA 6
 DB 64 KAVFFPA 69
 |||||
 RESULT 23
 AAW41085
 ID AAW41085 standard; protein; 74 AA.
 XX
 AC AAW41085;
 XX
 DT 08-JUN-1998 (first entry)
 XX
 DE Human matrix metalloproteinase huMMP-2 (aa439-512).
 XX
 KW Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;
 KW antagonist; integrin alpha-v beta-3; vitronectin receptor;
 KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;
 KW macular degeneration; restenosis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9745137-A1.
 XX
 PD 04-DEC-1997.
 XX
 PF 30-MAY-1997; 97WO-US009158.
 XX
 PR 31-MAY-1996; 96US-0015869P.
 XX
 PR 31-MAY-1996; 96US-0018733P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Brooks P, Cheres DA;
 XX
 DR WPI; 1998-032334/03.
 XX
 XX Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.
 PT
 XX Claim 2; Page 153; 234pp; English.
 PS
 XX This polypeptide comprises amino acid residues 439-512 of human mature
 CC matrix metalloproteinase 2 (huMMP-2). It can be produced by recombinant
 CC methods such as PCR amplification of huMMP-2 coding sequence and cloning
 CC into e.g. pGEX-3X vector for expression in E. coli as a fusion protein

CC with glutathione-S-transferase. The invention relates to the discovery
 CC that angiogenesis is mediated by the specific vitronectin receptor alpha-
 CC v beta-3, and that inhibition of alpha-v beta-3 function inhibits
 CC angiogenesis. Claimed antagonists of alpha-v beta-3 comprise C-terminal
 CC fragments (see AAW41083-94) of human or chicken MMP-2, fusion
 CC polypeptides, cyclic or linear polypeptides (see also AAW41098-110),
 CC derivatised polypeptides, a monoclonal antibody or organic mimetic
 CC compound. The antagonists are used to inhibit angiogenesis in: inflamed
 CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours
 CC or metastases, particularly to induce regression or to inhibit growth of
 CC tumours; and in ocular disorders such as diabetic retinopathy or macular
 CC degeneration (all claimed). They can also be used to treat restenosis
 CC caused by migration of smooth muscle cells following angioplasty and to
 CC reduce blood supply to selected tissues (claimed). The new antagonists
 CC are highly selective for angiogenesis. Only new blood vessels express
 CC alpha-v beta-3, so mature vessels are unaffected, and the antagonists
 CC should be of low toxicity

SQ Sequence 74 AA;

Query Match 100.0%; Score 29; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 DB 64 KAVFFA 69

RESULT 24

AAW41230
 ID AAW41230 standard; protein; 74 AA.

XX AAW41230;

XX 09-JUN-1998 (first entry)

XX Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.

XX Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation.

XX Synthetic.

OS Homo sapiens.

XX WO9745447-A1.

XX 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009099.

XX 31-MAY-1996; 96US-0015869P.

XX 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

XX Brooks P, Cheresch DA, Friedlander M;

XX WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav, betas
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

XX Claim 2; Page; 117pp; English.

XX Peptides AAW41228-33 are derived from the mature protein of human matrix
 CC metalloprotease-2 (MMP-2) (AAW41226). The present peptide is derived from
 CC amino acids 439-512. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an

CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
 CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

XX Sequence 74 AA;

Query Match 100.0%; Score 29; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 DB 64 KAVFFA 69

RESULT 25

ADT05998

ID ADT05998 standard; protein; 74 AA.

XX ADT05998;

XX 30-DEC-2004 (first entry)

XX Modified chicken MMP-2 Y517C, residues 445-518.

XX Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 KW cytotatic; antiinflammatory; antiarthritic; antirheumatic;
 KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
 KW hemopexin domain; cell attachment assay; ligand binding assay; chicken;
 KW mutant; mutein; cyclic.

XX Gallus gallus.

OS Synthetic.

XX Key Location/Qualifiers

FH Disulfide-bond 2..73

FT Misc-difference 73

FT /note= "Cys replaces wild-type Tyr. This residue
 corresponds to residue 517 of the mature MMP-2 protein"

XX WO2004087057-A2.

XX 14-OCT-2004.

XX 26-MAR-2004; 2004WO-US009321.

XX 28-MAR-2003; 2003US-00402212.

XX (SCRI) SCRIPPS RES INST.

XX Brooks PC, Cheresch DA;

XX WPI; 2004-737508/72.

XX Administration of composition comprising organic peptidomimetic alpha-v
 CC beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

```

PS Example 2; Page; 184pp; English.
XX
CC The invention relates to a method of inhibiting angiogenesis in a tissue
CC by the administration of a composition comprising an organic
CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
CC receptor). The integrin alpha-V beta-3 antagonist and compositions
CC containing it are useful for inhibiting angiogenesis in a variety of
CC medical conditions. The antagonist may be used to induce the regression
CC of solid tumours or solid tumour metastases; to inhibit the growth of
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
CC treat neovascularisation in retinal tissue (e.g., in diabetic
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
CC cell migration (such as that which occurs following angioplasty); and to
CC reduce the blood supply to a tissue required to support new growth of the
CC tissue. Sequences ADR05998-ADR06001 represent C-terminal (hemopexin
CC domain) fragments of chicken matrix metalloprotease 2 (MMP-2, gelatinase)
CC containing the amino acid substitutions Y517C and/or W551C which are
CC components of glutathione-S-transferase (GST)/MMP-2 fusion proteins used
CC in an example of the invention. Note: The present sequence is not shown
CC in the specification, but was derived from the wild-type chicken MMP-2 C-
CC terminal fragment ADR05971 and the information given on page 49.
XX
SQ Sequence 74 AA;

Query Match      100.0%; Score 29; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 64 KAVFFA 69
|||||

RESULT 26
ADR05965
ID ADR05965 standard; protein; 74 AA.
XX
AC ADR05965;
XX
DT 30-DEC-2004 (first entry)
XX
DE Human matrix metalloprotease (MMP-2) residues 439-512, SEQ ID NO:19.
XX
KW Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
KW cytotatic; antiinflammatory; antiarthritic; antirheumatic;
KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
KW hemopexin domain; cell attachment assay; ligand binding assay; human.
XX
OS Homo sapiens.
XX
FN WO2004087057-A2.
XX
PD 14-OCT-2004.
XX
PF 26-MAR-2004; 2004WO-US009321.
XX
PR 28-MAR-2003; 2003US-00402212.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Brooks PC, Cheres DA;
XX
DR WPI; 2004-737508/72.
XX
PT Administration of composition comprising organic peptidomimetic alpha-v
PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
XX
PS Example 1A; SEQ ID NO 19; 184pp; English.
XX
CC The invention relates to a method of inhibiting angiogenesis in a tissue
CC by the administration of a composition comprising an organic
CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
CC receptor). The integrin alpha-V beta-3 antagonist and compositions
CC containing it are useful for inhibiting angiogenesis in a variety of
CC medical conditions. The antagonist may be used to induce the regression
CC of solid tumours or solid tumour metastases; to inhibit the growth of
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
CC treat neovascularisation in retinal tissue (e.g., in diabetic
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
CC cell migration (such as that which occurs following angioplasty); and to
CC reduce the blood supply to a tissue required to support new growth of the
CC tissue. Sequences ADR05963-ADR05974 represent C-terminal (hemopexin
CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,
CC gelatinase) used in an example of the invention in assays of inhibition
CC of integrin alpha-V beta-3-mediated cell attachment and of ligand-
CC receptor binding.
XX
SQ Sequence 74 AA;

Query Match      100.0%; Score 29; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 64 KAVFFA 69
|||||

RESULT 27
ADR05971
ID ADR05971 standard; protein; 74 AA.
XX
AC ADR05971;
XX
DT 30-DEC-2004 (first entry)
XX
DE Chicken matrix metalloprotease (MMP-2) residues 445-518, SEQ ID NO:25.
XX
KW Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
KW cytotatic; antiinflammatory; antiarthritic; antirheumatic;
KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
KW hemopexin domain; cell attachment assay; ligand binding assay; chicken.
XX
OS Gallus gallus.
XX
FN WO2004087057-A2.
XX
PD 14-OCT-2004.
XX
PF 26-MAR-2004; 2004WO-US009321.
XX
PR 28-MAR-2003; 2003US-00402212.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Brooks PC, Cheres DA;
XX
DR WPI; 2004-737508/72.
XX
PT Administration of composition comprising organic peptidomimetic alpha-v
PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
XX
PS Example 1A; SEQ ID NO 25; 184pp; English.
XX

```

CC The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression
 CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat neovascularisation in retinal tissue (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to
 CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
 CC domain) fragments of human and chicken matrix metalloproteinase 2 (MMP-2,
 CC gelatinase) used in an example of the invention in assays of inhibition
 CC of integrin alpha-v beta-3-mediated cell attachment and of ligand-
 CC receptor binding.

XX SQ Sequence 74 AA;

Query Match 100.0%; Score 29; DB 8; Length 74;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
 |||||
 Db 64 KAVFFPA 69

RESULT 28

AAW41086
 ID AAW41086 standard; protein; 108 AA.

AC AAW41086;

XX 08-JUN-1998 (first entry)

DE Human matrix metalloproteinase huMMP-2 (aa439-546).

XX Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;
 KW antagonist; integrin alpha-v beta-3; vitronectin receptor;
 KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;
 KW macular degeneration; restenosis; therapy.

OS Homo sapiens.

XX WO9745137-A1.

PN 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009158.

XX 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

XX Brooks P, Cheresh DA;

PI WPI; 1998-032334/03.

XX Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

XX Claim 2; Page 154; 234pp; English.

XX This polypeptide comprises amino acid residues 439-546 of human mature
 CC matrix metalloproteinase 2 (huMMP-2). It can be produced by recombinant
 CC methods such as PCR amplification of huMMP-2 coding sequence and cloning
 CC into e.g. pGEX-3X vector for expression in E. coli as a fusion protein
 CC with glutathione-S-transferase. The invention relates to the discovery

CC that angiogenesis is mediated by the specific vitronectin receptor alpha-
 CC v beta-3, and that inhibition of alpha-v beta-3 function inhibits
 CC angiogenesis. Claimed antagonists of alpha-v beta-3 comprise C-terminal
 CC fragments (see AAW41083-94) of human or chicken MMP-2, fusion
 CC polypeptides, cyclic or linear polypeptides (see also AAW41098-110),
 CC derivatised polypeptides, a monoclonal antibody or organic mimetic
 CC compound. The antagonists are used to inhibit angiogenesis in: inflamed
 CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours
 CC or metastases, particularly to induce regression or to inhibit growth of
 CC tumours; and in ocular disorders such as diabetic retinopathy or macular
 CC degeneration (all claimed). They can also be used to treat restenosis
 CC caused by migration of smooth muscle cells following angioplasty and to
 CC reduce blood supply to selected tissues (claimed). The new antagonists
 CC are highly selective for angiogenesis. Only new blood vessels express
 CC alpha-v beta-3, so mature vessels are unaffected, and the antagonists
 CC should be of low toxicity

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 29; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
 |||||
 Db 64 KAVFFPA 69

RESULT 29

AAW41092
 ID AAW41092 standard; protein; 108 AA.

XX AAW41092;

XX 08-JUN-1998 (first entry)

DE Chicken matrix metalloproteinase chMMP-2 (aa445-552).

XX Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase; chicken;
 KW angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
 KW diabetic retinopathy; macular degeneration; restenosis; therapy.

XX Gallus sp.

XX WO9745137-A1.

XX 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009158.

XX 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

XX Brooks P, Cheresh DA;

XX WPI; 1998-032334/03.

XX Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

XX Claim 2; Page 160; 234pp; English.

XX This polypeptide comprises amino acid residues 445-552 of chicken mature
 CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by
 CC recombinant methods such as PCR amplification (see AAV12502) of chMMP-2
 CC coding sequence (see AAV03995) and cloning into e.g. pGEX-3X vector for
 CC expression in E. coli as a fusion protein with glutathione-S-transferase.
 CC The invention relates to the discovery that angiogenesis is mediated by
 CC the specific vitronectin receptor alpha-v beta-3, and that inhibition of

CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of
 CC alpha-v beta-3 comprise C-terminal fragments (see AAW41083-94) of human
 CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see
 CC also AAW41098-110), derivatised polypeptides, a monoclonal antibody or
 CC organic mimetic compound. The antagonists are used to inhibit
 CC angiogenesis in: inflamed tissue for treatment of arthritis or
 CC rheumatoid arthritis, solid tumours or metastases, particularly to induce
 CC tumour regression or inhibit growth of tumours; and in ocular disorders
 CC such as diabetic retinopathy or macular degeneration (all claimed). They
 CC can also be used to treat restenosis caused by migration of smooth muscle
 CC cells following angioplasty and to reduce blood supply to selected
 CC tissues (claimed). The new antagonists are highly selective for
 CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature
 CC vessels are unaffected, and the antagonists should be of low toxicity
 XX

XX Sequence 108 AA;
 Query Match 100.0%; Score 29; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 30

AAW41231
 ID AAW41231 standard; protein; 108 AA.

XX AC AAW41231;
 XX

DT 09-JUN-1998 (first entry)

XX Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.

XX Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation.

XX Synthetic.
 OS Homo sapiens.

XX WO9745447-A1.

PD 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009099.

XX 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

PI Brooks P, Cheres DA, Friedlander M;

XX WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav, beta5
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

XX Claim 2; Page; 117pp; English.

XX Peptides AAW41228-33 are derived from the mature protein of human matrix
 CC metalloprotease-2 (MMP-2) (AAW41226). The present peptide is derived from
 CC amino acids 439-546. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid

CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

XX Sequence 108 AA;

Query Match 100.0%; Score 29; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 31

AAW41237
 ID AAW41237 standard; protein; 108 AA.

XX AC AAW41237;
 XX

DT 09-JUN-1998 (first entry)

XX Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.

XX Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation.

XX Synthetic.
 OS Gallus sp.

XX WO9745447-A1.

PD 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009099.

XX 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

PI Brooks P, Cheres DA, Friedlander M;

XX WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav, beta5
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

XX Claim 2; Page; 117pp; English.

XX Peptides AAW41234-39 are derived from the chicken matrix metalloprotease-
 CC 2 (MMP-2) protein (AAW41227). The present peptide is derived from amino
 CC acids 445-552. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
 CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to

CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

XX
 SQ Sequence 108 AA;
 Query Match 100.0%; Score 29; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 90 KAVFFA 95

RESULT 32

ADT05972
 ID ADT05972 standard; protein; 108 AA.

XX AC ADT05972;

XX DT 30-DEC-2004 (first entry)

XX DE Chicken matrix metalloprotease (MMP-2) residues 445-552, SEQ ID NO:26.

XX KW Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 KW cystostatic; antiinflammatory; antiarthritic; antirheumatic;
 KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
 KW hemopexin domain; cell attachment assay; ligand binding assay; chicken.

XX OS Gallus gallus.

XX PN WO2004087057-A2.

XX PD 14-OCT-2004.

XX PF 26-MAR-2004; 2004WO-US009321.

XX PR 28-MAR-2003; 2003US-00402212.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Brooks PC, Cheres DA;

XX DR WPI; 2004-737508/72.

XX PT Administration of composition comprising organic peptidomimetic alpha-v
 beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX PS Example 1A; SEQ ID NO 26; 184pp; English.

XX CC The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression
 CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat restenosis in a tissue by inhibiting angiogenesis (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to

CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
 CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,
 CC gelatinase) used in an example of the invention in assays of inhibition
 CC of integrin alpha-v beta-3-mediated cell attachment and of ligand-
 CC receptor binding.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 29; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 33

ADT05966
 ID ADT05966 standard; protein; 108 AA.

XX AC ADT05966;

XX DT 30-DEC-2004 (first entry)

XX DE Human matrix metalloprotease (MMP-2) residues 439-546, SEQ ID NO:20.

XX KW Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 KW cystostatic; antiinflammatory; antiarthritic; antirheumatic;
 KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
 KW hemopexin domain; cell attachment assay; ligand binding assay; human.

XX OS Homo sapiens.

XX PN WO2004087057-A2.

XX PD 14-OCT-2004.

XX PF 26-MAR-2004; 2004WO-US009321.

XX PR 28-MAR-2003; 2003US-00402212.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Brooks PC, Cheres DA;

XX DR WPI; 2004-737508/72.

XX PT Administration of composition comprising organic peptidomimetic alpha-v
 beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX PS Example 1A; SEQ ID NO 20; 184pp; English.

XX CC The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression
 CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat restenosis in a tissue by inhibiting angiogenesis (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to
 CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin

CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,
 CC gelatinase) used in an example of the invention in assays of inhibition
 CC of integrin alpha-v beta-3-mediated cell attachment and of ligand-
 CC receptor binding.

XX Sequence 108 AA;

Query Match 100.0%; Score 29; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 34

ADT05999
 ID ADT05999 standard; protein; 108 AA.

XX AC

ADT05999;

XX DT 30-DEC-2004 (first entry)

DE DE Modified chicken MMP-2 Y517C/W551C, residues 445-552.

XX Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 KW cytotatic; antiinflammatory; antiarthritic; antirheumatic;
 KW ophthalmologic; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
 KW hemopexin domain; cell attachment assay; ligand binding assay; chicken;
 KW mutant; mutein.

XX Gallus gallus.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 73

FT /note= "Cys replaces wild-type Tyr. This residue
 corresponds to residue 517 of the mature MMP-2 protein"

FT Misc-difference 107

FT /note= "Cys replaces wild-type Trp. This residue
 corresponds to residue 551 of the mature MMP-2 protein"

XX WO2004087057-A2.

XX 14-OCT-2004.

XX 26-MAR-2004; 2004WO-US009321.

XX 28-MAR-2003; 2003US-00402212.

XX (SCRI) SCRIPPS RES INST.

XX Brooks PC, Cheres DA;

XX WPI; 2004-737508/72.

XX Administration of composition comprising organic peptidomimetic alpha-v
 PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX Example 2; Page; 184pp; English.

XX The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC Peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression

CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g. in rheumatoid arthritis); to
 CC treat neovascularisation in retinal tissue (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to
 CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. Sequences ADT05998-ADT06001 represent C-terminal (hemopexin
 CC domain) fragments of chicken matrix metalloprotease 2 (MMP-2, gelatinase)
 CC containing the amino acid substitutions Y517C and/or W551C which are
 CC components of glutathione-S-transferase (GST)/MMP-2 fusion proteins used
 CC in an example of the invention. Note: The present sequence is not shown
 CC in the specification, but was derived from the wild-type chicken MMP-2 C-
 CC terminal fragment ADT05971 and the information given on page 49.

XX Sequence 108 AA;

Query Match 100.0%; Score 29; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

|||||

Db 64 KAVFFA 69

RESULT 35

AAW41238
 ID AAW41238 standard; protein; 122 AA.

XX AC

AAW41238;

XX DT 09-JUN-1998 (first entry)

DE DE Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.

XX Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation.

XX Synthetic.

OS Gallus sp.

XX WO9745447-A1.

XX 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009099.

XX 31-MAY-1996; 96US-0015869P.

XX 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

XX Brooks P, Cheres DA, Friedlander M;

XX WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav, beta5
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

XX Claim 2; Page; 117pp; English.

XX Peptides AAW41234-39 are derived from the chicken matrix metalloprotease-
 CC 2 (MMP-2) protein (AAW41227). The present peptide is derived from amino
 CC acids 516-637. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid

CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

XX SQ Sequence 122 AA;

Query Match 100.0%; Score 29; DB 2; Length 122;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFPA 6

Db 19 KAVFFPA 24

RESULT 36

AAW41232
 ID AAW41232 standard; protein; 152 AA.

XX AC AAW41232;

XX DT 09-JUN-1998 (first entry)

XX DE Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.

XX KW Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 XX vitronectin receptor; inhibition; angiogenesis; tumour growth;
 XX restenosis; neovascularisation.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9745447-A1.

XX PD 04-DEC-1997.

XX PF 30-MAY-1997; 97WO-US009099.

XX PR 31-MAY-1996; 96US-0015869P.

XX PR 31-MAY-1996; 96US-0018733P.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Brooks P, Cheres DA, Friedlander M;

XX DR WPI; 1998-041758/04.

XX PT Packaging material containing polypeptide antagonist of alphav, betas
 XX integrin - used for inhibition of angiogenesis, and for treating tumours,
 XX inflammation, eye diseases etc.

XX PS Claim 2; Page; 117pp; English.

XX CC Peptides AAW41228-33 are derived from the mature protein of human matrix
 CC metalloproteinase-2 (MMP-2) (AAW41226). The present peptide is derived from
 CC amino acids 510-631. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
 CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to

CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

XX SQ Sequence 152 AA;

Query Match 100.0%; Score 29; DB 2; Length 152;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFPA 6

Db 23 KAVFFPA 28

RESULT 37

AAW41090
 ID AAW41090 standard; protein; 193 AA.

XX AC AAW41090;

XX DT 08-JUN-1998 (first entry)

XX DE Chicken matrix metalloproteinase chMMP-2 (aa445-637).

XX KW Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase; chicken;
 XX angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
 XX vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
 XX diabetic retinopathy; macular degeneration; restenosis; therapy.

XX OS Gallus sp.

XX PN WO9745137-A1.

XX PD 04-DEC-1997.

XX PF 30-MAY-1997; 97WO-US009158.

XX PR 31-MAY-1996; 96US-0015869P.

XX PR 31-MAY-1996; 96US-0018733P.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Brooks P, Cheres DA;

XX DR WPI; 1998-032334/03.

XX PT Packaging material containing polypeptide antagonist of alphav, betas
 XX integrin - used for inhibition of angiogenesis, and for treating tumours,
 XX inflammation, eye diseases etc.

XX PS Claim 2; Page 158-159; 234pp; English.

XX CC This polypeptide comprises amino acid residues 445-637 of chicken mature
 CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by
 CC recombinant methods such as PCR amplification (see AAV12502) of chMMP-2
 CC coding sequence (see AAV03995) and cloning into e.g. PGEX-3X vector for
 CC expression in E. coli as a fusion protein with glutathione-S-transferase.
 CC The invention relates to the discovery that angiogenesis is mediated by
 CC the specific vitronectin receptor alpha-v beta-3, and that inhibition of
 CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of
 CC alpha-v beta-3 comprise C-terminal fragments (see AAW41083-94) of human
 CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see
 CC also AAW41098-110), derivatised polypeptides, a monoclonal antibody or
 CC organic mimetic compound. The antagonists are used to inhibit
 CC angiogenesis in: inflamed tissue for treatment of arthritis or
 CC rheumatoid arthritis; solid tumours or metastases, particularly to induce
 CC tumour regression or inhibit growth of tumours; and in ocular disorders

CC such as diabetic retinopathy or macular degeneration (all claimed). They
 CC can also be used to treat restenosis caused by migration of smooth muscle
 CC cells following angioplasty and to reduce blood supply to selected
 CC tissues (claimed). The new antagonists are highly selective for
 CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature
 CC vessels are unaffected, and the antagonists should be of low toxicity
 XX

SQ Sequence 193 AA;
 Query Match 100.0%; Score 29; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 38
 AAW41084
 ID AAW41084 standard; protein; 193 AA.
 XX
 AC AAW41084;
 XX
 DT 08-JUN-1998 (first entry)
 XX
 DE Human matrix metalloproteinase huMMP-2 (aa439-631).
 XX
 KW Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;
 KW antagonist; integrin alpha-v beta-3; vitronectin receptor;
 KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;
 KW macular degeneration; restenosis; therapy.
 XX

OS Homo sapiens.
 XX
 PN WO9745137-A1.
 XX
 PD 04-DEC-1997.
 XX
 PF 30-MAY-1997; 97WO-US009158.
 XX
 PR 31-MAY-1996; 96US-0015869P.
 PR 31-MAY-1996; 96US-0018733P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Brooks P, Cheres DA;
 XX
 DR WPI; 1998-032334/03.
 XX

PT Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.
 XX

PS Claim 2; Page 152-153; 234pp; English.
 XX
 CC This polypeptide comprises amino acid residues 439-631 of human mature
 CC matrix metalloproteinase 2 (huMMP-2). It can be produced by recombinant
 CC methods such as PCR amplification (see AAV12510) of huMMP-2 coding
 CC sequence and cloning into e.g. pGEX-3X vector for expression in E. coli
 CC as a glutathione-S-transferase fusion protein. The invention relates to
 CC the discovery that angiogenesis is mediated by the specific vitronectin
 CC receptor alpha-v beta-3, and that inhibition of alpha-v beta-3 function
 CC inhibits angiogenesis. Claimed antagonists of alpha-v beta-3 comprise C-
 CC terminal fragments (see AAW1083-94) of human or chicken MMP-2, fusion
 CC polypeptides, cyclic or linear polypeptides (see also AAW1098-110),
 CC derivatised polypeptides, a monoclonal antibody or organic mimetic
 CC compound. The antagonists are used to inhibit angiogenesis in: inflamed
 CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours
 CC or metastases, particularly to induce tumour regression or inhibit growth
 CC of tumours; and in ocular disorders such as diabetic retinopathy or
 CC macular degeneration (all claimed). They can also be used to treat
 CC restenosis caused by migration of smooth muscle cells following

CC angioplasty and to reduce blood supply to selected tissues (claimed). The
 CC new antagonists are highly selective for angiogenesis. Only new blood
 CC vessels express alpha-v beta-3, so mature vessels are unaffected, and the
 CC antagonists should be of low toxicity
 XX

SQ Sequence 193 AA;
 Query Match 100.0%; Score 29; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 39
 AAW41229
 ID AAW41229 standard; protein; 193 AA.
 XX
 AC AAW41229;
 XX
 DT 09-JUN-1998 (first entry)
 XX
 DE Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.
 XX
 KW Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation.
 XX

OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9745447-A1.
 XX
 PD 04-DEC-1997.
 XX
 PF 30-MAY-1997; 97WO-US009099.
 XX
 PR 31-MAY-1996; 96US-0015869P.
 PR 31-MAY-1996; 96US-0018733P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Brooks P, Cheres DA, Friedlander M;
 XX
 DR WPI; 1998-041758/04.
 XX

PT Packaging material containing polypeptide antagonist of alphav, beta5
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.
 XX

PS Claim 2; Page; 117pp; English.
 XX
 CC Peptides AAW41228-33 are derived from the mature protein of human matrix
 CC metalloproteinase-2 (MMP-2) (AAW41226). The present peptide is derived from
 CC amino acids 439-631. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
 CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using

CC information provided

XX Sequence 193 AA;

SQ Query Match 100.0%; Score 29; DB 2; Length 193;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 64 KAVFFA 69

RESULT 40

AAW41235 ID AAW41235 standard; protein; 193 AA.

XX AC AAW41235;

XX DT 09-JUN-1998 (first entry)

XX DE Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.

XX KW Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;

XX KW vitronectin receptor; inhibition; angiogenesis; tumour growth;

XX KW restenosis; neovascularisation.

XX OS Synthetic.

XX OS Gallus sp.

XX OS WO9745447-A1.

XX PN 04-DEC-1997.

XX PD 30-MAY-1997; 97WO-US009099.

XX PF 31-MAY-1996; 96US-0015869P.

XX PR 31-MAY-1996; 96US-0018733P.

XX PS (SCRI) SCRIPPS RES INST.

XX PI Brooks P, Cheres DA, Friedlander M;

XX PI WPI; 1998-041758/04.

XX DR Packaging material containing polypeptide antagonist of alphav, betas

XX PT integrin - used for inhibition of angiogenesis, and for treating tumours,

XX PT inflammation, eye diseases etc.

XX PS Claim 2; Page; 117pp; English.

XX CC Peptides AAW41234-39 are derived from the chicken matrix metalloprotease-

XX CC 2 (MMP-2) protein (AAW41227). The present peptide is derived from amino

XX CC acids 445-637. The peptides are able to act as alpha-v-beta-5

XX CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of

XX CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a

XX CC novel labelled package that contains an inhibitor of angiogenesis i.e. an

XX CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-

XX CC beta-5 and includes a part of the C-terminal domain of MMP-2. The

XX CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid

XX CC tumours or metastases, and in a wide range of ocular disorders (e.g.

XX CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal

XX CC transplants). They are particularly used to induce regression or to

XX CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be

XX CC used to treat restenosis caused by migration of smooth muscle cells

XX CC following angioplasty and to reduce blood supply to selected tissues. The

XX CC antagonists particularly inhibit neovascularisation where this is induced

XX CC by cytokines, e.g. transforming growth factor alpha, epidermal growth

XX CC factor or especially vascular endothelial growth factor. note: this

XX CC sequence does not appear in the specification; it was created using

XX CC information provided

XX SQ Sequence 193 AA;

Query Match 100.0%; Score 29; DB 2; Length 193;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 90 KAVFFA 95

RESULT 41

ADT05964 ID ADT05964 standard; protein; 193 AA.

XX AC ADT05964;

XX DT 30-DEC-2004 (first entry)

XX DE Human matrix metalloprotease (MMP-2) residues 439-631, SEQ ID NO:18.

XX KW Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;

XX KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;

XX KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;

XX KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;

XX KW cytotatic; antiinflammatory; antiarthritic; antirheumatic;

XX KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;

XX KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;

XX KW hemopexin domain; cell attachment assay; ligand binding assay; human.

XX OS Homo sapiens.

XX OS WO2004087057-A2.

XX PN 14-OCT-2004.

XX PF 26-MAR-2004; 2004WO-US009321.

XX PR 28-MAR-2003; 2003US-00402212.

XX PS (SCRI) SCRIPPS RES INST.

XX PI Brooks PC, Cheres DA;

XX PI WPI; 2004-737508/72.

XX CC Administration of composition comprising organic peptidomimetic alpha-v

XX CC beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue

XX CC angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX PS Example 1A; SEQ ID NO 18; 184pp; English.

XX CC The invention relates to a method of inhibiting angiogenesis in a tissue

XX CC by the administration of a composition comprising an organic

XX CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin

XX CC receptor). The integrin alpha-V beta-3 antagonist and compositions

XX CC containing it are useful for inhibiting angiogenesis in a variety of

XX CC medical conditions. The antagonist may be used to inhibit the regression

XX CC of solid tumours or solid tumour metastases; to inhibit the growth of

XX CC solid tumours undergoing neovascularisation; to treat inflamed tissue in

XX CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to

XX CC treat neovascularisation in retinal tissue (e.g., in diabetic

XX CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle

XX CC cell migration (such as that which occurs following angioplasty); and to

XX CC reduce the blood supply to a tissue required to support new growth of the

XX CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin

XX CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,

XX CC gelatinase) used in an example of the invention in assays of inhibition

XX CC of integrin alpha-V beta-3-mediated cell attachment and of ligand-

XX CC receptor binding.

XX SQ Sequence 193 AA;

Query Match

100.0%; Score 29; DB 8; Length 193;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6 	
Db	64 KAVFFA 69	
RESULT 42		
ID	ADT05970	
XX	ADT05970 standard; protein; 193 AA.	
AC	ADT05970;	
XX		
DT	30-DEC-2004 (first entry)	
XX		
DE	Chicken matrix metalloprotease (MMP-2) residues 445-637, SEQ ID NO:24.	
XX		
KW	Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;	
KW	vitronectin receptor antagonist; neovascularisation; cancer; tumour;	
KW	inflammation; rheumatoid arthritis; retina; diabetic retinopathy;	
KW	restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;	
KW	cytostatic; antiinflammatory; antiarthritic; antirheumatic;	
KW	ophthalmological; antidiabetic; vasotropic; muscular-gen.;	
KW	peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;	
KW	hemopexin domain; cell attachment assay; ligand binding assay; chicken.	
XX		
OS	Gallus gallus.	
XX		
FN	WO2004087057-A2.	
XX		
PD	14-OCT-2004.	
XX		
PF	26-MAR-2004; 2004WO-US009321.	
XX		
PR	28-MAR-2003; 2003US-00402212.	
XX		
PA	(SCRI) SCRIPPS RES INST.	
XX		
PI	Brooks PC, Cheresch DA;	
XX		
DR	WPI; 2004-737508/72.	
XX		
PT	Administration of composition comprising organic peptidomimetic alpha-v	
PT	beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue	
PT	angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.	
XX		
PS	Example 1A; SEQ ID NO 24; 184pp; English.	
XX		
CC	The invention relates to a method of inhibiting angiogenesis in a tissue	
CC	by the administration of a composition comprising an organic	
CC	peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin	
CC	receptor). The integrin alpha-v beta-3 antagonist and compositions	
CC	containing it are useful for inhibiting angiogenesis in a variety of	
CC	medical conditions. The antagonist may be used to induce the regression	
CC	of solid tumours or solid tumour metastases; to inhibit the growth of	
CC	solid tumours undergoing neovascularisation; to treat inflamed tissue in	
CC	which neovascularisation is occurring (e.g., in rheumatoid arthritis); to	
CC	treat neovascularisation in retinal tissue (e.g., in diabetic	
CC	retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle	
CC	cell migration (such as that which occurs following angioplasty); and to	
CC	reduce the blood supply to a tissue required to support new growth of the	
CC	tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin	
CC	domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,	
CC	gelatinase) used in an example of the invention in assays of inhibition	
CC	of integrin alpha-v beta-3-mediated cell attachment and of ligand-	
CC	receptor binding.	
XX		
SQ	Sequence 193 AA;	
Query Match 100.0%; Score 29; DB 8; Length 193;		
Best Local Similarity 100.0%; Pred. No. 2.1e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2.4e+02;		
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KAVFFA 6	
Query Match 100.0%; Score 29; DB 2; Length 222;		
Best Local Similarity 100.0%; Pred. No. 2		

Db 93 KAVFFA 98

RESULT 44

AAW41228
ID AAW41228 standard; protein; 222 AA.AC
XX AAW41228;

DT 09-JUN-1998 (first entry)

DE Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.

KW Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
KW restenosis; neovascularisation.

OS Synthetic.

OS Homo sapiens.

FN W09745447-A1.

PD 04-DEC-1997.

PF 30-MAY-1997; 97WO-US009099.

PR 31-MAY-1996; 96US-0015869P.
PR 31-MAY-1996; 96US-0018733P.

PA (SCRI) SCRIPPS RES INST.

PI Brooks P, Cheres DA, Friedlander M;
PI WPI; 1998-041759/04.

DR WPI; 1998-041759/04.

PT Packaging material containing polypeptide antagonist of alphav, beta5
PT integrin - used for inhibition of angiogenesis, and for treating tumours,
PT inflammation, eye diseases etc.

PS Claim 2; Page; 117pp; English.

CC Peptides AAW41228-33 are derived from the mature protein of human matrix
CC metalloprotease-2 (MMP-2) (AAW41226). The present peptide is derived from
CC amino acids 410-631. The peptides are able to act as alpha-v-beta-5
CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
CC tumours or metastases, and in a wide range of ocular disorders (e.g.
CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
CC transplants). They are particularly used to induce regression or to
CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
CC used to treat restenosis caused by migration of smooth muscle cells
CC following angioplasty and to reduce blood supply to selected tissues. The
CC antagonists particularly inhibit neovascularisation where this is induced
CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
CC factor or especially vascular endothelial growth factor. note: this
CC sequence does not appear in the specification; it was created using
CC information provided

SQ Sequence 222 AA;

Query Match 100.0%; Score 29; DB 2; Length 222;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 93 KAVFFA 98

RESULT 45

ADT05963

ID ADT05963 standard; protein; 222 AA.

AC
XX ADT05963;

DT 30-DEC-2004 (first entry)

DE Human matrix metalloprotease (MMP-2) residues 410-631, SEQ ID NO:17.

KW Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;

KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
KW cytosolic; antiinflammatory; antiarthritic; antirheumatic;
KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
KW peptidomimetic; matrix metalloprotease 2; MMP-2; Gelatinase;
KW hemopexin domain; cell attachment assay; ligand binding assay; human.

OS Homo sapiens.

FN W02004087057-A2.

PD 14-OCT-2004.

PF 26-MAR-2004; 2004WO-US009321.

PR 28-MAR-2003; 2003US-00402212.

PA (SCRI) SCRIPPS RES INST.

PI Brooks PC, Cheres DA;
PI WPI; 2004-737508/72.

DR WPI; 2004-737508/72.

PT Administration of composition comprising organic peptidomimetic alpha-v
PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
XX Example 1A; SEQ ID NO 17; 184pp; English.

CC The invention relates to a method of inhibiting angiogenesis in a tissue
CC by the administration of a composition comprising an organic
CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
CC receptor). The integrin alpha-V beta-3 antagonist and compositions
CC containing it are useful for inhibiting angiogenesis in a variety of
CC medical conditions. The antagonist may be used to induce the regression
CC of solid tumours or solid tumour metastases; to inhibit the growth of
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
CC treat neovascularisation in retinal tissue (e.g., in diabetic
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
CC cell migration (such as that which occurs following angioplasty); and to
CC reduce the blood supply to a tissue required to support new growth of the
CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,
CC gelatinase) used in an example of the invention in assays of inhibition
CC of integrin alpha-V beta-3-mediated cell attachment and of ligand-
CC receptor binding.

SQ Sequence 222 AA;

Query Match 100.0%; Score 29; DB 8; Length 222;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 93 KAVFFA 98

RESULT 46

```

AAW41089
ID AAW41089 standard; protein; 228 AA.
XX
AC AAW41089;
AC
DT 08-JUN-1998 (first entry)
XX
DE Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.
XX
DE Chicken matrix metalloproteinase chMMP-2 (aa410-637).
XX
KW Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase; chicken;
KW angioinhibitor; antagonist; integrin alpha-v beta-3;
KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
KW diabetic retinopathy; macular degeneration; restenosis; therapy.
XX
OS Gallus sp.
XX
PN WO9745137-A1.
XX
PD 04-DEC-1997.
XX
PF 30-MAY-1997; 97WO-US009158.
XX
PR 31-MAY-1996; 96US-0015969P.
XX
PR 31-MAY-1996; 96US-0018733P.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Brooks P, Cheres DA;
XX
PI WPI; 1998-032334/03.
XX
DR Packaging material containing polypeptide antagonist of alphav, beta3
XX integrin - used for inhibition of angiogenesis, and for treating tumours,
XX inflammation, eye diseases etc.
XX
PS Claim 2; Page 157-158; 234pp; English.
XX
CC This polypeptide comprises amino acid residues 410-637 of chicken mature
CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by
CC recombinant methods such as PCR amplification (see AAV12501) of chMMP-2
CC coding sequence (see AAV03995) and cloning into e.g. pGEX-3X vector for
CC expression in E. coli as a fusion protein with glutathione-S-transferase.
CC The invention relates to the discovery that angiogenesis is mediated by
CC the specific vitronectin receptor alpha-v beta-3, and that inhibition of
CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of
CC alpha-v beta-3 comprise C-terminal fragments (see AAW41083-94) of human
CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see
CC also AAW41098-110), derivatised polypeptides, a monoclonal antibody or
CC organic mimetic compound. The antagonists are used to inhibit
CC angiogenesis in: inflamed tissue for treatment of arthritis or
CC rheumatoid arthritis; solid tumours or metastases, particularly to induce
CC tumour regression or inhibit growth of tumours; and in ocular disorders
CC such as diabetic retinopathy or macular degeneration (all claimed). They
CC can also be used to treat restenosis caused by migration of smooth muscle
CC cells following angioplasty and to reduce blood supply to selected
CC tissues (claimed). The new antagonists are highly selective for
CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature
CC vessels are unaffected, and the antagonists should be of low toxicity
XX
SQ Sequence 228 AA;
Query Match 100.0%; Score 29; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
DB 99 KAVFFA 104
RESULT 47
AAW41234
ID AAW41234 standard; protein; 228 AA.
XX
AC AAW41234;
AC
DT 09-JUN-1998 (first entry)
XX
DE Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.
XX
DE Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
KW restenosis; neovascularisation.
XX
OS Synthetic.
XX
OS Gallus sp.
XX
PN WO9745447-A1.
XX
PD 04-DEC-1997.
XX
PF 30-MAY-1997; 97WO-US009099.
XX
PR 31-MAY-1996; 96US-0015869P.
XX
PR 31-MAY-1996; 96US-0018733P.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Brooks P, Cheres DA, Friedlander M;
XX
PI WPI; 1998-041758/04.
XX
DR Packaging material containing polypeptide antagonist of alphav, beta5
XX integrin - used for inhibition of angiogenesis, and for treating tumours,
XX inflammation, eye diseases etc.
XX
PS Claim 2; Page; 117pp; English.
XX
CC Peptides AAW41234-39 are derived from the chicken matrix metalloproteinase-
CC 2 (MMP-2) protein (AAW41227). The present peptide is derived from amino
CC acids 410-637. The peptides are able to act as alpha-v-beta-5
CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
CC tumours or metastases, and in a wide range of ocular disorders (e.g.
CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
CC transplants). They are particularly used to induce regression or to
CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
CC used to treat restenosis caused by migration of smooth muscle cells
CC following angioplasty and to reduce blood supply to selected tissues. The
CC antagonists particularly inhibit neovascularisation where this is induced
CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
CC factor or especially vascular endothelial growth factor. note: this
CC sequence does not appear in the specification; it was created using
CC information provided
XX
SQ Sequence 228 AA;
Query Match 100.0%; Score 29; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
DB 125 KAVFFA 130
RESULT 48
ADT05969
ID ADT05969 standard; protein; 228 AA.
XX
AC ADT05969;
AC
XX

```

```

DT XX 30-DEC-2004 (first entry)
DE XX Chicken matrix metalloprotease (MMP-2) residues 410-637, SEQ ID NO:23.
XX XX
KW XX Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
KW XX vitronectin receptor antagonist; neovascularisation; cancer; tumour;
KW XX inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
KW XX restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
KW XX cytosolic; antiinflammatory; antiarthritic; antirheumatic;
KW XX ophthalmological; antidiabetic; vasotropic; muscular-gen.;
KW XX peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
KW XX hemopexin domain; cell attachment assay; ligand binding assay; chicken.
OS XX Gallus gallus.
XX XX
XX XX WO2004087057-A2.
XX XX
XX XX 14-OCT-2004.
XX XX
XX XX 26-MAR-2004; 2004WO-US009321.
XX XX
XX XX 28-MAR-2003; 2003US-00402212.
XX XX
XX XX (SCRI ) SCRIPPS RES INST.
XX XX
XX XX Brooks PC, Cheresh DA;
XX XX
XX XX WPI; 2004-737508/72.
XX XX
XX XX Administration of composition comprising organic peptidomimetic alpha-v
XX XX beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
XX XX angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
XX XX
XX XX Example 1A; SEQ ID NO 23; 184pp; English.
XX XX
XX XX The invention relates to a method of inhibiting angiogenesis in a tissue
XX XX by the administration of a composition comprising an organic
XX XX peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
XX XX receptor). The integrin alpha-v beta-3 antagonist and compositions
XX XX containing it are useful for inhibiting angiogenesis in a variety of
XX XX medical conditions. The antagonist may be used to induce the regression
XX XX of solid tumours or solid tumour metastases; to inhibit the growth of
XX XX solid tumours undergoing neovascularisation; to treat inflamed tissue in
XX XX which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
XX XX treat neovascularisation in retinal tissue (e.g., in diabetic
XX XX retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
XX XX cell migration (such as that which occurs following angioplasty); and to
XX XX reduce the blood supply to a tissue required to support new growth of the
XX XX tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
XX XX domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,
XX XX gelatinase) used in an example of the invention in assays of inhibition
XX XX of integrin alpha-v beta-3-mediated cell attachment and of ligand-
XX XX receptor binding.
XX XX
XX XX Sequence 228 AA;
XX XX
XX XX Query Match 100.0%; Score 29; DB 8; Length 228;
XX XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX QY 1 KAVFFFA 6
XX XX |||||
XX XX 99 KAVFFFA 104
XX XX
XX XX RESULT 49
XX XX ADT05661
XX XX ID ADT05661 standard; protein; 261 AA.
XX XX
XX XX AC ADT05661;
XX XX
XX XX 02-DEC-2004 (first entry)
XX XX
XX XX

```

```

DE XX Haemophilus influenzae (NTHi) protein - SEQ ID 697.
XX XX
XX XX middle ear bacterial infection; nasopharynx bacterial infection.
XX XX
XX XX Haemophilus influenzae.
XX XX
XX XX WO2004078949-A2.
XX XX
XX XX 16-SEP-2004.
XX XX
XX XX 05-MAR-2004; 2004WO-US007001.
XX XX
XX XX 06-MAR-2003; 2003US-0453134P.
XX XX
XX XX (CHIL-) CHILDRENS HOSPITAL INC.
XX XX
XX XX Bakaletz LO, Munson RS, Dyer DW;
XX XX
XX XX WPI; 2004-662422/64.
XX XX
XX XX N-PSDB; ADT05660.
XX XX
XX XX New polynucleotides of nontypeable strain of Haemophilus influenzae,
XX XX useful for treating or preventing NTHi bacterial infections of the middle
XX XX ear and/or nasopharynx.
XX XX
XX XX Claim 3; SEQ ID NO 697; 88pp; English.
XX XX
XX XX The invention comprises nucleotide sequences (genes) from the genome of a
XX XX nontypeable strain of Haemophilus influenzae (NTHi). The NTHi DNA
XX XX sequences of the invention are useful for treating or preventing NTHi
XX XX bacterial infections of the middle ear and/or nasopharynx. The present
XX XX amino acid sequence represents an NTHi protein of the invention.
XX XX
XX XX Sequence 261 AA;
XX XX
XX XX Query Match 100.0%; Score 29; DB 8; Length 261;
XX XX Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX QY 1 KAVFFFA 6
XX XX |||||
XX XX 205 KAVFFFA 210
XX XX
XX XX RESULT 50
XX XX AAW41112
XX XX ID AAW41112 standard; protein; 429 AA.
XX XX
XX XX AC AAW41112;
XX XX
XX XX 08-JUN-1998 (first entry)
XX XX
XX XX Human matrix metalloproteinase huMMP-2 (aa203-631).
XX XX
XX XX Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;
XX XX antagonist; integrin alpha-v beta-3; vitronectin receptor;
XX XX rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;
XX XX macular degeneration; restenosis; therapy.
XX XX
XX XX Homo sapiens.
XX XX
XX XX WO9745137-A1.
XX XX
XX XX 04-DEC-1997.
XX XX
XX XX 30-MAY-1997; 97WO-US009158.
XX XX
XX XX 31-MAY-1996; 96US-0015869P.
XX XX
XX XX 31-MAY-1996; 96US-0018733P.
XX XX
XX XX (SCRI ) SCRIPPS RES INST.
XX XX
XX XX Brooks P, Cheresh DA;
XX XX

```

XX
DR WPI; 1998-032334/03.
XX
PT Packaging material containing polypeptide antagonist of alphav, beta3
PT integrin - used for inhibition of angiogenesis, and for treating tumours,
PT inflammation, eye diseases etc.
XX
PS Example 4; Page 177-179; 234pp; English.
XX
CC This polypeptide comprises amino acid residues 203-631 of human mature
CC matrix metalloproteinase 2 (hMMP-2). It was produced by recombinant
CC methods involving PCR amplification (see AAV12509) of hMMP-2 coding
CC sequence and cloning into e.g. pGEX-lambda vector for expression in E.
CC coli as a glutathione-S-transferase fusion protein. The invention relates
CC to the discovery that angiogenesis is mediated by the specific
CC vitronectin receptor alpha-v beta-3, and that inhibition of alpha-v beta-
CC 3 function inhibits angiogenesis. Claimed antagonists of alpha-v beta-
CC 2, fusion polypeptides, cyclic or linear polypeptides (see also AAW41098-
CC 110), derivatised polypeptides, a monoclonal antibody or organic mimetic
CC compound. The antagonists are used to inhibit angiogenesis in: inflamed
CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours
CC or metastases, particularly to induce tumour regression or inhibit growth
CC of tumours; and in ocular disorders such as diabetic retinopathy or
CC macular degeneration (all claimed). They can also be used to treat
CC restenosis caused by migration of smooth muscle cells following
CC angioplasty and to reduce blood supply to selected tissues (claimed). The
CC new antagonists are highly selective for angiogenesis. Only new blood
CC vessels express alpha-v beta-3, so mature vessels are unaffected, and the
CC antagonists should be of low toxicity
XX
SQ Sequence 429 AA;
Query Match 100.0%; Score 29; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFFA 6
Db 300 KAVFFFA 305
|||||
RESULT 51
ADT05991
ID ADT05991 standard; protein; 429 AA.
AC
AC ADT05991;
XX
DT 30-DEC-2004 (first entry)
XX
DE Human matrix metalloprotease (MMP-2) residues 203-631, SEQ ID NO:45.
XX
KW Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
KW cytostatic; antiinflammatory; antiarthritic; antirheumatic;
KW ophthalmologic; antidiabetic; vasotropic; muscular-gen;
KW peptidomimetic; matrix metalloprotease 2; MMP-2; progelatinase; human;
KW C-terminal fragment; glutathione-S-transferase; GST fusion protein.
XX
OS Homo sapiens.
XX
XX WO2004087057-A2.
XX
XX 14-OCT-2004.
XX
XX 26-MAR-2004; 2004WO-US009321.
PF
XX 28-MAR-2003; 2003US-00402212.
PR
XX (SCRI) SCRIPPS RES INST.
PA
XX

PI Brooks PC, Chersesh DA;
XX
DR WPI; 2004-737508/72.
XX
CC Administration of composition comprising organic peptidomimetic alpha-v
PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
XX
PS Example 2; SEQ ID NO 45; 184pp; English.
XX
CC The invention relates to a method of inhibiting angiogenesis in a tissue
CC by the administration of a composition comprising an organic
CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
CC receptor). The integrin alpha-v beta-3 antagonist and compositions
CC containing it are useful for inhibiting angiogenesis in a variety of
CC medical conditions. The antagonist may be used to induce the regression
CC of solid tumours or solid tumour metastases; to inhibit the growth of
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
CC treat neovascularisation in retinal tissue (e.g., in diabetic
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
CC cell migration (such as that which occurs following angioplasty); and to
CC reduce the blood supply to a tissue required to support new growth of the
CC tissue. The present sequence represents residues 203-631 of human MMP-2
CC which is a component of a glutathione-S-transferase (GST)/MMP-2 fusion
CC protein produced in an example of the invention.
XX
SQ Sequence 429 AA;
Query Match 100.0%; Score 29; DB 8; Length 429;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFFA 6
Db 300 KAVFFFA 305
|||||
RESULT 52
ABG24001
ID ABG24001 standard; protein; 468 AA.
XX
AC ABG24001;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #23992.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
XX WO200175067-A2.
PN
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS88188.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX PS Claim 20; SEQ ID NO 54360; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridization probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activities. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 468 AA;

Query Match 100.0%; Score 29; DB 4; Length 468;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
 |||||
 Db 361 KAVFFFA 366

RESULT 53

ABM84057

ID ABM84057 standard; protein; 623 AA.

XX AC ABM84057;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:4306.

XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX OS Homo sapiens.

XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Deleane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Legace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D; Patury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

DR N-PSDB; ACN42709.

XX

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.

XX Claim 27; Page; 190pp; English.

XX CC The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX SQ Sequence 623 AA;

Query Match 100.0%; Score 29; DB 8; Length 623;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
 |||||
 Db 494 KAVFFFA 499

RESULT 54

ADG17622

ID ADG17622 standard; protein; 626 AA.

XX AC ADG17622;

XX DT 26-FEB-2004 (first entry)

XX DE Modified amyloid beta precursor protein-related fusion protein SeqID13.

XX KW amyloid beta precursor protein; APP; beta-selectase cleavage; alpha-selectase cleavage; Alzheimer's disease; dementia.

XX OS Unidentified.

XX PN WO2003102177-A1.

XX PD 11-DEC-2003.

XX PF 21-MAY-2003; 2003WO-JP006319.

XX PR 31-MAY-2002; 2002JP-00159472.

XX PA (SAKA) OTSUKA PHARM CO LTD.

XX PI Shimabuku A, Ogino K, Taki T, Shin R, Kitamoto T; WPI; 2004-053473/05.

XX PT Amyloid beta precursor protein cleaved by beta- but not alpha-selectase for screening for treatments for Alzheimer's disease.

XX PS Claim 15; SEQ ID NO 13; 89pp; Japanese.

XX CC This invention relates to a novel modified amyloid beta precursor protein (APP) which contains a beta-selectase cleavage site and a modification which prevents cleavage by alpha-selectase. The invention may be useful for screening for, treating and preventing Alzheimer's disease and

CC dementia. The present sequence is that of a protein which is related to
 CC the modified amyloid beta precursor proteins of the invention.

XX Sequence 626 AA;
 SQ Query Match 100.0%; Score 29; DB 8; Length 626;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 543 KAVFFA 548

RESULT 55

ADG17627
 ID ADG17627 standard; protein; 626 AA.

AC ADG17627;

XX 26-FEB-2004 (first entry)

XX Modified amyloid beta precursor protein-related fusion protein SeqID18.

XX amyloid beta precursor protein; APP; beta-selectase cleavage;

KW alpha-selectase cleavage; Alzheimer's disease; dementia.

XX Unidentified.

OS

XX WO2003102177-A1.

XX 11-DEC-2003.

XX 21-MAY-2003; 2003WO-JP006319.

XX 31-MAY-2002; 2002JP-00159472.

XX (SAKA) OTSUKA PHARM CO LTD.

XX Shimabuku A, Ogino K, Taki T, Shin R, Kitamoto T;

XX WPI; 2004-053473/05.

XX Amyloid beta precursor protein cleaved by beta- but not alpha-selectase
 PT for screening for treatments for Alzheimers disease.
 PS Claim 16; SEQ ID NO 18; 89pp; Japanese.

XX This invention relates to a novel modified amyloid beta precursor protein
 CC (APP) which contains a beta-selectase cleavage site and a modification
 CC which prevents cleavage by alpha-selectase. The invention may be useful
 CC for screening for, treating and preventing Alzheimer's disease and
 CC dementia. The present sequence is that of a protein which is related to
 CC the modified amyloid beta precursor proteins of the invention.

XX Sequence 626 AA;

Query Match 100.0%; Score 29; DB 8; Length 626;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 543 KAVFFA 548

RESULT 56

AAP96143
 ID AAP96143 standard; protein; 631 AA.

XX AAP96143;

XX 25-MAR-2003 (revised)

DT

DT 09-MAY-1991 (first entry)
 XX Sequence of human type IV collagenase (gelatinase) in pGEL 186.2.
 XX Hypertrophic scar; keloid; intervertebral disc disease; enzyme.

XX Homo sapiens.

XX GB2209526-A.

XX 17-MAY-1989.

XX 02-SEP-1988; 86GB-00820803.

XX 04-SEP-1987; 87US-00093421.

XX (UNIW) UNIV WASHINGTON.

XX Eisen AZ, Goldberg GI;

XX WPI; 1989-147011/20.

XX N-PSDB; AAN91700.

XX DNA encoding human type IV collagenase (gelatinase) - for use in the

XX treatment of hypertrophic scars, keloids and intervertebral disc disease.

XX Disclosure; Fig 3; 36pp; English.

XX The original source of the protein material was H-ras transformed human

XX bronchial epithelial cells (TBE-1). The AA sequence was then used to

XX develop oligonucleotide probes which were used to screen a cDNA library

XX of human skin fibroblast mRNA. The longest clone, pGEL 186.2, represented

XX almost the full gelatinase mRNA sequence except the leader sequence

XX encoding the first few AA's of the signal peptide. (Updated on 25-MAR-

XX 2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)

XX (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 631 AA;

Query Match 100.0%; Score 29; DB 1; Length 631;

Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||

Db 502 KAVFFA 507

RESULT 57

AAP91139

ID AAP91139 standard; protein; 631 AA.

XX AAP91139;

XX 25-MAR-2003 (revised)

XX 18-DEC-1989 (first entry)

XX Human type IV collagenase (gelatinase).

XX Human type IV collagenase; gelatinase; hypertrophic scars; keloids;

XX intervertebral disc disease; extracellular matrix metalloprotease;

XX bronchial epithelial cells; TBE-1 cells; pGEL186.2; type II motif;

XX fibonectin; collagen-binding domain.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..192

FT Domain 193..367

FT Duplication 197..254

FT Duplication 255..312

FT Duplication 313..368

FT Domain 368..631

XX GB2209526-A.
 XX 17-MAY-1989.
 XX 02-SEP-1988; 88GB-00820803.
 XX 04-SEP-1987; 87US-00093421.
 XX (UNIW) UNIV WASHINGTON.
 XX Eisen AZ, Goldberg GI;
 XX WPI; 1989-147011/20.
 XX DNA encoding human type IV collagenase (gelatinase) - for use in the
 XX treatment of hypertrophic scars, keloids and intervertebral disc disease.
 XX Claim 2; Fig 6; 36pp; English.
 XX Human type IV collagenase (gelatinase). Protein source was H-ras
 XX transformed human bronchial epithelial cells (TBE-1). The sequence was
 XX determined from clone pGel 186.2 which represents almost the full mRNA
 XX sequence. Feature 1 is the N-terminal domain, I; feature 2 is a middle
 XX domain, II, which is organised into 3 x 58 amino acid long head to tail
 XX repeats (features 4,5, and 6). These show homology to the type II motif
 XX collagen binding domain of fibronectin. Feature 3 is the C-terminal
 XX domain. The enzyme could be used in the treatment of hypertrophic scars,
 XX keloids, and intervertebral disc disease. See also AAN91700. (Updated on
 XX 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA
 XX field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX SQ Sequence 631 AA;

Query Match 100.0%; Score 29; DB 1; Length 631;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||||
 Db 502 KAVFFA 507

RESULT 58
 AAR07969
 ID AAR07969 standard; protein; 631 AA.

AC AAR07969;
 DT 25-MAR-2003 (revised)
 DT 17-DEC-2001 (revised)
 DT 16-JAN-1991 (first entry)

DE Complete type IV collagenase.

XX Type IV collagenase; peptide fragments; metalloproteinase detection;
 KW antibodies; metalloproteinase inhibition; angiogenesis; arthritis;
 KW tumour growth; metastasis; granulomatous inflammatory conditions;
 KW sarcoidosis.

OS Homo sapiens.

FH Key Location/Qualifiers
 FT Peptide 1. .18
 FT Peptide /label= 1
 FT Peptide 19. .33
 FT Peptide /label= 2
 FT Peptide 26. .42
 FT Peptide /label= 3
 FT Protein 34. .50
 FT Peptide /label= 4
 FT Peptide 51. .66
 FT Peptide /label= 5

FT Peptide 57. .89
 FT Peptide /label= 7
 FT Peptide 67. .80
 FT Peptide /label= 6
 FT Peptide 69. .75
 FT Peptide /label= 8
 FT Peptide 75. .94
 FT Peptide /label= 9
 FT Peptide 141. .150
 FT Peptide /label= 10
 FT Peptide 299. .307
 FT Peptide /label= 11
 FT Peptide 308. .318
 FT Peptide /label= 12
 FT Peptide 344. .368
 FT Peptide /label= 13
 FT Peptide 371. .386
 FT Peptide /label= 14
 FT Peptide 372. .375
 FT Peptide /label= 15
 FT Peptide 472. .491
 FT Peptide /label= 16

USN7317407-N.

21-AUG-1990.

01-MAR-1989; 89US-00317407.

01-MAR-1989; 89US-00317407.

(USSH) US NAT CANCER INST.

(USDC) US SEC OF COMMERCE.

Liotta LA, Stetlerste W, Krutzsch H;

WPI; 1990-290093/38.

New type-IV collagenase peptide fragments - used for metallo-proteinase
 detection and inhibition and for producing antibodies for enzyme
 detection.

Disclosure; Fig 1; -pp; English.

XX Type IV procollagenase was purified from human A2058 melanoma cells. The
 CC complete amino acid sequence was determined (see also Hoyhtya, M. et al,
 CC (1988) FEBS Letters 233, 109-113). Based on this sequence, peptides were
 CC synthesised (see features) having homology with a histidine contg. domain
 CC at residues 371-386, a cysteine contg. domain at residues 200-370, the 80
 CC residue amino terminus or a region 159 residues from the carboxy
 CC terminus. These regions correspond to the domain of the enzyme involved
 CC in enzyme activation and interaction of the enzyme with the substrate.
 CC The peptides are useful in metalloproteinase detection and inhibition.
 CC They can be used in the treatment of inappropriate angiogenesis,
 CC arthritis, tumour growth, invasion and metastasis and granulomatous
 CC inflammatory conditions such as sarcoidosis. The peptides can be used to
 CC produce antibodies. Peptide 6, at concn. of 0.1 mM inhibited 80% of the
 CC enzyme activity. See also US7494796-A and WO9010228. (Note: Revised entry
 CC submitted to correct the patent number format of US Government-owned NTIS
 CC applications to prevent clashes with ongoing US granted patent numbers.
 CC for further information please visit the Derwent web site at
 CC www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-MAR-2003 to
 CC correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX SQ Sequence 631 AA;

Query Match 100.0%; Score 29; DB 2; Length 631;

Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

|||||

Db 502 KAVFFA 507

```

DE XX Human mature matrix metalloprotease-2 (MMP-2) protein sequence.
KW Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
KW vitronectin receptor; inhibition; angiogenesis; integrin; tumour growth;
KW restenosis; neovascularisation.
XX OS Homo sapiens.
XX PN W09745447-A1.
XX PD 04-DEC-1997.
XX PF 30-MAY-1997; 97WO-US009099.
XX PR 31-MAY-1996; 96US-0015869P.
XX PR 31-MAY-1996; 96US-0018733P.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Brooks P, Chereah DA, Friedlander M;
XX WPI; 1998-041758/04.
XX PT Packaging material containing polypeptide antagonist of alphav, beta5
XX integrin - used for inhibition of angiogenesis, and for treating tumours,
XX inflammation, eye diseases etc.
XX PS Disclosure; Fig 16; 117pp; English.
XX CC The present sequence represents the mature protein of human matrix
XX metalloprotease-2 (MMP-2). Fragments of this protein (AAW41228-33) are
XX able to act as alpha-v-beta-5 antagonists. Alpha-v-beta-5 is a
XX vitronectin receptor. Inhibitors of alpha-v-beta-5 can inhibit
XX angiogenesis. The specification describes a novel labelled package that
XX contains an inhibitor of angiogenesis i.e. an alpha-v-beta-5 antagonising
XX polypeptide that binds to integrin alpha-v-beta-5 and includes a part of
XX the C-terminal domain of MMP. The antagonists are used to inhibit
XX angiogenesis in inflamed tissue, in solid tumours or metastases, and in a
XX wide range of ocular disorders (e.g. diabetic or other forms of
XX retinopathy, neovascular glaucoma, or corneal transplants). They are
XX particularly used to induce regression or to inhibit growth of tumours.
XX The alpha-v-beta-5 antagonists can also be used to treat restenosis
XX caused by migration of smooth muscle cells following angioplasty and to
XX reduce blood supply to selected tissues. The antagonists particularly
XX inhibit neovascularisation where this is induced by cytokines, e.g.
XX transforming growth factor alpha, epidermal growth factor or especially
XX vascular endothelial growth factor
XX SQ Sequence 631 AA;
Query Match 100.0%; Score 29; DB 2; Length 631;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 502 KAVFFA 507
|||||

RESULT 61
ADM48668
ID ADM48668 standard; protein; 631 AA.
XX AC ADM48668;
XX XX
XX DT 03-JUN-2004 (first entry)
XX DE Human matrix metalloprotease-2 (MMP-2) protein.
XX KW Cancer; metastasis; matrix metalloprotease-2; MMP-2; vaccine;
XX immune response; gene therapy; cytostatic; enzyme; human.
XX OS Homo sapiens.

RESULT 59
AAY07350
ID AAY07350 standard; protein; 631 AA.
XX AC AAY07350;
XX DT 25-MAR-2003 (revised)
XX DT 16-JUL-1999 (first entry)
XX DE Human type IV matrix metalloprotease protein.
XX KW Matrix metalloprotease; inhibitor; tissue damage; angiogenesis; antibody;
XX arthritis; tumour growth; granulomatous inflammatory condition; enzyme;
XX KW metastasis; sarcoidosis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 452
XX FT /note= "designated in specification as U"
XX PN W09010228-A.
XX PD 07-SEP-1990.
XX PF 01-MAR-1989; 89US-00317407.
XX PR 01-MAR-1989; 89US-00317407.
XX PR 26-FEB-1990; 90US-00488460.
XX PA (USDC ) US SEC OF COMMERCE.
XX PA (USSH ) NAT INST OF HEALTH.
XX PI Liotta LA, Stetlerste W, Krutzsh H;
XX WPI; 1990-290458/38.
XX DR Matrix metalloproteinase peptide(s) - used to inhibit enzyme in treating
XX tissue damage caused by activated enzyme.
XX PS Disclosure; Fig 1; 61pp; English.
XX CC This sequence represents a human type IV matrix metalloprotease (MMP)
XX zymogen (precursor protein). The invention relates to MMP inhibitor
XX peptides which can be used to treat tissue damage caused by activated
XX MMPs, e.g. for treating inappropriate angiogenesis, arthritis, tumour
XX growth, invasion and metastasis and granulomatous inflammatory conditions
XX such as sarcoidosis. Antibodies to the peptides can be used to detect the
XX MMPs and can distinguish activated from latent enzyme. (Updated on 25-MAR
XX -2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
XX (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 631 AA;
Query Match 100.0%; Score 29; DB 2; Length 631;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 502 KAVFFA 507
|||||

RESULT 60
AAW41226
ID AAW41226 standard; protein; 631 AA.
XX AC AAW41226;
XX XX
XX DT 09-JUN-1998 (first entry)
XX DE

```


KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase; mouse;
 KW murine; enzyme.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Domain 441..633
 FT /label = Hemopexin_domain
 XX
 PN WO2004087057-A2.
 XX
 PD 14-OCT-2004.
 XX
 XX 26-MAR-2004; 2004WO-US009321.
 XX
 XX 28-MAR-2003; 2003US-00402212.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 XX Brooks PC, Chereah DA;
 XX
 XX WPI; 2004-737508/72.
 XX
 XX Administration of composition comprising organic peptidomimetic alpha-v
 PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
 XX
 XX Example 2; Fig 7A-C; 184pp; English.
 XX
 XX The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression
 CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC treat neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat neovascularisation in retinal tissue (e.g., in diabetic
 CC retinopathy); to treat stenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to
 CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. The present sequence represents mouse mature matrix
 CC metalloprotease 2 (MMP-2, gelatinase) used in an example of the
 CC invention.
 XX
 XX Sequence 633 AA;
 SQ
 Query Match 100.0%; Score 29; DB 8; Length 633;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFFA 6
 Db 504 KAVFFFA 509
 |||||
 RESULT 64
 AAB20490
 ID AAB20490 standard; protein; 644 AA.
 XX
 XX AAB20490;
 AC
 DT 21-JUN-2001 (first entry)
 XX
 XX Human matrix metalloprotease-2 (MMP-2).
 DE
 XX Matrix metalloprotease-2; MMP-2; human; pain; analgesic;
 KW nerve tissue damage; stroke; haemorrhage; reperfusion injury;
 KW cerebral ischaemia; cerebral infarction; narcotic tolerance;
 KW narcotic withdrawal.
 XX

OS Homo sapiens.
 XX WO200126671-A1.
 XX
 XX 19-APR-2001.
 XX
 XX 11-OCT-2000; 2000WO-US027949.
 XX
 XX 12-OCT-1999; 99US-0158787P.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Romanic Arnold A, Barone FC, Bingham S;
 XX
 XX WPI; 2001-290654/30.
 DR N-PSDB; AAF30807.
 XX
 XX Polypeptide for the treatment of pain and the reduction of tissue damage
 PT comprises an inhibitor of human matrix metalloprotease.
 PT
 XX Claim 1; Fig 2; 61pp; English.
 XX
 XX The present sequence is that of human matrix metalloprotease-2 (MMP-2),
 CC previously known as 72 kDa gelatinase and gelatinase A. MMP-2 is capable
 CC of degrading the extracellular matrix components of the basement
 CC membrane. The invention relates to methods for treating pain in a patient
 CC by administering a dual inhibitor of MMP-2 and MMP-9 (see AAB20491). The
 CC administration of an inhibitor of MMP-2 is useful for treating nerve
 CC tissue damage (claimed), where the patient is suffering from a disease or
 CC disorder selected from stroke, haemorrhage, reperfusion injury, cerebral
 CC ischaemia and cerebral infarction (claimed). The method is useful for
 CC treating a disease, disorder or nerve tissue damage selected from
 CC enhanced or exaggerated sensitivity to acute pain, burn pain, atypical
 CC facial pain, neuropathic pain, back pain, complex regional pain syndrome
 CC I and II, arthritic pain, sports injury pain, pain related to virus
 CC infection, post-herpetic neuralgia, phantom limb pain, labour pain,
 CC cancer pain, post-chemotherapy pain, post-operative pain, post-stroke
 CC pain, physiological pain, inflammatory pain, acute inflammatory
 CC conditions/visceral pain, neuralgia, painful diabetic retinopathy,
 CC traumatic nerve injury, and tolerance to narcotics or withdrawal from
 CC narcotics (claimed). MMP-2 polypeptides can also be used to screen for
 CC agonist or antagonist (inhibitor) compounds
 XX
 XX Sequence 644 AA;
 SQ
 Query Match 100.0%; Score 29; DB 4; Length 644;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFFA 6
 Db 515 KAVFFFA 520
 |||||
 RESULT 65
 AAR06420
 ID AAR06420 standard; protein; 660 AA.
 XX
 XX AAR06420;
 AC
 XX 25-MAR-2003 (revised)
 DT 13-DEC-1990 (first entry)
 XX
 XX Type IV collagenase cDNA product.
 DE
 XX hypertrophic scars; keloids; intervertebral disc disease; ds.
 KW
 XX Homo sapiens.
 OS
 XX US4923818-A.
 PN
 XX 08-MAY-1990.
 PD

XX PF 15-MAY-1989; 89US-00352069.
 XX PR 15-MAY-1989; 89US-00352069.
 XX PA (UNIW) UNIV WASHINGTON.
 XX PI Goldberg GL, Eisen AZ;
 XX DR WPI; 1990-245482/32.
 XX DR N-PSDB; AAO05620.
 XX PT Recombinant human type IV collagenase - used in treatment of hypertrophic
 PT scars, keloids and intervertebral disc disease.
 XX PS Claim 3; Fig 9; 23pp; English.
 CC cDNA clone enables production of type IV collagenase, useful in
 CC catalyzing cleavage of extracellular matrix macromolecules, and in
 CC treatment of hypertrophic scars, keloids and intervertebral disc disease.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX SQ Sequence 660 AA;
 Query Match 100.0%; Score 29; DB 2; Length 660;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KAVFFA 6
 Db 531 KAVFFA 536
 RESULT 66
 AAB84607
 ID AAB84607 standard; protein; 660 AA.
 AC AAB84607;
 XX 05-SEP-2001 (first entry)
 DT
 DE Amino acid sequence of matrix metalloproteinase gelatinase A.
 XX Growth factor; protein inhibitor; protease; damaged tissue;
 KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
 KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;
 KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
 KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
 KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
 KW vascular endothelial growth factor; urokinase plasminogen activator;
 KW dermal ulcer; wound.
 XX Homo sapiens.
 OS
 XX WO200149309-A2.
 FN
 XX 12-JUL-2001.
 PD
 XX 21-DEC-2000; 2000WO-IB001935.
 PF
 XX 29-DEC-1999; 99GB-00030768.
 PR (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 XX Davies MJ, Huggins JP, McIntosh PS, Occleston NL;
 PI WPI; 2001-418351/44.
 DR N-PSDB; AAB28222.
 XX Composition for the treatment of damaged tissue i.e. chronic wounds and
 PT dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
 PT factor.

XX PS Disclosure; Page 552; 572pp; English.
 XX The specification describes a pharmaceutical composition, comprising a
 CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
 CC inhibits the action of at least one specific adverse protein, i.e. a
 CC protease, that is upregulated in a damaged tissue such as a wound
 CC environment. Growth factors which are included in the composition of the
 CC invention are platelet-derived growth factor (PDGF), fibroblast growth
 CC factor (FGF), connective tissue derived growth factor (CTGF),
 CC keratinocyte-derived growth factor (KGF), transforming growth factor-beta
 CC (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),
 CC epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),
 CC and chrysalin. Inhibitors which are included in the composition of the
 CC invention include inhibitors of urokinase-type plasminogen activator
 CC (uPA) and matrix metalloproteinase (MMP). The composition is useful for
 CC the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
 CC The present sequence represents a human MMP-2, and is used to produce the
 CC composition of the invention
 XX SQ Sequence 660 AA;
 Query Match 100.0%; Score 29; DB 4; Length 660;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KAVFFA 6
 Db 531 KAVFFA 536
 RESULT 67
 AAE10431
 ID AAE10431 standard; protein; 660 AA.
 AC AAE10431;
 XX 10-DEC-2001 (first entry)
 DT
 DE Human matrix metalloproteinase-2 (MMP-2) protein.
 XX Human; matrix metalloproteinase; MMP-2; hair growth; antisense therapy;
 KW endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT Peptide 1..27
 FT Protein /label= Signal_peptide
 FT Domain 28..660
 FT Domain /label= Mature_MMP_2_protein
 FT Domain 100..106
 FT Domain /label= Cysteine_switch_domain
 FT Domain 171..195
 FT /note= "Zinc and calcium binding domain"
 XX WO200166766-A2.
 FN
 XX 13-SEP-2001.
 PD
 XX 06-MAR-2001; 2001WO-US007167.
 PF
 XX 06-MAR-2000; 2000US-0187196P.
 PR (DARW-) DARWIN MOLECULAR CORP.
 PA (SCHA/) SCHATZMAN R.
 XX Fajardo M, Wang K, Smith R, Moss P;
 PI WPI; 2001-582276/65.
 DR Novel isolated matrix metalloproteinase-25 nucleic acid molecule and
 PT proteins encoded by them whose inhibition is useful for modulation of

PR 11-APR-2001; 2001US-0282850P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI St Croix B, Kinzler KW, Vogelstein B;
 XX
 DR WPI; 2002-291856/33.
 DR N-PSDB; ABL92092.
 XX
 XX An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth.
 PT
 XX Claim 54; Page 166-168; 31pp; English.
 PS
 CC The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects
 CC bearing a vascularised tumour, polycystic kidney disease, diabetic
 CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
 CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
 CC are disclosed, as are marker oligonucleotide sequences: tumour
 CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
 CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
 CC (PEM) ABL91903-ABL91995
 XX
 SQ Sequence 660 AA;
 Query Match 100.0%; Score 29; DB 5; Length 660;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 DB |||||
 531 KAVFFA 536
 RESULT 70
 AAU84348
 ID AAU84348 standard; protein; 660 AA.
 AC AAU84348;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Protein MMP2 differentially expressed in breast cancer tissue.
 XX
 KW Human; diagnosis of breast cancer; endometrial cancer; breast tumour;
 KW MAI; mitotic activity index; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200210436-A2.
 XX
 PD 07-FEB-2002.
 XX
 PP 27-JUL-2001; 2001WO-US023642.
 XX
 PR 28-JUL-2000; 2000US-0222093P.
 XX
 PA (BQHM) BRIGHAM & WOMENS HOSPITAL INC.
 PA (BAAK/) BAAK J.
 XX
 FI Baak J, Mutter GL;
 XX
 DR WPI; 2002-180084/23.
 DR N-PSDB; ABK35568.
 XX
 PT Diagnosing breast cancer comprises determining expression of nucleic acid
 PT molecules or expression products that are differentially expressed in

PT normal and malignant tissue.
 XX
 PS Claim 37; Page 185-187; 219pp; English.
 XX
 CC The present invention relates to a method for diagnosing breast cancer in
 CC a subject suspected of having endometrial cancer. The method comprises
 CC determining the expression of a set of human genes or expression products
 CC in an endometrial sample suspected of being cancerous. The human genes of
 CC the invention are differentially expressed in breast tumours
 CC characterised as high or low MAI (mitotic activity index). These sets of
 CC genes can be used to discriminate between high and low MAI breast
 CC tumours. The invention also provides DNA and protein microarrays for
 CC analysing the expression of the human genes and their protein products.
 CC The methods and arrays are useful for the diagnosis and prognosis of
 CC endometrial cancer, selecting and monitoring treatment regimes, and
 CC identification of compounds useful for the treatment of endometrial
 CC cancer. AAU84311-AAU84361 represent the human proteins of the invention
 CC that are differentially expressed in breast cancer tissue
 XX
 SQ Sequence 660 AA;
 Query Match 100.0%; Score 29; DB 5; Length 660;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 DB |||||
 531 KAVFFA 536
 RESULT 71
 ABU54445
 ID ABU54445 standard; protein; 660 AA.
 XX
 AC ABU54445;
 XX
 DT 12-MAR-2003 (first entry)
 XX
 DE Human tumour endothelial marker TEM 7.
 XX
 KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
 KW Tumour endothelial marker; normal endothelial marker; PEM;
 KW pan-endothelial marker; polycystic kidney disease; psoriasis;
 KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
 KW neoangiogenesis; immune response; cytostatic; antidiabetic;
 KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200283874-A2.
 XX
 PD 24-OCT-2002.
 XX
 PP 10-APR-2002; 2002WO-US008253.
 XX
 PR 11-APR-2001; 2001US-0282850P.
 PR 06-FEB-2002; 2002US-0354262P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
 XX
 DR WPI; 2003-093016/08.
 DR N-PSDB; ABX72017.
 XX
 PT New purified human transmembrane protein, designated as tumor endothelial
 PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
 PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
 PT psoriasis.
 XX
 PS Disclosure; Page 173-174; 374pp; English.
 XX
 CC The present invention relates to a novel method for the isolation of

CC endothelial cells (ECs), and the identification of genes expressed in
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
 CC identified in human ECs. The human EC marker proteins and the
 CC polynucleotide sequences encoding them are useful for detecting,
 CC diagnosing or treating tumours as well as polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
 CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for
 CC inducing an immune response to tumour endothelial cells in a patient, or
 CC for identifying candidate drugs for treating tumours. The present
 CC sequence represents a human TEM or NEM protein of the invention
 XX
 SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 6; Length 660;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 531 KAVFFA 536

RESULT 72
 ABP97136
 ID ABP97136 standard; protein; 660 AA.
 XX
 AC ABP97136;
 XX
 DT 24-JUN-2003 (first entry)
 XX
 DE Human matrix metalloproteinase 2 protein SEQ ID NO:14.
 XX
 KW Human; matrix metalloproteinase; MMP; anticancer; wound healing;
 KW matrix metalloproteinase inhibitor; antitumour; angiogenic; cardiac;
 KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;
 KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;
 KW dermatological; metastatic; non-metastatic; vascularised; heart disease;
 KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;
 KW macular degeneration; diabetic retinopathy; cleavage region.
 XX
 OS Homo sapiens.
 XX
 PN WO2003018748-A2.
 XX
 PD 06-MAR-2003.
 XX
 PF 15-AUG-2002; 2002WO-US026319.
 XX
 PR 16-AUG-2001; 2001US-0312726P.
 PR 21-DEC-2001; 2001US-00032376.
 PR 21-MAY-2002; 2002US-00153185.
 XX
 PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
 XX
 PI Quirk S, Weart IF;
 XX
 DR WPI; 2003-381408/36.
 XX
 PS Anti-angiogenic composition comprising peptide inhibitor of matrix
 FT metalloproteinase, useful for decreasing the expression of vascular
 PT endothelial growth factor and treating cancers and tissue injuries.
 XX
 PS Example 1; Page 43-44; 103pp; English.
 XX
 CC The present invention describes an anti-angiogenic composition (I) for
 CC inhibiting expression of vascular endothelial growth factor (VEGF). (I)
 CC comprises an effective amount of a peptide inhibitor of matrix
 CC metalloproteinase (MMP), where the peptide can inhibit the expression of
 CC VEGF. (I) has cytostatic, vulnary, cardiac, cerebroprotective,
 CC antidiabetic, ophthalmological and dermatological activities. (I) can be
 CC used for inhibiting expression of VEGF, and so can be used for inhibiting
 CC growth of tumours and diminishing tumours size. The tumour can be

CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.
 CC (I) is also useful for treating injuries including wounds, surgical
 CC incisions, chronic wounds, heart diseases and stroke. (I) is also useful
 CC for treating disorders characterised by excessive angiogenesis e.g.
 CC macular degeneration and diabetic retinopathy. The present sequence
 CC represents the human MMP-2 protein, which is used in the exemplification
 XX
 SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 6; Length 660;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 531 KAVFFA 536

RESULT 73
 AAO16608
 ID AAO16608 standard; protein; 660 AA.
 XX
 AC AAO16608;
 XX
 DT 08-MAY-2003 (first entry)
 XX
 DE Human matrix metalloproteinase 2 (MMP2) gelatinase protein.
 XX
 KW Human; enzyme; crystalline polypeptide; matrix metalloproteinase 9; MMP9;
 KW gelatinase; metalloproteinase mediated disease; drug design; arthritis;
 KW three-dimensional structure; MMP9 inhibitor; tumour growth;
 KW cancer metastasis; osteoarthritis; atherosclerosis; restenosis;
 KW periodontitis; multiple sclerosis; glomerulonephritis; MMP9 modulator;
 KW graft-versus-host disease; non-insulin dependent diabetes; MMP2;
 KW matrix metalloproteinase 2.
 XX
 OS Homo sapiens.
 XX
 PN WO2003002729-A1.
 XX
 PD 09-JAN-2003.
 XX
 PF 24-JUN-2002; 2002WO-SE001266.
 XX
 PR 27-JUN-2001; 2001SE-00002298.
 XX
 PA (ASTR) ASTRAZENCA AB.
 XX
 PI Jenson H, Minshull C, Paupit R, Rowsell S;
 XX
 DR WPI; 2003-201502/19.
 XX
 PT Novel crystalline form of a polypeptide corresponding to the catalytic
 FT domain of matrix metalloproteinase 9 protein, useful for selecting or
 PT designing chemical modulators which are used for treating diabetes,
 PT cancer, arthritis.
 XX
 PS Disclosure; Fig 7; 227pp; English.
 XX
 CC The invention comprises a crystalline form of a polypeptide corresponding
 CC to the catalytic domain of matrix metalloproteinase 9 (MMP9) protein - a
 CC gelatinase. The crystalline polypeptide of the invention is useful for
 CC treating a metalloproteinase mediated disease or condition in a warm-
 CC blooded animal. The crystalline polypeptide is also useful for
 CC determining the three-dimensional structure of the MMP9 catalytic domain
 CC to high resolution. The three-dimensional structure of the MMP9 catalytic
 CC domain is useful for rational drug design, and the atomic coordinates of
 CC the catalytic domain of MMP9 are useful for selecting or designing
 CC chemical modulators (preferably inhibitors) of MMP9. The crystalline
 CC polypeptide of the invention is useful in the treatment of a
 CC metalloproteinase mediated disease or condition, such as: tumour growth;
 CC metastasis in cancer; arthritis; osteoarthritis; atherosclerosis;

CC rectoriosis; periodontitis; multiple sclerosis; glomerulonephritis; graft-versus-host disease; and non-insulin dependent diabetes. The present amino acid sequence represents a human matrix metalloproteinase 2 (MMP2) protein

XX SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||

Db 531 KAVFFA 536

RESULT 74

ID ABG76322 standard; protein; 660 AA.

XX AC ABG76322;

XX DT 10-MAY-2003 (first entry)

XX DE Human matrix metalloproteinase-2 (MMP-2).

XX KW Human; peptide inhibitor; matrix metalloproteinase-2; MMP-2; cleavage region; proenzyme form; cellular proliferation; fibroblast; keratinocyte; healthy skin development; wound healing; scarring; skin tone; wrinkle; anti-aging; vulnerary.

XX OS Homo sapiens.

XX PN WO2003016520-A1.

XX PD 27-FEB-2003.

XX PF 15-AUG-2002; 2002WO-US026198.

XX PR 16-AUG-2001; 2001US-0312726P.

XX PR 21-DEC-2001; 2001US-00032376.

XX PR 21-MAY-2002; 2002US-00153185.

XX PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Quirk S, Malik S, Villanueva JM;

XX DR WPI; 2003-289980/28.

XX PT Novel peptide inhibitor of proteinase activity of matrix metalloproteinases, e.g. matrix metalloproteinase-2, useful for stimulating cellular proliferation of fibroblasts or keratinocytes.

XX PS Example 1; Page 41-42; 120pp; English.

XX CC The present invention relates to peptide inhibitors of metalloproteinases (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have peptide sequences related to the cleavage regions of the proenzyme forms of the MMPs. The peptide inhibitors are useful for stimulating cellular proliferation of fibroblasts or keratinocytes, promoting healthy skin development, treating wounds, preventing scarring, improving skin tone, reducing wrinkling and for stimulating the development of smooth, healthy skin. The peptide inhibitors are useful as anti-aging and wound healing compounds. The present sequence represents human MMP-2

XX SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||

Db 531 KAVFFA 536

RESULT 75

ID ADD18578

XX AC ADD18578 standard; protein; 660 AA.

XX AC ADD18578;

XX DT 15-JAN-2004 (first entry)

XX DE Human disease related protein SeqID9.

XX KW human; disease state; cytostatic; antiinflammatory; ophthalmological; antiarteriosclerotic; vulnerary; gene therapy;
XX KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
XX KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
XX KW glucose transport; catecholamine synthesis; iron transport;
XX KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
XX KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
XX KW inflammatory condition; wound healing.

XX OS Homo sapiens.

XX PN WO2003018621-A2.

XX PD 06-MAR-2003.

XX PF 23-AUG-2002; 2002WO-GB003892.

XX PR 23-AUG-2001; 2001GB-00020558.

XX PR 05-OCT-2001; 2001GB-00024037.

XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.

XX PI Kingman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;

XX DR WPI; 2003-290046/28.

XX DR N-PSDB; ADD18579.

XX PT New substantially purified polypeptide, useful for diagnosing or treating a hypoxia-regulated condition, such as cancer, ischemia, reperfusion injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or wound healing.

XX PS Claim 25; SEQ ID NO 9; 424pp; English.

XX CC This invention relates to novel human genes and gene product which are implicated in certain disease states. Compounds which modulate the proteins of the invention may have cytostatic, antiinflammatory, ophthalmological, antiarteriosclerotic or vulnerary activities. The sequences of the invention may be useful for gene therapy. The invention may be useful for diagnosing or treating a hypoxia-regulated condition, such as tumorigenesis, angiogenesis, apoptosis, inflammation, erythropoiesis, or the biological response to hypoxia conditions including processes such as glycolysis, gluconeogenesis, glucose transport, catecholamine synthesis, iron transport or nitric oxide synthesis. The disease includes cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, inflammatory conditions or wound healing. The present sequence is that of a disease related protein of the invention.

XX SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 7; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 531 KAVFFA 536
|||||

Search completed: December 29, 2005, 17:33:36
Job time : 91.7742 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78.1936 Seconds
(without alignments)
54.137 Million cell updates/sec

Title: US-10-009-122-4
Perfect score: 31
Sequence: 1 KPVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	47	Q8G9Y9	fugu rubrip
2	31	100.0	229	Q6RS99	tritricum tu
3	31	100.0	241	Q7XYC3	tritricum ae
4	31	100.0	331	Q6K5X9	oryza sativ
5	31	100.0	331	Q84NE7	ORYSA
6	31	100.0	335	Q615W9	ORYSA
7	31	100.0	353	Q8HQ66	CAMUP
8	31	100.0	519	Q5ATG9	EMENI
9	31	100.0	935	Q7XM01	ORYSA
10	31	100.0	3044	Q7QYR7	GIALA
11	30	96.8	224	Q84NG7	HORVU
12	30	96.8	395	Q98GC2	RHILO
13	30	96.8	397	Q22Y6C	RHIME
14	30	96.8	2643	Q5A3W3	CANAL
15	30	96.8	2643	Q5A3Q1	CANAL
16	28	90.3	23	Q4XXR5	PLACH
17	28	90.3	43	Q73M63	TREDE
18	28	90.3	49	Q9KAX7	BACHD
19	28	90.3	150	Q7R979	PLAYO
20	28	90.3	152	Q4J1Z2	AZOVI
21	28	90.3	177	Q20070	CAEEL
22	28	90.3	199	Q6LSA9	PHOPR
23	28	90.3	225	Q6UJY8	TRITU
24	28	90.3	226	Q8LKV8	ARGTA
25	28	90.3	241	Q7R8Y4	PLAYO
26	28	90.3	242	Q7RA05	PLAYO
27	28	90.3	250	Q7RNP5	PLAYO
28	28	90.3	251	Q7PDC0	PLAYO
29	28	90.3	251	Q7RPS1	PLAYO
30	28	90.3	252	Q7RA57	PLAYO
31	28	90.3	252	Q7RF37	PLAYO

32	28	90.3	255	Q7RLK2	PLAYO
33	28	90.3	262	Q7RCL4	PLAYO
34	28	90.3	265	Q7RC37	PLAYO
35	28	90.3	268	Q7RB86	PLAYO
36	28	90.3	285	Q529U4	MAGGR
37	28	90.3	293	Q94284	CAEEL
38	28	90.3	294	Q7RBU1	PLAYO
39	28	90.3	300	Q5UMP7	HALMA
40	28	90.3	321	Q7RBU3	PLAYO
41	28	90.3	326	Q74429	SYNY3
42	28	90.3	380	Q6KI05	MYCNO
43	28	90.3	388	Q4MSJ5	BACCE
44	28	90.3	388	Q6HLH8	BACHK
45	28	90.3	388	Q73BD3	BACCL
46	28	90.3	388	Q63S03	BACCC
47	28	90.3	388	Q81T98	BACAN
48	28	90.3	391	Q81G40	BACCR
49	28	90.3	398	Q5NEA9	FRATT
50	28	90.3	409	Q73V08	MYCPA
51	28	90.3	421	Q7Z2C3	CAEEL
52	28	90.3	422	Q9PQG2	UREPA
53	28	90.3	430	Q8FW04	BRUSU
54	28	90.3	432	Q6Q8W8	9GAMM
55	28	90.3	436	Q8M9J3	9AQUA
56	28	90.3	452	Q44595	CAEEL
57	28	90.3	456	Q6GVJ4	9BURK
58	28	90.3	465	1 RBL	NEPAL
59	28	90.3	472	Q9NSQ8	CAEEL
60	28	90.3	480	Q625W2	CAEER
61	28	90.3	482	Q5JU16	PYRKO
62	28	90.3	488	Q966D7	CAEEL
63	28	90.3	492	Q621X3	CAEER
64	28	90.3	506	Q38860	ARATH
65	28	90.3	508	1 MURE	BORBU
66	28	90.3	509	Q93058	BRATU
67	28	90.3	509	Q8LSC7	BRACM
68	28	90.3	509	Q8S384	BRATU
69	28	90.3	517	Q80729	ARATH
70	28	90.3	529	Q6NI23	CORDI
71	28	90.3	538	Q7PQ20	ANOAG
72	28	90.3	558	Q5TTR3	ANOAG
73	28	90.3	571	Q97KUB	CLOAB
74	28	90.3	584	Q4UGB4	THEAN
75	28	90.3	615	Q7PS12	ANOAG
76	28	90.3	664	Q966D8	CAEEL
77	28	90.3	746	Q9NSQ9	CAEEL
78	28	90.3	802	Q7R8Y2	PLAYO
79	28	90.3	853	Q7QTQ4	GIALA
80	28	90.3	922	1 GYRA	AERSA
81	28	90.3	1072	Q94537	SCHPO
82	28	90.3	1165	Q962L9	PLAVI
83	28	90.3	1285	Q9WXU3	THEMA
84	28	90.3	1558	Q5RH87	BRARE
85	27	87.1	31	Q4YNS6	PLABE
86	27	87.1	36	Q4XB83	PLACH
87	27	87.1	38	Q32187	EUGGR
88	27	87.1	46	Q867A4	TRAJA
89	27	87.1	60	Q4YKM8	PLABE
90	27	87.1	77	Q52R02	CHICK
91	27	87.1	90	Q4XC01	PLACH
92	27	87.1	92	Q8MPY0	CAEEL
93	27	87.1	96	Q61123	CAEEL
94	27	87.1	99	Q4T7Q1	TETNG
95	27	87.1	114	Q6ZB28	ORYSA
96	27	87.1	117	Q74KX8	LACJO
97	27	87.1	121	Q6R983	MAI2E
98	27	87.1	128	Q4MQN4	BACCE
99	27	87.1	128	Q6HNK6	BACHK
100	27	87.1	128	Q81116	BACCR
101	27	87.1	128	Q73DN7	BACCL
102	27	87.1	128	Q63G38	BACCC
103	27	87.1	128	Q81V92	BACAN
104	27	87.1	134	Q7R7Y0	PLAYO

Q7RLK2	plasmodium
Q7RCL4	plasmodium
Q7RC37	plasmodium
Q7RB86	plasmodium
Q529U4	magnaporthe
Q94284	caenorhabdi
Q7RBU1	plasmodium
Q5UMP7	haloarcula
Q7RBU3	plasmodium
P74429	mynechocyst
Q6KI05	mycoplasma
Q4MSJ5	bacillus ce
Q6HLH8	bacillus th
Q73BD3	bacillus ce
Q63S03	bacillus ce
Q81T98	bacillus an
Q81G40	bacillus ce
Q5NEA9	francisella
Q73V08	mycobacteri
Q7Z2C3	caenorhabdi
Q9PQG2	ureaplasma
Q8FW04	brucella su
Q6Q8W8	uncultured
Q8M9J3	illex pubesc
Q44595	caenorhabdi
Q6GVJ4	burkholderi
P28434	nepenthes a
Q9NSQ8	caenorhabdi
Q625W2	caenorhabdi
Q5JU16	pyrococcus
Q966D7	caenorhabdi
Q621X3	caenorhabdi
Q38860	arabidopsis
Q51219	borrelia bu
P93058	brassica ju
Q8LSC7	brassica ca
Q8S384	brassica ju
Q80729	arabidopsis
Q6NI23	corynebacte
Q5TTR3	anopheles g
Q97KUB	clostridium
Q4UGB4	theileria a
Q7PS12	anopheles g
Q966D8	caenorhabdi
Q9NSQ9	caenorhabdi
Q7R8Y2	plasmodium
Q7GTQ4	giardia lam
P48369	aeromonas s
Q94537	schizosacch
Q962L9	plasmodium
Q9WXU3	thermotoga
Q5RH87	brachydanio
Q4YNS6	plasmodium
Q4XB83	plasmodium
Q32187	euglena gra
Q867A4	tragulus ja
Q4YKM8	plasmodium
Q52R02	gallus gall
Q4XC01	plasmodium
Q8MPY0	caenorhabdi
Q61123	caenorhabdi
Q4T7Q1	tetradon n
Q6ZB28	oryza sativ
Q74KX8	lactobacill
Q6R983	zea mays (m
Q4MQN4	bacillus ce
Q6HNK6	bacillus th
Q81116	bacillus ce
Q73DN7	bacillus ce
Q63G38	bacillus ce
Q81V92	bacillus an
Q7R7Y0	plasmodium

105	27	87.1	134	2	Q4XU22_PLACH	Q4xu22 plasmodium	178	27	87.1	345	2	Q429Y8_9VRU	Q429y8 bacterioph
106	27	87.1	135	2	Q8MTN0_CABEL	Q8mtn0 caenorhabd1	179	27	87.1	345	2	Q8KZ48_9PROT	Q8kz48 uncultured
107	27	87.1	136	2	O51365_BORBU	O51365 borrelia bu	180	27	87.1	346	1	ACSF_GLOVI	Q7nfa1 gloebacter
108	27	87.1	140	2	O9G4E5_FASGI	O9g4e5 fasciola gi	181	27	87.1	349	1	ACSF_GRATL	Q6baul gracilaria
109	27	87.1	140	2	Q8I4D1_CABEL	Q8i4d1 caenorhabdi	182	27	87.1	349	1	ACSF_PORPU	P51277 porphyra pu
110	27	87.1	144	2	Q8IWA3_HUMAN	Q8iwa3 homo sapien	183	27	87.1	350	2	Q9Y370_HUMAN	Q9y370 homo sapien
111	27	87.1	144	2	Q6MGW2_EDEBA	Q6mgw2 bdellovibri	184	27	87.1	351	2	Q8TCX1_HUMAN	Q8tcx1 homo sapien
112	27	87.1	146	2	Q6MUK5_MYCNS	Q6muk5 mycoplasma	185	27	87.1	352	2	Q96J00_HUMAN	Q96j00 caenorhabdi
113	27	87.1	148	2	Q6ZUC5_HUMAN	Q6zuc5 homo sapien	186	27	87.1	352	2	O17576_CABEL	O17576 caenorhabdi
114	27	87.1	148	2	Q97657_CANFA	Q97657 canis fami1	187	27	87.1	354	1	ACSF_CVACA	Q9t1r8 cyanidium c
115	27	87.1	148	2	Q6QLX0_CANFA	Q6qlx0 canis fami1	188	27	87.1	356	1	ACSF_SYNXP	Q7u6y8 synecococc
116	27	87.1	151	2	Q4WKU9_ASPFU	Q4wku9 aspergillus	189	27	87.1	356	2	Q5NPT3_ZYPMO	Q5npt3 zymomonas m
117	27	87.1	164	2	Q6KAU3_MOUSE	Q6kau3 mus musculu	190	27	87.1	358	1	ACSF1_SYNY3	P72584 synecocycet
118	27	87.1	171	1	RT25_MOUSE	Q9d125 mus musculu	191	27	87.1	358	1	ACSF3_ANASP	Q8yrc22 anaabaena sp
119	27	87.1	171	2	Q4QRW0_RAT	Q4qrw0 rattus norv	192	27	87.1	362	2	Q75AT8_ASHGO	Q75at8 ashya goss
120	27	87.1	172	2	Q4RQJ4_TETNG	Q4rjq4 tetraodon n	193	27	87.1	362	2	O7RGM5_PLAYO	Q7rgm5 plasmodium
121	27	87.1	173	1	RT25_HUMAN	P82663 homo sapien	194	27	87.1	365	1	ACSF_RHOPA	Q6n9j7 rhodopseudo
122	27	87.1	176	2	Q63507_9TREM	O63507 echinostoma	195	27	87.1	369	2	Q6ZM18_BRARE	Q6zmi8 brachydanio
123	27	87.1	176	2	Q63508_9TREM	O63508 echinostoma	196	27	87.1	370	2	Q40093_IPONI	Q40093 ipomoea nil
124	27	87.1	176	2	Q63509_9TREM	O63509 echinostoma	197	27	87.1	370	2	Q8A715_BACTN	Q8a715 bacteroides
125	27	87.1	179	2	Q4ZOC8_PLABB	Q4zoc8 plasmodium	198	27	87.1	370	2	Q98QH7_MYCPU	Q98qh7 mycoplasma
126	27	87.1	185	1	LEP1_BACAM	P41026 bacillus am	199	27	87.1	371	2	Q84RD7_TOBAC	Q84rd7 nicotiana t
127	27	87.1	185	2	O51736_BORBU	O51736 borrelia bu	200	27	87.1	375	2	Q6FVI2_CANGA	Q6fvi2 candida gla
128	27	87.1	193	1	LEP2_BACAM	P41025 bacillus am	201	27	87.1	376	2	Q95NI2_CABEL	Q95ni2 caenorhabdi
129	27	87.1	193	1	LEPT_BACSU	F71013 bacillus su	202	27	87.1	393	2	Q8LEE4_ARATH	Q8lee4 arabidopsis
130	27	87.1	194	2	Q50XJ3_ENTHI	Q50xj3 entamoeba h	203	27	87.1	405	1	CRD1_EUPES	Q945b7 euphorbia e
131	27	87.1	194	2	Q5NT24_ENTHI	O5nt24 entamoeba h	204	27	87.1	405	1	CTH1_CHLRE	Q6e1v8 gosypium h
132	27	87.1	201	2	O96B03_HUMAN	O96b03 homo sapien	205	27	87.1	407	1	O45653_CABEL	Q9ar22 chlamydomon
133	27	87.1	201	2	Q6PDB2_HUMAN	O6pdb2 homo sapien	206	27	87.1	408	2	O45653_CABEL	O45653 caenorhabdi
134	27	87.1	208	2	Q83455_ADEP3	Q83455 porcine ade	207	27	87.1	408	2	Q9SDJ2_ORISA	Q9sdj2 oryza sativ
135	27	87.1	211	2	Q7RNU3_PLAYO	Q7rnu3 plasmodium	208	27	87.1	409	1	CRD1_ARATH	Q9m591 a magnesium
136	27	87.1	227	2	Q6PMQ4_XENLA	Q6pmq4 xenopus lae	209	27	87.1	415	2	Q5LHI5_BACFN	Q5lhi5 bacteroides
137	27	87.1	228	2	Q9LHM5_ARATH	Q9lhm5 arabidopsis	210	27	87.1	415	2	Q64YF9_BACFR	Q64yf9 bacteroides
138	27	87.1	232	2	Q8ZDV0_YERPE	Q8zdv0 versinia pe	211	27	87.1	417	1	CRD1_HORVU	O5etu4 hordeum vul
139	27	87.1	238	1	YO14_BFL2	P42549 bacterioph	212	27	87.1	423	2	Q6NKY4_ARATH	Q6nky4 arabidopsis
140	27	87.1	239	2	Q5HRC1_STAEO	O5hrc1 staphylococ	213	27	87.1	428	2	Q60IR3_MYCHY	Q60ir3 mycoplasma
141	27	87.1	244	2	Q8CTN5_STAEP	Q8ctn5 staphylococ	214	27	87.1	431	2	Q98TF3_ORYLA	Q98tf3 oryza lat
142	27	87.1	244	2	Q5B4B1_EMENI	O5b4b1 aspergillus	215	27	87.1	432	2	Q681Y3_ARATH	Q681y3 arabidopsis
143	27	87.1	246	2	Q4N8X3_THEPA	Q4n8x3 theileria p	216	27	87.1	435	2	Q6XRC0_9BACT	Q6xrc0 uncultured
144	27	87.1	246	2	Q8FB21_ECOL6	Q8fb21 escherichia	217	27	87.1	436	2	Q9C954_ARATH	Q9c954 arabidopsis
145	27	87.1	247	2	Q81B21_PLAF7	Q81b21 plasmodium	218	27	87.1	437	2	O5LEE2_ENTHI	O5lee2 entamoeba h
146	27	87.1	256	2	O5L209_GEOKA	O5l209 geobacillus	219	27	87.1	438	1	ENGA_CLOPE	Q8xfj1 clostridium
147	27	87.1	258	2	Q9C1L0_NEUCR	Q9c1l0 neurospora	220	27	87.1	459	2	Q9WZ33_THEME	Q9wz33 thermotoga
148	27	87.1	262	2	Q9BGL3_SHEEP	Q9bgl3 ovis aries	221	27	87.1	467	2	Q8YUW4_STAHO	Q8yuvw4 staphylococ
149	27	87.1	262	2	Q6PMQ5_XENLA	Q6pmq5 xenopus lae	222	27	87.1	469	2	O51FM2_ENTHI	Q51fm2 entamoeba h
150	27	87.1	274	2	Q9WZS5_THEME	Q9wzs5 thermotoga	223	27	87.1	472	2	Q4UDY3_THEAN	Q4udy3 theileria a
151	27	87.1	278	2	Q9U336_CABEL	Q9u336 caenorhabdi	224	27	87.1	478	2	Q6UR08_ANOGA	Q6ur08 anopheles g
152	27	87.1	287	2	Q72P77_LEPIC	Q72p77 leptospira	225	27	87.1	479	2	Q7QCC7_ANOGA	Q7qcc7 anopheles g
153	27	87.1	287	2	Q8F779_LEFIN	Q8f779 leptospira	226	27	87.1	488	2	Q18760_CABEL	Q18760 caenorhabdi
154	27	87.1	300	2	Q34521_FASHE	Q34521 fasciola he	227	27	87.1	499	2	P87212_9APHY	P87212 polyporacea
155	27	87.1	300	2	Q9B8Y4_FASHE	Q9b8y4 fasciola he	228	27	87.1	504	2	Q8NKF3_9AGAR	Q8nkf3 termitomyce
156	27	87.1	300	2	Q88XR9_LACPL	Q88xr9 lactobacill	229	27	87.1	522	2	Q6ONE9_CABEL	Q6one9 caenorhabdi
157	27	87.1	301	2	Q7XJ11_TRIRP	Q7xj11 trifolium r	230	27	87.1	522	2	Q9LPY0_ARATH	Q9lpy0 arabidopsis
158	27	87.1	301	2	Q7XJ16_WHEAT	Q7xj16 triticum ae	231	27	87.1	524	2	Q75819_ASHGO	Q75819 ashya goss
159	27	87.1	308	2	Q7XJ12_ERANA	Q7xj12 brassica na	232	27	87.1	527	1	IPT1_YEAST	P38954 saccharomyc
160	27	87.1	308	2	Q66917_YERPS	Q66917 versinia ps	233	27	87.1	543	2	Q7QXS6_GIALA	Q7qxs6 giardia lam
161	27	87.1	309	2	Q5LLS8_SILPO	Q5lls8 silicibacte	234	27	87.1	546	2	Q98TF2_ORYLA	Q98tf2 oryza lat
162	27	87.1	310	1	Y160_BUCAP	Q8k9x4 buchnera ap	235	27	87.1	553	2	Q4SKD2_TETNG	Q4skd2 tetraodon n
163	27	87.1	321	1	YCR39_CVAPA	P48279 cyanophora	236	27	87.1	560	2	Q4SOT5_TETNG	Q4sot5 tetraodon n
164	27	87.1	324	2	Q6HKI3_BACHK	Q6hki3 bacillus th	237	27	87.1	574	2	Q7T2J2_BRARE	Q7t2j2 brachydanio
165	27	87.1	325	2	Q81SA4_BACAN	Q81sa4 bacillus an	238	27	87.1	575	2	Q2USC3_XENLA	Q2usc3 xenopus lae
166	27	87.1	332	2	Q84RD6_CUCSA	Q84rd6 cucumis sat	239	27	87.1	576	2	Q6DCW8_XENLA	Q6dcw8 xenopus lae
167	27	87.1	333	2	Q7XJ13_9ROSA	Q7xj13 rosa davuri	240	27	87.1	578	2	Q5BL52_XENTR	Q5bl52 xenopus tro
168	27	87.1	333	2	Q7XJ14_9ROSI	Q7xj14 salix babyl	241	27	87.1	580	1	MMPL4_FIG	Q9xt90 sus scrofa
169	27	87.1	335	1	ACSP_CYAME	Q85fx6 cyanidiosch	242	27	87.1	581	2	O68921_NEIGO	O68921 neisseria g
170	27	87.1	335	2	O5LE41_BACFN	Q5le41 bacteroides	243	27	87.1	581	2	Q5F8K1_NEIGI	Q5f8k1 neisseria g
171	27	87.1	335	2	Q9F749_BACFR	Q9f749 bacteroides	244	27	87.1	581	2	Q9UZ93_NEIMB	Q9uz93 neisseria m
172	27	87.1	336	2	Q68BQ2_ORYSA	Q68bq2 oryza sativ	245	27	87.1	581	2	Q9JUB8_NEIMA	Q9jub8 neisseria m
173	27	87.1	339	2	Q9XDJ2_BACFR	Q9xdj2 bacteroides	246	27	87.1	582	1	MMPL4_HUMAN	P50281 homo sapien
174	27	87.1	339	2	O5LGH6_BACFN	O5lgh6 bacteroides	247	27	87.1	582	1	MMPL4_MOUSE	P35690 mus musculu
175	27	87.1	340	2	O5LIR4_BACFN	O5lir4 bacteroides	248	27	87.1	582	1	MMPL4_RABIT	P52220 coryctolagus
176	27	87.1	340	2	Q64ZV1_BACFR	Q64zv1 bacteroides	249	27	87.1	582	1	MMPL4_RAT	Q10739 rattus norv
177	27	87.1	345	2	Q6Y7P5_9VRU	Q6y7p5 staphylococ	250	27	87.1	582	2	Q6GSF3_HUMAN	Q6gsf3 homo sapien

251 27 87.1 582 2 Q9GLE4_BOVIN
 252 27 87.1 582 2 Q5RES1_PONPY
 253 27 87.1 582 2 Q9XSP0_CAPHI
 254 27 87.1 582 2 Q99PG1_CRIGR
 255 27 87.1 582 2 Q8BTK2_MOUSE
 256 27 87.1 582 2 Q6DFU5_mus musculus
 257 27 87.1 582 2 Q6IN06_rattus norv
 258 27 87.1 585 2 Q7RDB0_PLAYO
 259 27 87.1 585 2 Q4NRP3_THEPA
 260 27 87.1 592 2 Q4RWY3_TETNG
 261 27 87.1 599 2 Q752M5_ASHGO
 262 27 87.1 607 2 Q76LU7_ORYLA
 263 27 87.1 610 2 Q4W889_ORYLA
 264 27 87.1 621 2 Q72J1_BRARE
 265 27 87.1 626 2 Q98HT9_RHILO
 266 27 87.1 689 1 S01B2_MOUSE
 267 27 87.1 695 2 Q419U8_GIBZE
 268 27 87.1 698 2 Q5BD98_EWENI
 269 27 87.1 721 2 Q16363_CABEL
 270 27 87.1 732 2 Q4SKK7_TETNG
 271 27 87.1 763 2 Q4Y7S4_PLACH
 272 27 87.1 773 1 YOD3_CABEL
 273 27 87.1 780 2 Q6A1B3_ECHMU
 274 27 87.1 789 2 Q5AG44_CANAL
 275 27 87.1 794 2 Q7R8G4_PLAYO
 276 27 87.1 796 2 Q91SC5_9ALPH
 277 27 87.1 833 1 HMDH_AGRIP
 278 27 87.1 846 2 Q4SL98_TETNG
 279 27 87.1 856 1 HMDH_BLAG
 280 27 87.1 923 2 Q73L77_TREDE
 281 27 87.1 1024 1 CAR12_HUMAN
 282 27 87.1 1049 2 Q528F0_MAGGR
 283 27 87.1 1068 2 Q55DX7_DICDI
 284 27 87.1 1099 2 Q8IE72_PLAF7
 285 27 87.1 1126 2 Q73ME8_TREDE
 286 27 87.1 1144 2 Q86JE2_DICTOSTELI
 287 27 87.1 1145 2 Q5SA20_DICTOSTELI
 288 27 87.1 1269 2 Q4YNH1_PLABE
 289 27 87.1 1279 2 Q76IL3_BRACHYDANIO
 290 27 87.1 1469 2 Q4YZQ1_PLABE
 291 27 87.1 1508 2 Q7RHFS_PLAYO
 292 27 87.1 1563 2 Q61CM5_CAENORHABDI
 293 27 87.1 1897 2 Q8IBK2_PLAF7
 294 27 87.1 1917 2 Q7RR57_PLAYO
 295 27 87.1 2118 2 Q7RR57_PLAYO
 296 27 87.1 2921 2 Q5WNK5_CAENORHABDI
 297 27 87.1 3978 2 Q97236_PLAF7
 298 27 87.1 6739 2 Q7QYB8_GIALA
 299 26 83.9 24 2 Q4X467_PLACH
 300 26 83.9 27 2 Q4Z519_PLABE

ALIGNMENTS

RESULT 1
 Q8QGY9_FUGRU
 ID Q8QGY9_FUGRU PRELIMINARY; PRT; 47 AA.
 AC Q8QGY9;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Guanine nucleotide binding protein (Fragment).
 GN Name=Gnat2;
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97129408; PubMed=8973916;

RA Sarwal M.M., Sontag J.M., Hoang L., Brenner S., Wilkie T.M.;
 RT "G protein alpha subunit multigene family in the Japanese puffer fish
 Fugu rubripes: PCR from a compact vertebrate genome.";
 RL Genome Res. 6:1207-1215(1996).
 DR EMBL; L79897; AAL77630.1; -; Genomic_DNA.
 DR HSSP; P04695; 1TND.
 DR GO; GO:0004871; P:signal transducer activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR001019; Gprotein_alpha.
 DR Pfam; PF00503; G-alpha; 1.
 DR NON_TER 1 1
 FT NON_TER 47 47
 SQ SEQUENCE 47 AA; 5255 MW; 9770A35D36E1FAEC CRC64;

Query Match 100.0%; Score 31; DB 2; Length 47;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
 Db 15 KVFVFA 20
 |||||

RESULT 2

Q6RS99_TRITU
 ID Q6RS99_TRITU PRELIMINARY; PRT; 229 AA.
 AC Q6RS99;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Globulin.
 OS Triticum turgidum (Poulard wheat) (Rivet wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4571;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15122014; DOI=10.1104/pp.103.038083;
 Gu Y.Q., Coleman-Derr D., Kong X., Anderson O.D.;
 RT "Rapid Genome Evolution Revealed by Comparative Sequence Analysis of
 Orthologous Regions from Four Triticeae Genomes.";
 RL Plant Physiol. 135:459-470(2004).
 DR EMBL; AY494981; AAK95703.1; -; Genomic_DNA.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR001419; Glutenin.
 DR Pfam; PF00234; Tryp_alpha_amyl; 1.
 DR PRINTS; PR00210; GLUTENIN.
 DR SMART; SM00499; AAI; 1.
 SQ SEQUENCE 229 AA; 25000 MW; 18E769DAB08E41E3 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 229;
 Best Local Similarity 100.0%; Pred. No. 11e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
 Db 3 KVFVFA 8
 |||||

RESULT 3

Q7XYC3_WHEAT
 ID Q7XYC3_WHEAT PRELIMINARY; PRT; 241 AA.
 AC Q7XYC3;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE 19 kDa globulin (Fragment).
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Triticum.

```

OX NCBI_TaxID=4565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Seed;
RA Li J.R., Wang F., Li Q.Z., Zhang X.S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF475121; AAP80642.1; -; mRNA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF00234; Tryp alpha amyl; 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
FT NON TER
SQ SEQUENCE 241 AA; 26139 MW; AAD8F2BB859DA016 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 15 KVFVFA 20

RESULT 4
Q6K5X9 ORYSA
ID Q6K5X9 ORYSA PRELIMINARY; PRT; 331 AA.
AC Q6K5X9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Transmembrane protein-like.
GN Name=OJ2055 H10.27-1; Synonyms=P0407A09.6-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005300; BAD19727.1; -; Genomic DNA.
DR EMBL; AF004747; BAD19452.1; -; Genomic DNA.
DR Gramene; Q6K5X9; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004853; DUF250.
DR Pfam; PF03151; DUF250; 1.
KW Transmembrane.
SQ SEQUENCE 331 AA; 36397 MW; EACAC4769463E9EA CRC64;

Query Match 100.0%; Score 31; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 80 KVFVFA 85

RESULT 5
Q84NE7 ORYSA
ID Q84NE7 ORYSA PRELIMINARY; PRT; 331 AA.
AC Q84NE7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative transmembrane protein.

```

```

OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Lee R.H., Chen S.C.G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY030360; AAKS0365.1; -; mRNA.
DR Gramene; Q84NE7; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004853; DUF250.
DR Pfam; PF03151; DUF250; 1.
KW Transmembrane.
SQ SEQUENCE 331 AA; 36384 MW; 289C89F3D3F8229A CRC64;

Query Match 100.0%; Score 31; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 80 KVFVFA 85

RESULT 6
Q61SW9 ORYSA
ID Q61SW9 ORYSA PRELIMINARY; PRT; 335 AA.
AC Q61SW9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transmembrane protein.
GN Name=OJ1076 H08.6;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC108498; AAT47018.1; -; Genomic DNA.
DR Gramene; Q61SW9; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004853; DUF250.
DR Pfam; PF03151; DUF250; 1.
KW Transmembrane.
SQ SEQUENCE 335 AA; 36826 MW; 5A0EF43F8578B46F CRC64;

Query Match 100.0%; Score 31; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 80 KVFVFA 85

RESULT 7
Q4HQ66 CAMUP
ID Q4HQ66 CAMUP PRELIMINARY; PRT; 353 AA.
AC Q4HQ66;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

```

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE GDP-fucose synthetase.
GN Name=fcl; ORFNames=CUP1255;
OS Campylobacter upsaliensis RM3195.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=306264;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=RM3195;
RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
RA Nelson K.E.;
RT "Major structural and novel potential virulence mechanisms from the
RT genomes of multiple Campylobacter species.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC preliminary data.
DR EMBL; AAFU01000007; EAL52977.1; -; Genomic DNA.
SQ SEQUENCE 353 AA; 39798 MW; 59CC8A43D31EPAE CRC64;
Query Match 100.0%; Score 31; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVFFA 6
DQ |||||
DB 58 KVFVFFA 63
RESULT 8
Q5ATG9_EMENI PRELIMINARY; PRT; 519 AA.
AC Q5ATG9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AN8411.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Borkhater B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Fato S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihoava T., Menga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkharp P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome Sequence of Aspergillus nidulans.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: Hydroxylation of N-alkanes at the terminal
CC position.
CC -1- CATALYTIC ACTIVITY: Obtusifolios + 3 O(2) + 3 NADPH = 4-alpha-
CC methyl-5-alpha-ergosta-8,14,24(28)-trien-3-beta-ol + formate + 3
CC NADP(+) + 3 H(2)O.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AACD01000153; EAA67033.1; -; Genomic DNA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0016126; P:sterol biosynthesis; IEA.
DR InterPro; IPR001128; Cytochrome P450.
DR InterPro; IPR002974; EP450_IL_CYP52.
DR InterPro; IPR002403; EP450IV.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR01239; EP450IICYP52.
DR PRINTS; PR00465; EP450IV.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
KW Heme; Hypothetical protein; Iron; Lipid synthesis; Membrane;
KW Metal-binding; Monooxygenase; Oxidoreductase; Steroid biosynthesis;
KW Sterol biosynthesis.
SQ SEQUENCE 519 AA; 60440 MW; B367EE6EB6PFA287 CRC64;
Query Match 100.0%; Score 31; DB 2; Length 519;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVFFA 6
DQ |||||
DB 26 KVFVFFA 31
RESULT 9
Q7XM01_ORYSA PRELIMINARY; PRT; 935 AA.
AC Q7XM01;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE OSJNBa0086006.8 protein.
GN Names=OSJNBa0086006.8;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
[1]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=12447439; DOI=10.1038/nature01183;
RX Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Wang Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL; AL662981; CA804860.2; -; Genomic DNA.
DR Gramene; Q7XM01; -;
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 2.
DR SMART; SM00256; FBOX; 2.
DR PROSITE; PS50181; FBOX; 1.
SQ SEQUENCE 935 AA; 103910 MW; 735DD287C6E1BC69 CRC64;
Query Match 100.0%; Score 31; DB 2; Length 935;

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 1 KVFVFA 6
|||
Db 74 KVFVFA 79

RESULT 10

Q7QYR7 GIALA
ID Q7QYR7 GIALA PRELIMINARY; PRT; 3044 AA.
AC Q7QYR7;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE GLP_70_49040_39906.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D., Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC EMBL: AACB01000048; EAA40229.1; -; Genomic_DNA.
DR InterPro; IPR012351; Cytochrome_4_hlx.
KW Cytochrome.
SQ SEQUENCE 3044 AA; 347085 MW; 24F737600F128C6D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 3044;
Best Local Similarity 100.0%; Pred. No. 9.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 1 KVFVFA 6
|||
Db 382 KVFVFA 387

RESULT 11

Q84NG7 HORVU
ID Q84NG7 HORVU PRELIMINARY; PRT; 224 AA.
AC Q84NG7;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Globulin.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=14663527; DOI=10.1139/g03-071;
RA Gu Y.Q., Anderson O.D., Londeore C.F., Kong X., Chibbar R.N., Lazo G.R.;
RT "Structural organization of the barley D-hordein locus in comparison with its orthologous regions of wheat genomes."
RL Genome 46:1084-1097(2003).
DR EMBL: AY268139; AAP31050.1; -; Genomic DNA.
DR GO: GO:0045735; F.nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF00234; Tryp_alpha_amy1; 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 224 AA; 24561 MW; 91A5BFF15C86394D CRC64;

Query Match 96.8%; Score 30; DB 2; Length 224;
Best Local Similarity 83.3%; Pred. No. 1.8e+02; Mismatches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
Db 3 KVFVFA 8

RESULT 12

Q98GC2 RHIL
ID Q98GC2 RHIL PRELIMINARY; PRT; 395 AA.
AC Q98GC2;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative peptidase.
GN OrderedLocusNames=ml13393;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idekawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL: BA000012; BAB50294.1; -; Genomic DNA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0004239; F:methionyl aminopeptidase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000994; Peptidase M24.
DR InterPro; IPR001714; Pept_M24_MAP.
DR Pfam; PF00557; Peptidase_M24_1.
DR PRINTS; PR00599; MAPEPTIDASE.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 395 AA; 43302 MW; E9ADFA4ADB1D472 CRC64;

Query Match 96.8%; Score 30; DB 2; Length 395;
Best Local Similarity 83.3%; Pred. No. 2.9e+02; Mismatches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
Db 48 KVFVFA 53

RESULT 13

Q92YY6 RHIME
ID Q92YY6 RHIME PRELIMINARY; PRT; 397 AA.
AC Q92YY6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Putative proline dipeptidase.
GN OrderedLocusNames=RAO726; ORFNames=SM1329;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymA.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798; Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

QY 1 KFVFPA 6
|||: |||

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.M.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajadream M.A., Carucci D.J., Yates J.R., Kafatos
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Minden R.S.,

```

RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RL transcriptomic, and proteomic analyses.";
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01002391; CNH78296.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 23 AA; 3051 MW; ECFB64E8BCC09AA0 CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 23;
  Best Local Similarity 83.3%; Pred. No. 74;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFFA 6
Db 16 KVFVFFA 21

RESULT 17
ID Q73M63 TREDE PRELIMINARY; PRT; 43 AA.
AC Q73M63;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TDE1646;
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35405 / DSM 14222;
RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidson T.M., Deboy R.T., Fouts D.E., Haft D.H.,
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebregeorgis E., Geer K., Teagave G., Malek J.K., Ayodeji B.,
RA Shatnam S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
DR EMBL; AR017251; AAS12163.1; -; Genomic_DNA.
DR TIGR; TDE1646; -.
KW Complete proteome.
SQ SEQUENCE 43 AA; 5202 MW; E1189303B62C9173 CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 43;
  Best Local Similarity 83.3%; Pred. No. 1.2e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFFA 6
Db 20 KVFVFFA 25

RESULT 18
Q9KAX7 BACHD
ID Q9KAX7 BACHD PRELIMINARY; PRT; 49 AA.
AC Q9KAX7;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE BH2159 protein.
GN OrderedLocusNames=BH2159;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;

```

```

RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=205112582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; BA000004; BAB05878.1; -; Genomic_DNA.
DR PIR; G83919; G83919.
KW Complete proteome.
SQ SEQUENCE 49 AA; 5463 MW; D669731B6DCD0B1 CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 49;
  Best Local Similarity 83.3%; Pred. No. 1.4e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFFA 6
Db 34 KVFVFFS 39

RESULT 19
Q7R979 PLAYO
ID Q7R979 PLAYO PRELIMINARY; PRT; 150 AA.
AC Q7R979;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06986;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22555706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguoli S.V., Suh B.B., Kooij T.W., Perteu M.,
RA Silva J.C., Emolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidblyum S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002464; EAA19320.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 150 AA; 17794 MW; DA68536D398B37AC CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 150;
  Best Local Similarity 83.3%; Pred. No. 3.5e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFFA 6
Db 7 KVFVFFS 12

RESULT 20
Q4J1Z2_AZOVI

```

```
ID Q4J1Z2_AZOVI PRELIMINARY; PRT; 152 AA.
AC Q4J1Z2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Glyoxalase/Bleomycin resistance protein/dioxygenase domain.
DE ORNames=AVINDRAFT_6949;
GN Azotobacter vinelandii AVOP.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=322710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Ibrani S., Pitluck S., Richardson P.,
RA "Sequencing of the draft genome assembly of Azotobacter vinelandii
RT AVOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.,
RA "Annotation of the draft genome assembly of Azotobacter vinelandii
RT AVOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RA US DOE Joint Genome Institute;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Ibrani S., Pitluck S., Richardson P.,
RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAU03000001; EAM08399.1; -; Genomic_DNA.
KW Dioxygenase.
SQ SEQUENCE 152 AA; 16984 MW; 05A60BD5879ED93 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 152;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 111 RFVFFA 116
|||||

RESULT 21
Q20070_CABEL PRELIMINARY; PRT; 177 AA.
AC Q20070;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein F35H10.6.
GN ORNames=F35H10.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
```

```
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; U40934; AAA81680.1; -; Genomic_DNA.
DR PIR; T16280; T16280.
DR Ensemble; F35H10.6; Caenorhabditis elegans.
DR GO; GO:0016272; C:prefoldin complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR004127; PFD_alpha_like.
DR Pfam; PF02996; Prefoldin; 1.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 177 AA; 21142 MW; E8B71144250DB915 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 177;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 10 KVFVFS 15
|||||

RESULT 22
Q6LSA9_PROPR PRELIMINARY; PRT; 199 AA.
AC Q6LSA9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=BPRA1406;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746425; DOI=10.1126/science.1103341;
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N.,
RA Lauro F.M., Cestaro A., Malacrida G., Simonato B., Cannata N.,
RA Romualdi C., Bartlett D.H., Valle G.;
RA "Life at depth: Photobacterium profundum genome sequence and
RT expression analysis.";
RL Science 307:1459-1461(2005).
DR EMBL; CR378667; CAG19817.1; -; Genomic DNA.
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR InterPro; IPR000182; GCN5acetyl_trans.
DR Pfam; PF00583; Acetyltransf_1; 1.
DR Complete proteome.
SQ SEQUENCE 199 AA; 22203 MW; AF44E115663FD3F6 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 199;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 47 KFLFFA 52
|||||

RESULT 23
Q6UJY8_TRITU PRELIMINARY; PRT; 225 AA.
AC Q6UJY8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Globulin.
GN Triticum turgidum (Poulard wheat) (Rivet wheat).
OS Eukaryota; Viridiplantae; Streptophyta; Poales; Poaceae; Pooideae;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poaceae; Pooideae;
```

```

OC  Triticeae; Triticum.
OX  NCBI_TaxID=4571;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  PubMed=15159634; DOI=10.1023/B:PLAN.0000028768.21587.dc;
RA  Kong X.Y., Gu Y.Q., You F.M., Dubcovsky J., Anderson O.D.;
RT  "Dynamics of the evolution of orthologous and paralogous portions of a
RL  complex locus region in two genomes of allopolyploid wheat.";
RN  Plant Mol. Biol. 54:55-69(2004).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RA  Kong X.-Y., Gu Y.Q., Anderson O.D.;
RL  Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY368673; AAQ93632.1; -; Genomic DNA.
DR  GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR  InterPro; IPR003612; AAI.
DR  InterPro; IPR001419; Glutenin.
DR  Pfam; PF00234; Tryp_alpha_amy1; 1.
DR  PRINTS; PR00210; GLUTENIN.
DR  SMART; SM00499; AAI; 1.
SQ  SEQUENCE 225 AA; 24502 MW; 45F4D19403BCDCC2 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 225;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 KVFVFA 6
Db  :|||||
   3 RFVFFA 8

RESULT 24
Q8LKV8 AEGTA
ID  Q8LKV8 AEGTA PRELIMINARY; PRT; 226 AA.
AC  Q8LKV8
DT  01-OCT-2002 (TrEMBLrel. 22, Created)
DT  01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Seed globulin.
GN  Names=Glo-2;
OS  Aegilops tauschii (Tausch's goatgrass) (Aegilops squarrosa).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC  Triticeae; Aegilops.
OX  NCBI_TaxID=37682;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=22478028; PubMed=12590343;
RA  Anderson O.D., Rausch C., Moullet O., Lagudah E.S.;
RT  "The wheat D-genome HMW-glutenin locus: BAC sequencing, gene
RT  distribution, and retrotransposon clusters.";
RL  Funct. Integr. Genomics 3:56-68(2003).
DR  EMBL; AF497474; AAM77580.1; -; Genomic DNA.
DR  GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR  InterPro; IPR003612; AAI.
DR  InterPro; IPR001419; Glutenin.
DR  Pfam; PF00234; Tryp_alpha_amy1; 1.
DR  PRINTS; PR00210; GLUTENIN.
DR  SMART; SM00499; AAI; 1.
SQ  SEQUENCE 226 AA; 24515 MW; 95397E83C63D50AD CRC64;

Query Match 90.3%; Score 28; DB 2; Length 226;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 KVFVFA 6
Db  :|||||
   3 RFVFFA 8

RESULT 25
Q7R8Y4 PLAYO
ID  Q7R8Y4 PLAYO PRELIMINARY; PRT; 241 AA.

```

```

AC  Q7R8Y4;
DT  01-MAR-2004 (TrEMBLrel. 26, Created)
DT  01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Hypothetical protein.
GN  Name=PY07086;
OS  Plasmodium yoelii yoelii.
OC  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX  NCBI_TaxID=73239;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=17XNL;
RX  MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA  Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA  Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA  Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA  Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA  Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA  Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA  Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA  van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA  Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA  Carucci D.J.;
RT  "Genome sequence and comparative analysis of the model rodent malaria
RT  parasite Plasmodium yoelii yoelii.";
RL  Nature 419:512-519(2002).
CC  -!- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
DR  EMBL; ABL01002524; EAAL9443.1; -; Genomic DNA.
DR  InterPro; IPR006484; PYST-B.
DR  TIGRFAMs; TIGR01597; PYST-B; 1.
KW  Hypothetical protein.
SQ  SEQUENCE 241 AA; 28789 MW; BE9AD8A3E5924873 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 241;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 KVFVFA 6
Db  :|||||
   7 KVFVFS 12

RESULT 26
Q7RA05 PLAYO
ID  Q7RA05 PLAYO PRELIMINARY; PRT; 242 AA.
AC  Q7RA05
DT  01-MAR-2004 (TrEMBLrel. 26, Created)
DT  01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Hypothetical protein.
GN  Name=PY06703;
OS  Plasmodium yoelii yoelii.
OC  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX  NCBI_TaxID=73239;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=17XNL;
RX  MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA  Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA  Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA  Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA  Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA  Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA  Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA  Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA  van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA  Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA  Carucci D.J.;
RT  "Genome sequence and comparative analysis of the model rodent malaria
RT  parasite Plasmodium yoelii yoelii.";
RL  Nature 419:512-519(2002).

```

CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABL01002310; EAA18966.1; -; Genomic_DNA.
 DR InterPro; IPR006484; PYST-B.
 DR TIGRFAMs; TIGR01597; PYST-B; 1.
 KW Hypothetical protein.

SQ SEQUENCE 242 AA; 28514 MW; FF31C7DDBB82957BF CRC64;

Query Match 90.3%; Score 28; DB 2; Length 242;

Best Local Similarity 83.3%; Pred. No. 5.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6

Db 7 KVFVFS 12

RESULT 27

Q7RNP5 PLAYO

ID Q7RNP5 PLAYO PRELIMINARY; PRT; 250 AA.

AC Q7RNP5;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein.

GN Name=PY01770;

OS Plasmodium yoelii yoelii.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=73239;

RN STRAIN=17XNL;

RC MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;

RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,

RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,

RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,

RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,

RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,

RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,

RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,

RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,

RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,

RA Carucci D.J.;

RT "Genome sequence and comparative analysis of the model rodent malaria

RT parasite Plasmodium yoelii yoelii."

RL Nature 419:512-519(2002).

CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AABL01000477; EAA21136.1; -; Genomic_DNA.

DR InterPro; IPR006484; PYST-B.

DR TIGRFAMs; TIGR01597; PYST-B; 1.

KW Hypothetical protein.

SQ SEQUENCE 250 AA; 29944 MW; EFFF3D5B5C001C8C CRC64;

Query Match 90.3%; Score 28; DB 2; Length 250;

Best Local Similarity 83.3%; Pred. No. 5.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6

Db 7 KVFVFS 12

RESULT 28

Q7PDC0 PLAYO

ID Q7PDC0 PLAYO PRELIMINARY; PRT; 251 AA.

AC Q7PDC0;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein.

GN Name=PY01770;

OS Plasmodium yoelii yoelii.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=73239;

RN STRAIN=17XNL;

RC MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;

RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,

RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,

RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,

GN Name=PY00554; Synonym=PY01592;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 [1]
 RN STRAIN=17XNL;
 RC MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;

RT "Genome sequence and comparative analysis of the model rodent malaria

RT parasite Plasmodium yoelii yoelii."

RL Nature 419:512-519(2002).

CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

CC EMBL; AABL01000150; EAA16801.1; -; Genomic_DNA.

DR InterPro; IPR006484; PYST-B.

DR TIGRFAMs; TIGR01597; PYST-B; 1.

KW Hypothetical protein.

SQ SEQUENCE 251 AA; 30043 MW; 3D608A4EC7F432D5 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 251;

Best Local Similarity 83.3%; Pred. No. 5.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6

Db 7 KVFVFS 12

RESULT 29

Q7RPS1 PLAYO

ID Q7RPS1 PLAYO PRELIMINARY; PRT; 251 AA.

AC Q7RPS1;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein.

GN Name=PY01385;

OS Plasmodium yoelii yoelii.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=73239;

RN STRAIN=17XNL;

RC MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;

RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,

RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,

RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,

RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,

RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,

RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,

RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,

RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,

RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,

RA Carucci D.J.;

RT "Genome sequence and comparative analysis of the model rodent malaria

RT parasite Plasmodium yoelii yoelii."

RL Nature 419:512-519(2002).

CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

CC EMBL; AABL01000363; EAA20702.1; -; Genomic_DNA.

DR InterPro; IPR006484; PYST-B.

```

DR TIGRFAMS; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 251 AA; 30054 MW; 3D6A80BE6DFE9275 CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 251;
  Best Local Similarity 83.3%; Pred. No. 5.4e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db      |||||:
       7 KVFVFS 12

RESULT 30
Q7RA57 PLAYO
ID Q7RA57 PLAYO PRELIMINARY; PRT; 252 AA.
AC Q7RA57;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Names=PY06647;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Sedegah M., Shoabi A., Cummings L.M.,
RA Cho J.K., Quackenbush J., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Florens L., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519 (2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL01001507; EAA16812.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMS; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 252 AA; 29757 MW; 64EB5B4C1P49786D CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 252;
  Best Local Similarity 83.3%; Pred. No. 5.4e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db      |||||:
       7 KVFVFS 12

RESULT 32
Q7RLK2 PLAYO
ID Q7RLK2 PLAYO PRELIMINARY; PRT; 255 AA.
AC Q7RLK2;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY02539;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Sedegah M., Shoabi A., Cummings L.M.,
RA Cho J.K., Quackenbush J., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Florens L., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519 (2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL0100695; EAA21989.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMS; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 255 AA; 30283 MW; 51F1FD33PED980B3 CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 255;
  Best Local Similarity 83.3%; Pred. No. 5.4e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db      |||||:
       7 KVFVFS 12

RESULT 31
Q7RF37 PLAYO
ID Q7RF37 PLAYO PRELIMINARY; PRT; 252 AA.
AC Q7RF37;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Names=PY04873;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]

```

```

Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 7 KVFVFS 12

RESULT 33
Q7RC37 PLAYO
ID Q7RC37 PLAYO PRELIMINARY; PRT; 262 AA.
AC Q7RC37
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY05766;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., Yates J.R. III, Raine J.D., Shumway M.F., Bidwell S.L.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RA "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RT Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABL01001873; EAA17841.1; -; Genomic_DNA.
DR InterPro; IPR006484; PFST-B.
DR TIGRFAMs; TIGR01597; PFST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 262 AA; 7A520F097AEF0573 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 262;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 7 KVFVFS 12

RESULT 34
Q7RC37 PLAYO
ID Q7RC37 PLAYO PRELIMINARY; PRT; 265 AA.
AC Q7RC37
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY05947;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,

```

```

RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Shumway M.F., Bidwell S.L.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RA "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RT Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABL01001955; EAA18074.1; -; Genomic_DNA.
DR InterPro; IPR006484; PFST-B.
DR TIGRFAMs; TIGR01597; PFST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 265 AA; 7CCD7DBCC3A26FF CRC64;

Query Match 90.3%; Score 28; DB 2; Length 265;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 7 KVFVFS 12

RESULT 35
Q7RB86 PLAYO
ID Q7RB86 PLAYO PRELIMINARY; PRT; 268 AA.
AC Q7RB86
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE Hypothetical protein (Fragment).
GN Name=PY06262;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Shumway M.F., Bidwell S.L.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RA "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RT Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABL01002095; EAA18444.1; -; Genomic_DNA.
DR InterPro; IPR006484; PFST-B.
DR TIGRFAMs; TIGR01597; PFST-B; 1.
KW Hypothetical protein.
FT NON-TER 268
SQ SEQUENCE 268 AA; D273B20E61AA181C CRC64;

Query Match 90.3%; Score 28; DB 2; Length 268;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6

```

Db |||||:
7 KVFVFS 12

RESULT 36

Q529U4 MAGGR PRELIMINARY; PRT; 285 AA.
AC Q529U4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG02290.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Alt-zahra M., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Ambruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blithsteyn B., Bloom I., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Darjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnikre A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseles M., Karlsson E.,
RA Kelis C., Kieu A., Kishner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Legler J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokitysang T., Lokitysang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Meneus L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mienga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Picani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Riese C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schubach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Teamlia T., Tsomo N., Vallée D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe grisea";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

DR EMBL; AACU01000444; EAA54305.1; -; Genomic_DNA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR Pfam; PF04479; RTA1.
DR Pfam; PF04479; RTA1; 1.
KW Hypothetical protein.
SQ SEQUENCE 285 AA; 31531 MW; DCB48A5EB9E4D1BD CRC64;

Query Match 90.3%; Score 28; DB 2; Length 285;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||:|
DB 6 KVFVFA 11

RESULT 37

Q94284_CAEEL PRELIMINARY; PRT; 293 AA.
AC Q94284;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein M02B7.4.
GN ORFNames=M02B7.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology";
RL Science 282:2012-2018 (1998).
DR EMBL; U70851; AAB09129.1; -; Genomic_DNA.
DR PIR; T29899; T29899.
DR Ensemble; M02B7.4; Caenorhabditis elegans.
DR WormBase; WBGene00019725; M02B7.4.
DR WormPep; M02B7.4; CEl2326.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 293 AA; 33247 MW; 90CEE020650E5065 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 293;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||:|
DB 258 KVFVFS 263

RESULT 38

Q7RBUL_PLAYO PRELIMINARY; PRT; 294 AA.
AC Q7RBUL;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06045;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,


```

RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002005; EAA18193.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 294 AA; 34611 MW; 281A85D322326659 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 294;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 7 KVFVFS 12

RESULT 39
QSUMP7_HALMA PRELIMINARY; PRT; 300 AA.
ID QSUMP7;
AC QSUMP7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Sugar ABC transport system permease protein.
GN Name=malFG-9; OrderedLocustNames=rrn80104;
OS Haloarcula marismortui (Haloacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxID=2238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 43049;
RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;
RT "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
RT the Dead Sea.";
RL Genome Res. 14:2221-2234(2004).
CC -1- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
DR EMBL; AY596298; AAV48306.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD transp.
DR Pfam; PF00528; BPD transp.1; 1.
DR PROSITE; PS50928; ABC_TM1; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 300 AA; 32975 MW; 9C230B44EF19CE5A CRC64;

Query Match 90.3%; Score 28; DB 2; Length 300;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6

```

```

Db 86 KVFVFA 91

RESULT 40
Q7RBJ3_PLAYO PRELIMINARY; PRT; 321 AA.
ID Q7RBJ3;
AC Q7RBJ3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06150;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perlea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002053; EAA18307.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 321 AA; 38948 MW; E1127BA81EB58FDB CRC64;

Query Match 90.3%; Score 28; DB 2; Length 321;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 51 KVFVFS 56

RESULT 41
P74429_SYNV3 PRELIMINARY; PRT; 326 AA.
ID P74429;
AC P74429;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ycf39 gene product.
GN Name=ycf39; OrderedLocustNames=blr0399;
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugita M., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the

```

```

RT  entire genome and assignment of potential protein-coding regions.";
RL  DNA Res. 3:109-136(1996).
DR  EMBL; BA000022; BAA18529.1; -; Genomic_DNA.
DR  PIR; S76400; S76400.
DR  GO; GO:0003824; F:catalytic activity; IEA.
DR  GO; GO:0051287; F:NAD binding; IEA.
DR  GO; GO:0009225; F:nucleotide-sugar metabolism; IEA.
DR  InterPro; IPR001509; Epimerase_Dh.
DR  Pfam; PF01370; Epimerase; 1.
KW  Complete proteome.
SQ  SEQUENCE 326 AA; 36519 MW; 99F522C1E980B943 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 326;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 KVFVFA 6
    |||||
Db  104 KVFVFS 109

RESULT 42
Q6KI05 MYCWO
ID  Q6KI05 MYCWO PRELIMINARY; PRT; 380 AA.
AC  Q6KI05;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  Restriction-modification enzyme mpuUVIII 8 subunit (EC 3.1.21.3).
GN  Name=hds; OrderedLocusNames=MMOB2850;
OS  Mycoplasma mobile.
OC  Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX  NCBI_TaxID=2118;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=163K / ATCC 43663;
RX  PubMed=15289470; DOI=10.1101/gr.2674004;
RA  Jaife J.D., Stange-Thomann N., Smith C., DeCaprio D., Fisher S.,
RA  Butler J., Calvo S., Elkins T., Fitzgerald M.G., Hafez N.,
RA  Kodira C.D., Major J., Wang S., Wilkinson J., Nicol R., Nusbaum C.,
RA  Birren B., Berg H.C., Church G.M.;
RT  "The complete genome and proteome of Mycoplasma mobile.";
RL  Genome Res. 14:1447-1461(2004).
DR  EMBL; AB017338; AAT27771.1; -; Genomic_DNA.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  GO; GO:0016787; F:hydrolase activity; IEA.
DR  GO; GO:0009035; F:type I site-specific deoxyribonuclease acti...; IEA.
DR  GO; GO:0006304; P:DNA modification; IEA.
DR  InterPro; IPR000055; Rest_mod_DNA.
DR  Pfam; PF01420; Methylase_S; 2.
KW  Complete proteome; Hydrolase.
SQ  SEQUENCE 380 AA; 44463 MW; D42428E38774F9CE CRC64;

Query Match          90.3%; Score 28; DB 2; Length 380;
Best Local Similarity 83.3%; Pred. No. 7.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 KVFVFA 6
    |||||
Db  294 KVFVFA 299

RESULT 43
Q4MSJ5 BACCE
ID  Q4MSJ5 BACCE PRELIMINARY; PRT; 388 AA.
AC  Q4MSJ5;
DT  13-SEP-2005 (TrEMBLrel. 31, Created)
DT  13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT  13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE  Basic membrane protein DtlB.
GN  Name=dtlB; ORFNames=BCE_G9241_1384;
OS  Bacillus cereus G9241.
OC  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;

```

```

OC  Bacillus cereus group.
OX  NCBI_TaxID=269801;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=G9241;
RX  PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA  Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA  Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA  Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA  Rilestone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA  Popovic T., Fraser C.M.;
RT  "Identification of anthrax toxin genes in a Bacillus cereus associated
RT  with an illness resembling inhalation anthrax.";
RL  Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC  -!- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
DR  EMBL; ABK0100009; EAL15142.1; -; Genomic_DNA.
SQ  SEQUENCE 388 AA; 45590 MW; E21AEA22BA0511CF CRC64;

Query Match          90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 KVFVFA 6
    :|||||
Db  286 RVVFFA 291

RESULT 44
Q6HLH8 BACHK
ID  Q6HLH8 BACHK PRELIMINARY; PRT; 388 AA.
AC  Q6HLH8;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  D-alanyl transfer protein.
GN  Name=ditB; OrderedLocusNames=BT9727_1258;
OS  Bacillus thuringiensis (subsp. konkukian).
OC  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC  Bacillus cereus group.
OX  NCBI_TaxID=180856;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=97-27;
RA  Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA  Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA  Richardson P., Rubin E., Rice H.;
RT  "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL  Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AE017355; AAT61956.1; -; Genomic_DNA.
DR  InterPro; IPR004299; MBOAT_fam.
DR  Pfam; PF03062; MBOAT; 1.
KW  Complete proteome.
SQ  SEQUENCE 388 AA; 45999 MW; DFB6794B3247A66B CRC64;

Query Match          90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 KVFVFA 6
    :|||||
Db  286 RVVFFA 291

RESULT 45
Q73BD3 BACCI
ID  Q73BD3 BACCI PRELIMINARY; PRT; 388 AA.
AC  Q73BD3;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  DltB protein.

```

```

GN Name=dltB; OrderedLocusNames=PCE1486;
OS Bacillus cereus (strain ATCC 10987);
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1."
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017269; AAS40415.1; -; Genomic_DNA.
DR TIGR; BCE1486; -.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 388 AA; 45590 MW; 74CBF3D745A83BC6 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFPVFFA 6
Db 286 RFVFFA 291

RESULT 46
ID Q63E03 BACCZ PRELIMINARY; PRT; 388 AA.
AC Q63E03;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE D-alanyl transfer protein.
GN Name=dltB;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18989.1; -; Genomic_DNA.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 388 AA; 45590 MW; 009F62D46DF6FC7 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFPVFFA 6
Db 286 RFVFFA 291

RESULT 47
ID Q81T98 BACAN PRELIMINARY; PRT; 388 AA.
AC Q81T98; Q611H5; Q6KVC6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE DltB protein.

```

```

GN Name=dltB; OrderedLocusNames=BAL388, BAS1286, GBAA1388;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Oekstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics."
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=Sterne;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017028; AAP25332.1; -; Genomic_DNA.
DR EMBL; AE017334; AAT30485.1; -; Genomic_DNA.
DR EMBL; AE017225; AAT53606.1; -; Genomic_DNA.
DR TIGR; BAL388; -.
DR TIGR; GBAA1388; -.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 388 AA; 45590 MW; 009F62D46DF6FC7 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFPVFFA 6
Db 286 RFVFFA 291

RESULT 48
ID Q81G40 BACCR PRELIMINARY; PRT; 391 AA.
AC Q81G40;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein dltB.
GN OrderedLocusNames=BC1371;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

```

RX MEDLINE-22608415; PubMed-12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapratral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen G., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyripides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL; AB017002; AAP08353.1; -; Genomic_DNA.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
DR Complete proteome.
SQ SEQUENCE 391 AA; 46119 MW; E8755D0033C91C54 CRC64;

    Query Match          90.3%; Score 28; DB 2; Length 391;
    Best Local Similarity 83.3%; Pred. No. 7.9e+02;
    Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 289 RFVFFA 294
:|||||

RESULT 49
Q5NEA9 FRATT PRELIMINARY; PRT; 398 AA.
ID Q5NEA9;
AC Q5NEA9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Aromatic amino acid transporter of the HAAAP family.
GN OrderedLocusNames=FTII732c;
OS Francisella tularensis (subsp. tularensis).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales;
OC Francisellaceae; Francisella.
OX NCBI_TaxID=119856;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCHU S4 / Schu 4;
RC PubMed=15640799; DOI=10.1038/ng1499;
RA Larsson P., Oyston P.C.F., Chain P., Chu M.C., Duffield M.,
RA Fuxelius H.-H., Garcia E., Haelterl G., Johansson D., Isherwood K.E.,
RA Karp P.D., Larsson E., Liu Y., Michell S., Prior J., Prior R.,
RA Malfatti S., Sjoestedt A., Svensson K., Thompson N., Vergez L.,
RA Wagg J.K., Wren B.W., Lindler L.E., Andersson S.G.E., Forsman M.,
RA Titball R.W.;
RT "The complete genome sequence of Francisella tularensis, the causative
RT agent of tularemia."
RL Nat. Genet. 37:153-159(2005).
DR EMBL; AJ749949; CAG46365.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002293; AA/re1_permease1.
DR InterPro; IPR002422; AA/re1_permease2.
DR InterPro; IPR002091; ARAA_permease.
DR Pfam; PF03222; Txp_Typ perm. 1.
DR PRINTS; PR00166; AROAPRMEASE.
DR Complete proteome; Transmembrane.
SQ SEQUENCE 398 AA; 44437 MW; 1A93FFD1D8AA4A38 CRC64;

    Query Match          90.3%; Score 28; DB 2; Length 398;
    Best Local Similarity 83.3%; Pred. No. 8e+02;
    Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 152 KLFVFA 157
:|||||

RESULT 50

```

```

Q73V08 MYCPA
ID Q73V08 MYCPA PRELIMINARY; PRT; 409 AA.
AC Q73V08;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Nuoh.
GN Name=nuoh; OrderedLocusNames=MAP3208;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium avium complex (MAC).
OX NCBI_TaxID=1770;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K10;
RA Li L., Bannantine J., Zhang Q., Anonsin A., Alt D., Kapur V.;
RL Submitted (SEF-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017238; AAS05756.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001694; Resp_NADH_dhl.
DR Pfam; PF00146; NADHdh; 1.
DR PROSITE; PS00667; COMPLEX1_ND1_1; 1.
DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
KW Complete proteome.
SQ SEQUENCE 409 AA; 44971 MW; 693518B9DDF94B11 CRC64;

    Query Match          90.3%; Score 28; DB 2; Length 409;
    Best Local Similarity 83.3%; Pred. No. 8.2e+02;
    Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 67 KFVYFA 72
:|||||

RESULT 51
Q722C3 CAEL PRELIMINARY; PRT; 421 AA.
ID Q722C3 CAEL PRELIMINARY; PRT; 421 AA.
AC Q722C3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Y19D10A.8;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; AC006722; AAK68421.2; -; Genomic_DNA.
DR Ensembl; Y19D10A.8; Caenorhabditis elegans.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS.1.
DR Pfam; PF07690; MFS 1; 1.
DR PROSITE; PS50850; MFS; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 421 AA; 46361 MW; 75B7CF15ABE2C432 CRC64;

    Query Match          90.3%; Score 28; DB 2; Length 421;

```

Best Local Similarity 83.3%; Pred. No. 8.4e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KFVFFA 6
Db 291 RFVFFA 296

RESULT 52

ID Q9PQ2_UREPA PRELIMINARY; PRT; 422 AA.
AC Q9PQ2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unique hypothetical.
GN OrderedLocusNames=U0329;
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 700970;
RX MEDLINE=20500219; PubMed=11048724; DOI=10.1038/35037619;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RA "The complete sequence of the mucosal pathogen Ureaplasma
RT urealyticum".
RL Nature 407:757-762(2000).
RW EMBL; AB002130; AAF30738.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 422 AA; 49219 MW; 8EA05B3F2F76C8E8 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 422;
Best Local Similarity 83.3%; Pred. No. 8.4e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KFVFFA 6
Db 208 KYVFFA 213

RESULT 53

ID Q8FW04_BRUSU PRELIMINARY; PRT; 430 AA.
AC Q8FW04;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Uracil-xanthine permease, putative.
GN OrderedLocusNames=BRA0661;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kaul M., Shetty J., Malek J.A.,
RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AE014292; AAN33850.1; -; Genomic DNA.
DR TIGR; BRA0661; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004711; Bene.
DR InterPro; IPR006043; Xant/urac/vitc.
DR Pfam; PF00860; Xan ur permease; 1.
DR ProDom; PD024853; Bene; 1.
KW Complete proteome.
SQ SEQUENCE 430 AA; 44661 MW; B69F2E03E9A28C39 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 430;
Best Local Similarity 83.3%; Pred. No. 8.5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KFVFFA 6
Db 424 RFVFFA 429

RESULT 54

Q6Q8W8_9GAMM PRELIMINARY; PRT; 432 AA.
ID Q6Q8W8_9GAMM
AC Q6Q8W8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Predicted preprotein translocase subunit SecY.
GN ORFNames=Red20809_103;
OS uncultured marine gamma proteobacterium EBAC20E09.
OC Bacteria; Proteobacteria; Gammaproteobacteria; SAR86 cluster;
OC environmental samples.
OX NCBI_TaxID=266134;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15305915; DOI=10.1111/j.1462-2920.2004.00676.x;
RA Sabehi G., Reja O., Suzuki M.T., Preston C.M., DeLong E.P.;
RT "Different SAR86 subgroups harbour divergent proteorhodopsins.";
RL Environ. Microbiol. 6:903-910(2004).
DR EMBL; AY552545; AAS73104.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015450; F:protein translocase activity; IEA.
DR GO; GO:0009306; P:protein secretion; IEA.
DR GO; GO:0006605; P:protein targeting; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
DR InterPro; IPR002208; SecY.
DR Pfam; PF00344; SecY; 1.
DR PRINTS; PR00303; SECYTRNLCASE.
DR TIGRFAMs; TIGR00967; 3a05018007; 1.
DR PROSITE; PS00756; SECY_2; 1.
KW Protein transport; Translocation; Transmembrane; Transport.
SQ SEQUENCE 432 AA; 47276 MW; CCOF2DA782EB8F79 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 432;
Best Local Similarity 83.3%; Pred. No. 8.5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KFVFFA 6
Db 15 RFVFFA 20

RESULT 55

Q8M9J3_9AQUA PRELIMINARY; PRT; 436 AA.
ID Q8M9J3_9AQUA
AC Q8M9J3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribulose-bisphosphate carboxylase (EC 4.1.1.39) (Fragment).
GN Name=rbcl;
OS Ilex pubescens.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; campanulids; Aquifoliales; Aquifoliaceae; Ilex.
 OX NCBI_TaxID=185543;
 RN [1]
 RA NUCLEOTIDE SEQUENCE.
 RA Manen J.F.;
 RA "The complex history of the genus Ilex L. (Aquifoliaceae): evidence
 RT from the comparison of plastid and nuclear DNA sequences and from
 RT fossil data.";
 RL Plant Syst. Evol. 0:0-0(0).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RA Manen J.F.;
 RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic
 CC carbon dioxide fixation, as well as the oxidative fragmentation of
 CC carbon dioxide fixation, as well as the oxidative fragmentation of
 CC the pentose substrate in the photorepiration process (By
 CC similarity).
 CC -I- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic
 CC carbon dioxide fixation, as well as the oxidative fragmentation of
 CC the pentose substrate in the photorepiration process. Both
 CC reactions occur simultaneously and in competition at the same
 CC active site (By similarity).
 CC -I- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) + H(2)O =
 CC 2 3-phospho-D-glycerate.
 CC -I- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) = 3-
 CC phospho-D-glycerate + 2-phosphoglycolate.
 CC -I- SUBUNIT: 8 large chains + 8 small chains (By similarity).
 CC -I- SUBCELLULAR LOCATION: Chloroplast (By similarity).
 CC -I- SIMILARITY: Belongs to the RuBisCO large chain family.
 DR EMBL; AJ492722; CAD37439.1; -; Genomic_DNA.
 DR SRR; Q8M9J3; 9-436.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0009573; C:ribulose biphosphate carboxylase complex (. . .); IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.
 DR GO; GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA.
 DR GO; GO:0015977; P:carbon utilization by fixation of carbon di. . .; IEA.
 DR GO; GO:0009853; P:photorepiration; IEA.
 DR GO; GO:0015979; P:photosynthesis; IEA.
 DR InterPro; IPR000685; RuBisCO_large.
 DR Pfam; PF00016; RuBisCO_large; 1.
 DR Pfam; PF02788; RuBisCO_large; 1.
 KW Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase;
 KW Oxidoreductase; Photorepiration; Photosynthesis.
 FT NON_TER 436 436
 SQ SEQUENCE 436 AA; 48367 MW; E1A65FFCF93985A1 CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 436;
 Best Local Similarity 83.3%; Pred. No. 8.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 Db 217 RVVFFA 222
 RESULT 56
 ID O44595_CABEL PRELIMINARY; PRT; 452 AA.
 AC O44595;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein F56A4.10.
 GN ORFNames=F56A4.10;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=9906613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018 (1998).
 DR EMBL; AC006645; AAF39848.1; -; Genomic_DNA.
 DR PIR; C88969; C88969.
 DR Ensembl; F56A4.10; Caenorhabditis elegans.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; F:transport; IEA.
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR011701; MFS.
 DR Pfam; PF07690; MFS_1; 1_
 DR PROSITE; PS50850; MFS; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 452 AA; 49858 MW; F1BED2FBE60CAE59 CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 452;
 Best Local Similarity 83.3%; Pred. No. 8.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 Db 291 RVVFFA 296
 RESULT 57
 Q6GVJ4_9BURK PRELIMINARY; PRT; 456 AA.
 ID Q6GVJ4;
 AC Q6GVJ4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Glycosyltransferase.
 GN Name=wbcE;
 OS Burkholderia cenocepacia.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
 OX NCBI_TaxID=95486;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=K56-2;
 RX PubMed=15687196; DOI=10.1128/JB.187.4.1324-1333.2005;
 RA Ortega X., Hunt T.A., Loutet S., Vinion-Dubiel A.D., Datta A.,
 RA Choudhury B., Goldberg J.B., Carlson R., Valvano M.A.;
 RT "Reconstitution of O-Specific Lipopolysaccharide Expression in
 RT Burkholderia cenocepacia Strain J2315, Which Is Associated with
 RT Transmissible Infections in Patients with Cystic Fibrosis.";
 RL J. Bacteriol. 187:1324-1333(2005).
 DR EMBL; AY633623; AAT48329.1; -; Genomic_DNA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0009058; F:biosynthesis; IEA.
 DR InterPro; IPR001296; Glyco_transf_1.
 DR Pfam; PF00534; Glycos_transf_1; 1.
 KW Transferase.
 SQ SEQUENCE 456 AA; 50801 MW; E5B3648E1BE54A54 CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 456;
 Best Local Similarity 83.3%; Pred. No. 8.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 Db 6 KFLFFA 11
 RESULT 58
 REL_NEPAL
 ID_RBL_NEPAL STANDARD; PRT; 465 AA.
 AC P28434;

DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ribulose biphosphate carboxylase large chain (EC 4.1.1.39) (RuBisCO
 DE large subunit) (Fragment).
 GN Namearbel;
 OS Nepenthes alata (Winged pitcher plant).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Caryophyllales; Nepenthaceae; Nepenthes.
 OX NCBI_TaxID=4376;
 RN [1]

NUCLEOTIDE SEQUENCE.
 RP MEDLINE=3237008; PubMed=1523408;
 RA Albert V.A., Williams S.E., Chase M.W.;
 RT "Carnivorous plants: phylogeny and structural evolution.";
 RL Science 257:1491-1495(1992).
 CC -1- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic
 CC carbon dioxide fixation, as well as the oxidative fragmentation of
 CC the pentose substrate in the photorespiration process. Both
 CC reactions occur simultaneously and in competition at the same
 CC active site.
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) + H(2)O =
 CC 2 3-phospho-D-glycerate + 2 H(+).
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) = 3-
 CC phospho-D-glycerate + 2-phosphoglycolate.
 CC -1- COPACTOR: Binds 1 magnesium ion per subunit (By similarity).
 CC -1- SUBUNIT: Heterohexameric of 8 large chains and 8 small chains;
 CC disulfide-linked. The disulfide link is formed within the large
 CC subunit homodimers (By similarity).
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- DOMAIN: The basic functional RuBisCO is composed of a large chain
 CC homodimer in a "head-to-tail" conformation. In form I RuBisCO this
 CC homodimer is arranged in a barrel-like tetramer with the small
 CC subunits forming a tetrameric "cap" on each end of the "barrel"
 CC (By similarity).
 CC -1- PTM: The disulfide bond which can form in the large chain dimeric
 CC partners within the hexadecamer appears to be associated with
 CC oxidative stress and protein turnover (By similarity).
 CC -1- SIMILARITY: Belongs to the RuBisCO large chain family. Type I
 CC subfamily.

 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; L01936; AAA84502.2; -; Genomic_DNA.
 CC HSSP; P00875; LAUS.
 CC SWP; P28434; 1-465.
 CC HAMAP; MF_01338; -; 1.
 CC InterPro; IPR000685; RuBisCO_large.
 CC Pfam; PF00016; RuBisCO_large; 1.
 CC Pfam; PF02788; RuBisCO_large N; 1.
 CC PROSITE; PS00157; RUBISCO_LARGE; 1.
 CC Calvin cycle; Carbon dioxide fixation; Chloroplast; Lyase; Magnesium;
 KW Metal-binding; Methylation; Monooxygenase; Oxidoreductase;
 KW Photorespiration; Photosynthesis.
 FT ACT SITE 165 165 Proton acceptor (By similarity).
 FT ACT SITE 165 165 Proton acceptor (By similarity).
 FT ACT SITE 284 284 Magnesium (via carboxylate group) (By
 FT METAL 191 191 similarity).
 FT METAL 193 193 Magnesium (By similarity).
 FT METAL 194 194 Magnesium (By similarity).
 FT BINDING 113 113 Substrate (in homodimeric partner) (By
 FT similarity).
 FT BINDING 163 163 Substrate; C1 phosphate group (By
 FT similarity).
 FT BINDING 167 167 Substrate (By similarity).
 FT BINDING 285 285 Substrate; C5 phosphate group (By

FT BINDING 317 317 similarity).
 FT Substrate; C5 phosphate group (By
 FT similarity).
 FT BINDING 369 369 Substrate; C5 phosphate group (By
 FT similarity).
 FT SITE 324 324 Transition state stabilizer (By
 FT similarity).
 FT MOD_RES 4 4 N6,N6,N6-trimethyllysine (By similarity).
 FT MOD_RES 191 191 N6-carboxyllysine (By similarity).
 FT DISULFID 237 237 Interchain (in linked form) (By
 FT similarity).
 FT NON_TER 1 1'
 SQ SEQUENCE 465 AA; 51614 MW; 29E322894FE92451 CRC64;
 Query Match 90.3%; Score 28; DB 1; Length 465;
 Best Local Similarity 83.3%; Pred. No. 9.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KFVFFA 6
 Db 207 RFVFFA 212

RESULT 59
 Q9NSQ8_CABEL PRELIMINARY; PRT; 472 AA.
 ID Q9NSQ8_CABEL PRELIMINARY;
 AC Q9NSQ8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein F56A4.12.
 DE ORFNames=F56A4.12;
 GN Caenorhabditis elegans.
 OC Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; AC006645; AAF39850.1; -; Genomic DNA.
 DR Ensembl; F56A4.12; Caenorhabditis elegans.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR011701; MFS_1.
 DR Pfam; PF07690; MFS_1; 1.
 DR PROSITE; PS50850; MFS; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 472 AA; 52251 MW; C06DFDB6AA6755AE CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 472;
 Best Local Similarity 83.3%; Pred. No. 9.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KFVFFA 6
 Db 340 RFVFFA 345

RESULT 60
 Q625W2_CABER
 ID Q625W2_CABER PRELIMINARY; PRT; 480 AA.
 AC Q625W2;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein CBG01115.

```

GN Name=CBG01115;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]_TaxID=6238;
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; CAAC0100007; CAE58039.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
DR PROSITE; PS50850; MFS; 1.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 53324 MW; BDC75B20A6CC51 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 480;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 343 RVVFFA 348

RESULT 61
Q5JJ16_PYRKO
ID Q5JJ16_PYRKO PRELIMINARY; PRT; 482 AA.
AC Q5JJ16;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical membrane protein, conserved.
GN OrderedLocusNames=TK1728;
OS Pyrococcus kodakaraensis (Thermococcus kodakaraensis).
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCBI_TaxID=69014;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KOD1;
RA Fukui T., Atomi H., Kanai T., Matsumi R., Fujiwara S., Imanaka T.;
RT "Complete genome sequence of the hyperthermophilic archaeon
Thermococcus kodakaraensis KOD1 and comparison with Pyrococcus
genomes."
RL Genome Res. 15:352-363(2005).
DR EMBL; AP006878; BAD85917.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 482 AA; 54068 MW; 097052D348C3BB4D CRC64;

Query Match 90.3%; Score 28; DB 2; Length 482;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 336 RVVFFA 341

RESULT 62
Q966D7_CAEEL
ID Q966D7_CAEEL PRELIMINARY; PRT; 488 AA.
AC Q966D7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Y19D10A.11;

```

```

OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]_TaxID=6239;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; AC006722; AAK68411.2; -; Genomic DNA.
DR Ensembl; Y19D10A.11; Caenorhabditis elegans.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
DR PROSITE; PS50850; MFS; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 488 AA; 54121 MW; A145401A124DB716 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 488;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 356 RVVFFA 361

RESULT 63
Q621X3_CAEER
ID Q621X3_CAEER PRELIMINARY; PRT; 492 AA.
AC Q621X3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG02310 (Fragment).
GN Name=CBG02310;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]_TaxID=6238;
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; CAAC01000012; CAE59030.1; -; Genomic DNA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc_phsphtase.
DR Pfam; PF00328; Acid_phosphat_A; 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 492
SQ SEQUENCE 492 AA; 57471 MW; 4F1D61BB64DC5CFB CRC64;

Query Match 90.3%; Score 28; DB 2; Length 492;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 188 RVVFFA 193

```

RESULT 64


```

Q38860 ARATH PRELIMINARY; PRT; 506 AA.
ID Q38860 ARATH PRELIMINARY; PRT; 506 AA.
AC Q38860;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-FEB-2005 (TEMBLrel. 29, Last annotation update)
DE Fatty acid elongase 1.
GN Names: Synonyms=At4g34520, T4L20.100;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WS;
RX MEDLINE=95252821; PubMed=7734965; DOI=10.1105/tpc.7.3.309;
RA James D.W. Jr., Lim E., Keller J., Plooy I., Ralston E., Dooner H.K.;
RT "Directed tagging of the Arabidopsis FATTY ACID ELONGATION1 (FAE1)
RT gene with the maize transposon activator.";
RL Plant Cell 7:309-319(1995).
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Terryn N., Ardiles W., Buyssehaert C., Dasseville R.,
RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
RA Villarroel R., Gielen J., Van Montagu M., Jesse T., Heijnen L., Vos P.,
RA Hohelsel J., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RA Terryn N., Ardiles W., Buyssehaert C., Dasseville R., De Clerck R.,
RA De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarroel R.,
RA Gielen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RA EMBL; U29142; AAA70154.1; -; Genomic DNA.
RA EMBL; AL023094; CAA18831.1; -; Genomic DNA.
RA EMBL; AL161585; CAB80169.1; -; Genomic DNA.
DR PTR; T05272; T05272.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; F:biosynthesis; IEA.
SQ SEQUENCE 506 AA; 56263 MW; 4516D0E8E453D18 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 506;
Best Local Similarity 83.3%; Pred. No. 9.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
Db 356 KFLFFA 361

RESULT 65
MURE BORBU STANDARD; PRT; 508 AA.
AC O51219;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase
DE (EC 6.3.2.13) (UDP-N-acetylmuramyl-tripeptide synthetase) (Meso-
DE diaminopimelate-adding enzyme) (UDP-MurNAC-tripeptide synthetase).
GN Name=mure; OrderedLocName=BB0201;
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;

Borrelia burgdorferi group.
NCBI_TaxID=139;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
RA Winn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
RA Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,
RA Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
RA Gocayne J.D., Weidman J.F., Utterback T.R., Wathey L., McDonald L.A.,
RA Artiach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,
RA Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586 (1997).
CC -1- FUNCTION: Cell wall formation. Diaminopimelic acid adding enzyme
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanyl-D-
CC glutamate + meso-2,6-diaminoheptanedioate = ADP + phosphate + UDP-
CC N-acetylmuramoyl-L-alanyl-D-gamma-glutamyl-meso-2,6-diamino-
CC heptanedioate.
CC -1- PATHWAY: Peptidoglycan biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the murCDF family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AE001130; AAC66588.1; -; Genomic DNA.
DR PTR; A70125; A70125.
DR TIGR; B80201; -; 1.
DR HAMAP; MF_00208; -; 1.
DR InterPro; IPR004101; Mur_ligase_C.
DR InterPro; IPR00713; Mur_ligase_N.
DR InterPro; IPR005761; MurE.
DR InterPro; IPR012237; UDP-NACM_Align.
DR Pfam; PF01225; Mur_ligase_1.
DR Pfam; PF02875; Mur_ligase_C_1.
DR TIGRFAMS; TIGR01085; mure; 1.
DR PIRSF; PIRSF001562; UDP-NACM_Align; 1.
KW ATP-binding; Cell cycle; Cell division; Cell shape; Cell wall;
KW Complete proteome; Ligase; Nucleotide-binding;
KW Peptidoglycan synthesis.
FT NE_BIND 118 124 ATP (Potential).
SQ SEQUENCE 508 AA; 57149 MW; 44043B05F3683B8C CRC64;

Query Match 90.3%; Score 28; DB 1; Length 508;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
Db 41 RFVFFA 46

RESULT 66
P93058 BRAJU PRELIMINARY; PRT; 509 AA.
ID P93058 BRAJU PRELIMINARY; PRT; 509 AA.
AC P93058;
DT 01-MAY-1997 (TEMBLrel. 03, Created)
DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Fatty acid elongation 1.
GN Name=fael;
OS Brassica juncea (Leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Brassica.

```

```

OX NCBI_TaxID=3707;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Hypocotyl;
RA Venkateswari J., Kanwar S., Kirti P.B., Malathi V.G., Chopra V.L.;
RT "Molecular cloning and characterization of fatty acid elongation 1
RT (fae 1) gene of Brassica juncea cv. Pusa Bold.";
RL J. Plant Biochem. Biotechnol. 8:53-55(1999).
DR EMBL; Y11007; CAA71898.1; -; Genomic DNA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 509 AA; 56661 MW; B204DASAB5887C5C CRC64;

Query Match          90.3%; Score 28; DB 2; Length 509;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 359 KFLFFA 364

RESULT 67
Q8LSC7_BRACM
ID Q8LSC7_BRACM PRELIMINARY; PRT; 509 AA.
AC Q8LSC7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fatty acid elongase.
OS Brassica campestris (field mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3711;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Yadav P., Bhat S., Chopra V.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF491878; AAM33539.1; -; Genomic DNA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 509 AA; 56661 MW; 59ED8F07457CB6F5 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 509;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 358 KFLFFA 363

RESULT 68
Q8S384_BRAJU
ID Q8S384_BRAJU PRELIMINARY; PRT; 509 AA.
AC Q8S384;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Fatty acid elongase.
GN Name=Fael.2; Synonyms=fae 1.1;
OS Brassica juncea (leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3707;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Yadav P., Bhat S., Chopra V.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

```

```

DR EMBL; AF491877; AAM11648.1; -; Genomic DNA.
DR EMBL; AF491876; AAM34043.1; -; Genomic DNA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 509 AA; 56616 MW; F6C553739AD86C23 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 509;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 358 KFLFFA 363

RESULT 69
O80729_ARATH
ID O80729_ARATH PRELIMINARY; PRT; 517 AA.
AC O80729;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative cytochrome P450 (At2g46950).
GN Name=At2g46950;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Renning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RN NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RN NUCLEOTIDE SEQUENCE.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Ecker J.R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RN NUCLEOTIDE SEQUENCE.
RA Kim C.J., Chen H., Cheuk R., Shinn P., Ecker J.R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: belongs to the cytochrome P450 family.
DR EMBL; AC004411; AAC34228.1; -; Genomic DNA.
DR EMBL; BT014808; AAT41791.1; -; mRNA.
DR EMBL; BT011625; AAS47631.1; -; mRNA.
DR PIR; T02192; T02192.
DR HSP; P14779; 1JZP.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP4501.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PRO0063; EP4501.
DR PRINTS; PRO0385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
DR Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
KW Transmembrane.
SQ SEQUENCE 517 AA; 59021 MW; 3963BCEC988C19A2 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 517;
Best Local Similarity 83.3%; Pred. No. 9.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 123 KVFVFS 128

```

```

RESULT 70
Q6NI23 CORDI PRELIMINARY; PRT; 529 AA.
AC Q6NI23;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative peptide transport system secreted protein.
GN OrderedLocusNames=DIP0956;
OS Corynebacterium diphtheriae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1717;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Biotype gravis / NCTC 13129;
RX MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
RA Cerdeno-Jarraga A.-M., Efstathiou A., Dover L.G., Holden M.T.G.,
RA Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,
RA De Zuyasa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
RA Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A.,
RA Rabinowitsch E., Rutherford K.M., Thomson N.R., Unwin L.,
RA Whitehead S., Barrell B.G., Parkhill J.;
RT "The complete genome sequence and analysis of Corynebacterium
RT diphtheriae NCTC13129.";
RL Nucleic Acids Res. 31:6516-6523(2003).
DR EMBL; BX248356; CAB49475.1; -; Genomic DNA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000914; SBP_bac_5.
DR Pfam; PF00496; SBP_bac_5; 1.
DR PROSITE; PS01040; SBP_BACTERIAL_5; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 529 AA; 57407 MW; 0B8BF5955BA6818A CRC64;

Query Match 90.3%; Score 28; DB 2; Length 529;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFPA 6
Db 234 KFVFYA 239

RESULT 71
Q7PQZ0 ANOGA PRELIMINARY; PRT; 538 AA.
AC Q7PQZ0;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE ENSANGP0000001154 (Fragment).
GN ORFNames=ENSANG00000001003;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008859; EAL40926.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR003595; PTPc_motif.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.

Query Match 90.3%; Score 28; DB 2; Length 538;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFPA 6
Db 503 KFVFYA 508

RESULT 72
Q5TTR3 ANOGA PRELIMINARY; PRT; 558 AA.
AC Q5TTR3;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE ENSANGP00000029277 (Fragment).
GN ORFNames=ENSANG00000001003;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008859; EAL40926.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR003595; PTPc_motif.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.

```

DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PRTPHPHTASE.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00194; PTPC; 1.
 DR SMART; SM00404; PTPC_motif; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS00001; SH2; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_FTP; 1.
 KW Hydrolase.
 FT NON_TER 1 1
 FT NON_TER 558 558
 SQ SEQUENCE 558 AA; 63773 MW; 2EC7E5D5BAFE310 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 558;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 :|||:
 Db 519 KVFVFA 524

RESULT 73
 Q97K08_CLOAB PRELIMINARY; PRT; 571 AA.
 AC Q97K08_CLOAB PRELIMINARY;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Diguanilate cyclase/phosphodiesterase domain (GGDEF) containing protein.
 GN OrderedLocusNames-CAC0818;
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RX DOI=10.1128/JB.183.16.4823-4838.2001;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
 RA "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum."
 RT J. Bacteriol. 183:4823-4838(2001).
 RL EMBL; AS007597; AAK78794.1; -; Genomic_DNA.
 DR PIR; G97000; G97000.
 DR InterPro; IPR011623; 7TMR-DISM_7TM.
 DR InterPro; IPR000160; GGDEF.
 DR Pfam; PF07695; 7TMR-DISM_7TM; 1.
 DR Pfam; PF00990; GGDEF; 1.
 DR SMART; SM00267; DUFL; 1.
 DR TIGRFAMs; TIGR00254; GGDEF; 1.
 DR PROSITE; PS00887; GGDEF; 1.
 KW Complete proteome.
 SQ SEQUENCE 571 AA; 66225 MW; 64B51A5D9F5BD23F CRC64;

Query Match 90.3%; Score 28; DB 2; Length 571;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 :|||:
 Db 314 KVFVFA 319

RESULT 74
 Q4UGB4_THEAN PRELIMINARY; PRT; 584 AA.
 AC Q4UGB4_
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE SerYl-trna synthetase, putative (EC 6.1.1.11).
 GN ORFNames=TA19195;
 OS Theileria annulata.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
 OC Theileria.
 OX NCBI_TaxID=5874;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ankara isolate clone C9;
 RA Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M., Hall N., Barrell B.G.;
 RA "The chromosome 1 sequence of Theileria annulata."
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR940347; CAI73875.1; -; Genomic_DNA.
 KW Aminoacyl-tRNA synthetase; Ligase.
 SQ SEQUENCE 584 AA; 66617 MW; 76FEB10EEF7C6691 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 584;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 :|||:
 Db 13 RVVFFA 18

RESULT 75
 Q7PS12_ANOGA PRELIMINARY; PRT; 615 AA.
 ID Q7PS12_ANOGA PRELIMINARY;
 AC Q7PS12;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE ENSANGP00000017331.
 GN ORFNames=ENSANGG000000021622;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RT "Anopheles gambiae re-annotation."
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
 CC EMBL; AAB0100846; EAA06305.3; -; Genomic_DNA.
 DR SMR; Q7PS12; 1-355.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0005856; C:cytoskeleton; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008092; F:cytoskeletal protein binding; IEA.
 DR InterPro; IPR000299; Band 4.1.
 DR InterPro; IPR011174; ERM_
 DR InterPro; IPR011259; ERM_C.
 DR InterPro; IPR000798; Ez/Fad/moesin.
 DR Pfam; PF00373; Band_41; 1.
 DR Pfam; PF00769; ERM; 1.

DR PIRSF; PIRSF002305; ERM; 1.
DR PRINTS; PR00661; ERMFAMILY.
DR SMART; SM00295; B41; 1.
DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS50057; FERM_3; 1.
SQ SEQUENCE 615 AA; 72579 MW; 804168798B4C5DDC CRC64;
Query Match 90.3%; Score 28; DB 2; Length 615;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVFVFA 6
Db 96 KVFVFS 101

Search completed: December 29, 2005, 17:47:10
Job time : 90.1936 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:57 ; Search time 12.9677 Seconds
(without alignments)
44.518 Million cell updates/sec

Title: US-10-009-122-4

Perfect score: 31

Sequence: 1 KFPVFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : PIR 80.*

1: piri.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	96.8	397	2	P95352
2	28	90.3	49	2	G83919
3	28	90.3	177	2	T16280
4	28	90.3	293	2	T29899
5	28	90.3	326	2	S76400
6	28	90.3	422	2	E82904
7	28	90.3	452	2	C89699
8	28	90.3	506	2	T05272
9	28	90.3	508	2	A70125
10	28	90.3	517	2	T02192
11	28	90.3	571	2	G97000
12	28	90.3	1072	2	T37742
13	28	90.3	1285	2	B72420
14	27	87.1	38	4	S07937
15	27	87.1	138	2	C70150
16	27	87.1	185	2	I40051
17	27	87.1	185	2	C70199
18	27	87.1	193	2	S45022
19	27	87.1	193	2	G69707
20	27	87.1	232	2	AH0299
21	27	87.1	274	2	E73239
22	27	87.1	298	2	T29189
23	27	87.1	321	2	T06845
24	27	87.1	349	2	S73198
25	27	87.1	358	2	S74431
26	27	87.1	358	2	A82218
27	27	87.1	370	2	H90559
28	27	87.1	408	2	T23285
29	27	87.1	409	2	T47754

30	27	87.1	436	2	E96635
31	27	87.1	459	2	B72361
32	27	87.1	488	2	T20124
33	27	87.1	522	2	H86248
34	27	87.1	527	2	S49827
35	27	87.1	581	2	B81107
36	27	87.1	581	2	B81909
37	27	87.1	582	2	I38028
38	27	87.1	582	2	I84471
39	27	87.1	689	2	JC7286
40	27	87.1	856	2	S30338
41	27	87.1	857	2	S44883
42	27	87.1	870	2	T31795
43	26	83.9	107	2	S56500
44	26	83.9	127	2	G87731
45	26	83.9	171	2	C81280
46	26	83.9	183	2	T47707
47	26	83.9	188	2	A86806
48	26	83.9	203	2	S73449
49	26	83.9	216	2	G70437
50	26	83.9	218	2	F86844
51	26	83.9	243	2	T22101
52	26	83.9	255	2	B81693
53	26	83.9	265	2	T44414
54	26	83.9	289	2	B81857
55	26	83.9	289	2	D81085
56	26	83.9	294	2	A27692
57	26	83.9	294	2	B36351
58	26	83.9	297	2	S75656
59	26	83.9	323	2	D86216
60	26	83.9	324	2	T24424
61	26	83.9	337	2	S08459
62	26	83.9	344	2	E90564
63	26	83.9	381	2	T34333
64	26	83.9	389	2	S68155
65	26	83.9	390	2	T22810
66	26	83.9	395	2	T00516
67	26	83.9	395	2	D81040
68	26	83.9	395	2	B81986
69	26	83.9	397	2	T46710
70	26	83.9	397	2	A11250
71	26	83.9	397	2	AE1613
72	26	83.9	398	2	T44331
73	26	83.9	401	2	H69833
74	26	83.9	404	2	C95990
75	26	83.9	405	1	CEQFR
76	26	83.9	406	2	T43120
77	26	83.9	416	2	T23977
78	26	83.9	431	2	B81254
79	26	83.9	432	2	AD3311
80	26	83.9	436	2	A81443
81	26	83.9	438	2	H82974
82	26	83.9	443	2	AB2841
83	26	83.9	443	2	D97618
84	26	83.9	462	2	AF0057
85	26	83.9	483	2	T20895
86	26	83.9	486	2	S50644
87	26	83.9	503	2	AC3296
88	26	83.9	544	2	T40058
89	26	83.9	664	2	T14132
90	26	83.9	749	2	S62171
91	26	83.9	780	2	T02939
92	26	83.9	841	2	T48508
93	26	83.9	884	2	T25205
94	26	83.9	903	2	G82516
95	26	83.9	1772	2	A45532
96	26	83.9	1785	2	A45546
97	26	83.9	2149	2	C96695
98	26	83.9	2948	2	T22664
99	25	80.6	33	2	S23094
100	25	80.6	42	2	PN0512
101	25	80.6	50	2	A69055
102	25	80.6	57	2	A60045

hypothetical prote
conserved hypochet
hypothetical prote
protein T23J18.22
probable membrane
exodeoxyribonuclea
exodeoxyribonuclea
matrix metalloprot
liver-specific org
hydroxymethylgluta
ZC262.3 protein -
hypothetical prote
probable membrane
protein W10C8.3 [i
hypothetical prote
transcription regu
MG028 homolog B01
soluble hydrogenas
hypothetical prote
hypothetical prote
conserved hypochet
hypothetical prote
probable acetyltra
HcrB/MSB family p
sarcotoxin IIA pre
sarcotoxin II-2 -
hypothetical prote
protein T23G18.8 [i
hypothetical prote
potassium channel
hypothetical prote
ubiquinol-cytochro
ubiquinol-cytochro
hypothetical prote
cytochrome c-type
probable membrane
multidrug resistanc
multidrug-efflux t
multidrug-efflux t
hypothetical prote
conserved hypochet
probable sugar upt
ubiquinol-cytochro
conserved hypochet
hypothetical prote
probable transmembr
ubiquinol-cytochro
probable transmembr
probable MFS trans
MFS permease[proli
probable mfs trans
probable transport
hypothetical prote
cytochrome oxidase
proline/betaine tr
probable chromatin
NADH2 dehydrogenas
probable membrane
chloride channel p
beta-adaptin-like
hypothetical prote
hypothetical prote
major merozoite su
major merozoite su
ribulose biphosph
hypothetical prote
beta-amyloid prote
beta-amyloid prote
hypothetical prote
Alzheimer's diseas

103	25	80.6	57	2	F60045	Alzheimer's diseases	176	25	80.6	711	2	C49219	toxin apxIII secre
104	25	80.6	57	2	D60045	Alzheimer's diseases	177	25	80.6	747	2	JH0773	Alzheimer's diseases
105	25	80.6	57	2	E60045	Alzheimer's diseases	178	25	80.6	764	2	T48446	hypothetical prote
106	25	80.6	57	2	G60045	Alzheimer's diseases	179	25	80.6	770	1	QRHUA4	Alzheimer's diseases
107	25	80.6	57	2	B60045	Alzheimer's diseases	180	25	80.6	771	2	AD3126	ATP-dependent DNA
108	25	80.6	78	2	E69969	hypothetical prote	181	25	80.6	771	2	E98161	probable ATP-depen
109	25	80.6	82	2	FQ0438	Alzheimer's diseases	182	25	80.6	841	2	AD3254	protein-tyrosine-p
110	25	80.6	114	2	T33289	hypothetical prote	183	25	80.6	901	2	D70116	transcription elon
111	25	80.6	152	2	T06645	hypothetical prote	184	25	80.6	942	2	T20287	hypothetical prote
112	25	80.6	159	2	T30445	hypothetical prote	185	25	80.6	962	2	G86479	FlADP7.6 protein -
113	25	80.6	169	2	T15611	hypothetical prote	186	25	80.6	975	2	T22788	hypothetical prote
114	25	80.6	174	2	T15658	hypothetical prote	187	25	80.6	1016	2	S30236	genome polyprotein
115	25	80.6	177	2	T22603	hypothetical prote	188	25	80.6	1046	2	F71432	hypothetical prote
116	25	80.6	179	2	T17915	hypothetical prote	189	25	80.6	1436	2	S67655	probable membrane
117	25	80.6	191	2	A96765	hypothetical prote	190	25	80.6	1549	2	T13940	ankyrin - fruit fl
118	25	80.6	198	2	H84646	hypothetical prote	191	25	80.6	1683	2	S56811	probable membrane
119	25	80.6	210	2	F64609	conserved hypotet	192	25	80.6	1717	2	T50247	probable helicase
120	25	80.6	210	2	B71906	hypothetical prote	193	25	80.6	1848	2	S37771	ankyrin, erythrocy
121	25	80.6	220	2	T41562	hypothetical wtf p	194	25	80.6	1856	2	B35049	ankyrin 1, erythro
122	25	80.6	222	2	AB3114	hypothetical prote	195	25	80.6	1862	2	I49502	ankyrin - mouse
123	25	80.6	231	2	H85138	hypothetical prote	196	25	80.6	1880	2	A35049	ankyrin 1, erythro
124	25	80.6	237	2	AC1953	rubrerythrin limpo	197	25	80.6	1881	1	SJHUK	ankyrin 1, erythro
125	25	80.6	242	2	A82512	hypothetical prote	198	24	77.4	39	2	S00318	photosystem I chai
126	25	80.6	267	2	A40269	cyclin C - fruit f	199	24	77.4	47	2	G70191	hypothetical prote
127	25	80.6	270	2	H98172	amino acid ABC tra	200	24	77.4	51	2	T07326	hypothetical prote
128	25	80.6	273	2	B85896	probable dimethyl	201	24	77.4	71	2	T26661	hypothetical prote
129	25	80.6	273	2	F91051	probable dimethyl	202	24	77.4	71	2	T26662	hypothetical prote
130	25	80.6	277	2	E75187	sugar abc transpor	203	24	77.4	72	2	T26662	hypothetical prote
131	25	80.6	277	2	D71220	probable sugar tra	204	24	77.4	84	2	S77771	probable ribonucle
132	25	80.6	286	2	H86564	outer membrane lip	205	24	77.4	93	2	A89057	protein K09H11.5 l
133	25	80.6	288	2	T37709	hypothetical prote	206	24	77.4	94	2	F90448	hypothetical prote
134	25	80.6	300	2	T26245	hypothetical prote	207	24	77.4	109	2	S57547	hypothetical prote
135	25	80.6	303	2	T25501	hypothetical prote	208	24	77.4	113	2	PN0091	pullulanase (BC 3.
136	25	80.6	327	2	A83766	hypothetical prote	209	24	77.4	126	2	G96930	glyoxalase I (glyo
137	25	80.6	339	2	A30754	hypothetical prote	210	24	77.4	134	2	G89382	response regulator
138	25	80.6	342	2	A48454	cathepsin B-like c	211	24	77.4	134	2	B83804	small multidrug ex
139	25	80.6	342	2	T09355	hypothetical prote	212	24	77.4	138	2	T25620	hypothetical prote
140	25	80.6	346	2	A83686	hypothetical prote	213	24	77.4	139	2	G69543	conserved hypotet
141	25	80.6	349	2	T26247	hypothetical prote	214	24	77.4	140	2	H81959	patch repair prote
142	25	80.6	352	2	T48903	wax synthase limpo	215	24	77.4	143	2	S20937	photosystem I chai
143	25	80.6	356	2	G72386	conserved hypotet	216	24	77.4	143	2	A89093	hypothetical prote
144	25	80.6	361	2	T24111	hypothetical prote	217	24	77.4	143	2	F85938	hypothetical prote
145	25	80.6	389	2	T20811	hypothetical prote	218	24	77.4	143	2	B65069	hypothetical prote
146	25	80.6	397	2	A96925	uncharacterized co	219	24	77.4	149	2	A13586	xanthine/uracil pe
147	25	80.6	404	2	F87753	protein C43E11.7 l	220	24	77.4	156	2	T43957	hypothetical prote
148	25	80.6	406	2	C86904	transporter yxbD l	221	24	77.4	161	2	F72861	AcOrf-93 protein -
149	25	80.6	421	2	A99309	membrane transport	222	24	77.4	161	2	T41833	AcMNPV orf93 - Bom
150	25	80.6	428	2	T48008	hypothetical prote	223	24	77.4	167	1	F1SP5	photosystem I chai
151	25	80.6	439	2	E70371	apolipoprotein N-a	224	24	77.4	171	2	C86367	protein F26F24.18
152	25	80.6	497	2	AD3514	D-serine/D-alanine	225	24	77.4	171	2	D86475	unknown protein, 3
153	25	80.6	501	2	C70420	NADH2 dehydrogen	226	24	77.4	176	2	G90120	hypothetical prote
154	25	80.6	508	2	T05156	probable Glucose t	227	24	77.4	177	2	S34499	hypothetical prote
155	25	80.6	516	2	S34525	hypothetical prote	228	24	77.4	177	2	AE1410	hypothetical prote
156	25	80.6	520	2	D90014	hypothetical prote	229	24	77.4	184	2	S23381	signal peptidase 1
157	25	80.6	534	2	E82269	conserved hypotet	230	24	77.4	186	1	WMR219	19K globulin precu
158	25	80.6	543	2	S62012	probable membrane	231	24	77.4	186	2	JC4784	alpha-globulin pre
159	25	80.6	568	2	D90525	hypothetical prote	232	24	77.4	188	2	B85481	yaah protein [simi
160	25	80.6	573	2	AB2401	hypothetical prote	233	24	77.4	188	2	B90630	yaah protein [simi
161	25	80.6	582	2	E71052	hypothetical prote	234	24	77.4	188	2	E56688	protein yaah - Esc
162	25	80.6	584	2	F75090	archaeosine tna-r	235	24	77.4	191	2	T09553	conserved hypotet
163	25	80.6	616	2	B90554	lipoprotein limpo	236	24	77.4	197	2	S42129	light-harvesting c
164	25	80.6	632	2	A25784	hypothetical 70K p	237	24	77.4	197	2	T33525	hypothetical prote
165	25	80.6	663	2	T26835	hypothetical prote	238	24	77.4	211	2	T05276	hypothetical prote
166	25	80.6	692	2	C87644	fatty oxidation co	239	24	77.4	211	2	T12013	cuticular protein
167	25	80.6	695	1	A49795	Alzheimer's diseases	240	24	77.4	217	2	T1830	hypothetical prote
168	25	80.6	695	2	A27485	Alzheimer's diseases	241	24	77.4	219	2	C85834	hypothetical prote
169	25	80.6	695	2	S00550	Alzheimer's diseases	242	24	77.4	219	2	A98989	hypothetical prote
170	25	80.6	703	2	H45456	NADH2 dehydrogen	243	24	77.4	220	2	S62598	cuticular protein
171	25	80.6	707	1	LEBBB	hemolysin secretio	244	24	77.4	220	2	C89800	conserved hypotet
172	25	80.6	707	1	LEECB	hemolysin secretio	245	24	77.4	231	2	T12012	cuticular protein
173	25	80.6	707	2	A61378	leukotoxin express	246	24	77.4	236	2	A97233	uncharacterized co
174	25	80.6	707	2	D43599	hemolysin I secret	247	24	77.4	239	2	S27789	hypothetical prote
175	25	80.6	708	2	C30169	leukotoxin express	248	24	77.4	250	2	F84977	deoxyribonuclease

249 24 77.4 255 2 E82813
250 24 77.4 257 2 AC1290
251 24 77.4 257 2 A11661
252 24 77.4 259 2 E72218
253 24 77.4 263 2 D72303
254 24 77.4 267 2 S52347
255 24 77.4 268 2 A82498
256 24 77.4 270 2 T44049
257 24 77.4 277 2 T50722
258 24 77.4 279 2 B37849
259 24 77.4 284 2 H86183
260 24 77.4 285 2 F71851
261 24 77.4 286 2 AH2943
262 24 77.4 294 2 G81318
263 24 77.4 297 2 T25817
264 24 77.4 298 2 H95195
265 24 77.4 298 2 B98062
266 24 77.4 301 2 S50737
267 24 77.4 307 2 C90549
268 24 77.4 312 2 G70114
269 24 77.4 313 2 B98339
270 24 77.4 314 2 G86835
271 24 77.4 315 2 T07314
272 24 77.4 317 2 B98208
273 24 77.4 317 2 AG3078
274 24 77.4 319 2 S73159
275 24 77.4 320 2 T16311
276 24 77.4 321 2 H71729
277 24 77.4 327 2 AH2312
278 24 77.4 328 2 AH2399
279 24 77.4 334 2 T19127
280 24 77.4 335 2 T04029
281 24 77.4 340 1 MMBE5
282 24 77.4 345 2 C45456
283 24 77.4 347 2 T15672
284 24 77.4 348 2 T20167
285 24 77.4 358 2 A64424
286 24 77.4 358 2 T50897
287 24 77.4 361 2 A86841
288 24 77.4 364 2 T16376
289 24 77.4 368 2 D90596
290 24 77.4 375 2 A39622
291 24 77.4 385 2 T05049
292 24 77.4 391 2 T20752
293 24 77.4 394 2 T19028
294 24 77.4 397 2 T19029
295 24 77.4 398 2 F72335
296 24 77.4 401 2 S49393
297 24 77.4 404 2 T32998
298 24 77.4 405 2 B97171
299 24 77.4 406 2 T32922
300 24 77.4 409 2 E97218

ALIGNMENTS

RESULT 1

probable proline dipeptidase [imported] - Sinorhizobium meliloti (strain 1021) megaplasm
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: F95352
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: F95352
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-397 <KUR>
A:Cross-references: UNIPROT:Q92YY6; UNIPARC:UPI00000CB1AA; GB:AE006469; PIDN:AAK65384.1;

A:Experimental source: strain 1021, megaplaamid pSyma
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMal329
A:Genome: plasmid

Query Match 96.8%; Score 30; DB 2; Length 397;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFPVFFA 6
|||:
Db 25 KFIFFA 30

RESULT 2

G83919
hypothetical protein BH2159 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: G83919
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G83919
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-49 <STO>
A:Cross-references: UNIPROT:Q9KAX7; UNIPARC:UPI000000C3E07; GB:AP001514; GB:BA0000004; NI
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2159

Query Match 90.3%; Score 28; DB 2; Length 49;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFPVFFA 6
|||:
Db 34 KFPVFS 39

RESULT 3

TL6280
hypothetical protein F35H10.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: TL6280
R;Woessner, J.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid F35H10.
A:Reference number: Z18490
A:Accession: TL6280
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-177 <WOB>
A:Cross-references: UNIPROT:Q20070; UNIPARC:UPI0000007F0D0; EMBL:U40934; NID:g1072149;
C:Genetics:
A:Gene: CESP:F35H10.6
A:Introns: 18/1, 39/2, 74/3, 97/2

Query Match 90.3%; Score 28; DB 2; Length 177;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
 |||||:
 Db 10 KFVFFS 15

RESULT 4
 T29899
 hypothetical protein M02B7.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T29899
 R;Nelson, J.; Wohlmann, P.
 submitted to the EMBL Data Library, September 1996
 A:Description: The sequence of C. elegans cosmid M02B7.
 A:Reference number: Z20706
 A:Accession: T29899
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-293 <NEL>
 A:Cross-references: UNIPROT:Q94284; UNIPARC:UPI0000078391; EMBL:U70851; PIDN:AAB09129.1;
 A:Experimental source: strain Bristol N2; clone M02B7
 C:Genetics:
 A:Gene: CESP:M02B7.4
 A:Map position: 4
 A:Introns: 42/3; 150/2; 198/1; 230/3; 276/3

Query Match 90.3%; Score 28; DB 2; Length 293;
 Best Local Similarity 83.3%; Pred. No. 69;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
 |||||:
 Db 258 KFVFFS 263

RESULT 5
 S76400
 hypothetical protein - Synechocystis sp. (strain PCC 6803)
 C:Species: Synechocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C:Accession: S76400
 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 S.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S76400
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-326 <KAN>
 A:Cross-references: UNIPROT:P74429; UNIPARC:UPI00000C1025; EMBL:D90915; GB:AB001339; NID
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 90.3%; Score 28; DB 2; Length 326;
 Best Local Similarity 83.3%; Pred. No. 76;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
 |||||:
 Db 104 KFVFFS 109

RESULT 6
 E82904
 hypothetical protein U0329 [imported] - Ureaplasma urealyticum
 C:Species: Ureaplasma urealyticum
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: E82904
 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 submitted to GenBank, February 2000

A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a m
 A:Reference number: A82870
 A:Accession: E82904
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-422 <GLA>
 A:Cross-references: UNIPARC:UPI00000C1C1F; GB:AE002130; GB:AF222894; NID:g6899302; PIDN
 A:Experimental source: serovar 3; biovar 1
 C:Genetics:
 A:Gene: U0329
 A:Genetic code: SGC3

Query Match 90.3%; Score 28; DB 2; Length 422;
 Best Local Similarity 83.3%; Pred. No. 96;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
 |||||:
 Db 208 KYVFFA 213

RESULT 7
 C88969
 protein F15B11.8 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: C88969
 R;anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_el
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
 A:Accession: C88969
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-452 <STO>
 A:Cross-references: UNIPROT:O44595; UNIPARC:UPI0000075D10; GB:chr_V; PIDN:AAB94205.1; P
 C:Genetics:
 A:Gene: F15B11.8
 A:Map position: 5

Query Match 90.3%; Score 28; DB 2; Length 452;
 Best Local Similarity 83.3%; Pred. No. 1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
 |||||:
 Db 291 RFVFFA 296

RESULT 8
 T05272
 fatty acid elongase 1 - Arabidopsis thaliana
 N:Alternate names: protein T4L20.100
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T05272
 R;Sevan, M.; Terry, N.; Ardiles, W.; Buysaert, C.; Dasseville, R.; De Clerck, R.; De
 ewes, H.W.; Mayer, K.F.X.; Schueller, C.
 submitted to the Protein Sequence Database, September 1998
 A:Reference number: Z15406
 A:Accession: T05272
 A:Molecule type: DNA
 A:Residues: 1-506 <BEV>
 A:Cross-references: UNIPROT:Q38860; UNIPARC:UPI0000047264; EMBL:AL023094
 A:Experimental source: cultivar Columbia; BAC clone T4L20
 C:Genetics:
 A:Map position: 4
 A:Note: T4L20.100
 C:Superfamily: very-long-chain 3-ketoacyl-CoA synthase

Query Match 90.3%; Score 28; DB 2; Length 506;

Best Local Similarity 83.3%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVFVFFA 6
Db 356 KFLFFA 361

RESULT 9
A70125
UDP-N-acetylmuramoyl-D-glutamate-2,6-diaminopimelate ligase (murE) homolog - Lyme
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-Oct-2004
C;Accession: A70125
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kervilavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: A70125
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-508 <KLE>
A;Cross-references: UNIPROT:O51219; UNIPARC:UPI00000573B3; GB:AE001130; GB:AE000783; NID
A;Experimental source: strain B31
C;Superfamily: UDP-N-acetylmuramate-alanine ligase

Query Match 90.3%; Score 28; DB 2; Length 508;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVFVFFA 6
Db 41 RFVFFA 46

RESULT 10
T02192
probable cytochrome P450 At2g46950 [imported] - Arabidopsis thaliana
N;Alternate names: cytochrome P450 homolog F14M4.22
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02192; C84909
R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Ron
submitted to the EMBL Data Library, September 1998
A;Description: Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.
A;Reference number: Z14609
A;Accession: T02192
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-517 <ROU>
A;Cross-references: UNIPROT:O80729; UNIPARC:UPI00000A147A; EMBL:AC004411; NID:G3522932;
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84909
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-517 <STO>
A;Cross-references: UNIPARC:UPI00000A147A; GB:AE002093; NID:G3522946; PIDN:AAC34228.1; G
C;Genetics:
A;Gene: At2g46950; F14M4.22
A;Map position: 2
A;Introns: 95/1; 169/3; 252/2; 374/3
C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology
C;Keywords: heme; iron; metalloprotein
F;321-485/Domain: cytochrome P450 homology <P45>

F;463/Binding site: heme iron (Cys) (axial ligand) #status predicted
Query Match 90.3%; Score 28; DB 2; Length 517;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVFVFFA 6
Db 123 KVFVFFS 128

RESULT 11
G97000
diguanylate cyclase/phosphodiesterase domain (GGDEF) containing protein [imported] - Cl
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97000
R;Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-571 <KUR>
A;Cross-references: UNIPROT:Q97KUS; UNIPARC:UPI000000C9FBF; GB:AE001437; PIDN:AAK78794.1
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0818

Query Match 90.3%; Score 28; DB 2; Length 571;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVFVFFA 6
Db 314 KFMFFA 319

RESULT 12
T37742
serine threonine-protein kinase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
C;Accession: T37742
R;Rieger, M.; Wood, V.; Rajandream, M.A.; Barrrell, B.G.
submitted to the EMBL Data Library, January 1999
A;Reference number: Z21743
A;Accession: T37742
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1072 <RIB>
A;Cross-references: UNIPROT:O94537; UNIPARC:UPI00000069EBD; EMBL:AL035248; PIDN:CRAA22846
A;Experimental source: strain 972h-; cosmid c167
C;Genetics:
A;Gene: spac167.01; SPDB:SPAC167.01
A;Map position: 1
A;Introns: 1015/3

Query Match 90.3%; Score 28; DB 2; Length 1072;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVFVFFA 6
Db 13 KVFVFFS 18

RESULT 13
B72420
hypothetical protein TM0088 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: B72420
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A;Reference number: A72200; MUID:99287316; PMID:10360571
 A;Accession: B72420
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1285 <ARN>
 A;Cross-references: UNIPROT:Q9WUX3; UNIPARC:UPI0000003DA9B; GB:AE001695; GB:AE000512; NID
 A;Experimental source: strain MSB8
 C;Genetics:
 A;Gene: TW0088

Query Match 90.3%; Score 28; DB 2; Length 1285;
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 |||||
 Db 341 KVFVFA 346

RESULT 14
 S07937
 hypothetical protein atpH 5'-region - Euglena gracilis chloroplast (fragment)
 C;Species: chloroplast Euglena gracilis
 C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 09-Jul-2004
 C;Accession: S07937
 R;Passavant, C.W.; Hallick, R.B.
 Plant Mol. Biol. 4, 347-354, 1985
 A;Title: Location, nucleotide sequence and expression of the proton-translocating subunit
 A;Reference number: S07400
 A;Accession: S07937
 A;Molecule type: DNA
 A;Residues: 1-38 <PAS>
 A;Cross-references: UNIPROT:Q32187; UNIPARC:UPI00000965CB; EMBL:M16844; NID:g336867; PID
 C;Comment: This is the hypothetical translation of a sequence that was not reported as a
 C;Genetics:
 A;Genome: chloroplast
 C;Keywords: chloroplast

Query Match 87.1%; Score 27; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
 |||||
 Db 18 KVFVFF 22

RESULT 15
 C70150
 hypothetical protein BB0404 - Lyme disease spirochete
 C;Species: Borrelia burgdorferi (Lyme disease spirochete)
 C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
 C;Accession: C70150
 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
 Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A;Authors: Smith, H.O.; Venter, J.C.
 A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
 A;Reference number: A70100; MUID:98065943; PMID:9403685
 A;Accession: C70150
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-138 <KLE>
 A;Cross-references: UNIPROT:O51365; UNIPARC:UPI00000547C; GB:AE001146; GB:AE000783; NID
 A;Experimental source: strain B31

C;Superfamily: Borrelia burgdorferi hypothetical protein BB0404
 Query Match 87.1%; Score 27; DB 2; Length 138;
 Best Local Similarity 66.7%; Pred. No. 57;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 |||||
 Db 40 KVFVFA 45

RESULT 16
 I40051
 signal peptidase I (EC 3.4.21.89) - Bacillus amyloliquefaciens
 N;Alternate names: leader peptidase
 C;Species: Bacillus amyloliquefaciens
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C;Accession: I40051; S38885
 R;Tomlinson, I.M.; Cook, G.P.; Carter, N.P.; Elaszarapu, R.; Smith, S.; Walter, G.; Bul
 Hum. Mol. Genet. 3, 853-860, 1994
 A;Title: Human immunoglobulin VH and D segments on chromosomes 15q11.2 and 16p11.2.
 A;Reference number: I37619; MUID:95038735; PMID:7951227
 A;Accession: I40051
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-185 <RES>
 A;Cross-references: UNIPROT:P41026; UNIPARC:UPI000012E452; EMBL:Z27458; NID:g429069; PFI
 C;Genetics:
 A;Gene: sipa
 A;Start codon: TTG
 C;Superfamily: signal peptidase I sips
 C;Keywords: hydrolase; serine proteinase

Query Match 87.1%; Score 27; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
 |||||
 Db 172 KVFVFF 176

RESULT 17
 C70199
 hypothetical protein BB0796 - Lyme disease spirochete
 C;Species: Borrelia burgdorferi (Lyme disease spirochete)
 C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
 C;Accession: C70199
 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
 Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A;Authors: Smith, H.O.; Venter, J.C.
 A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
 A;Reference number: A70100; MUID:98065943; PMID:9403685
 A;Accession: C70199
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-185 <KLE>
 A;Cross-references: UNIPROT:O51736; UNIPARC:UPI00000575FE; GB:AE001178; GB:AE000783; NID
 A;Experimental source: strain B31

Query Match 87.1%; Score 27; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
 |||||
 Db 7 KVFVFF 11

RESULT 18
 S45022

signal peptidase I (EC 3.4.21.89) - *Bacillus amyloliquefaciens*

N;Alternate names: leader peptidase

C;Species: *Bacillus amyloliquefaciens*

C;Date: 06-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Accession: S59966; S45022

R;Hoang, V.; Hofemeister, J.

Biochim. Biophys. Acta 1269, 64-68, 1995

A;Title: *Bacillus amyloliquefaciens* possesses a second type I signal peptidase with exte

A;Reference number: S59965; MUID:96049527; PMID:7578273

A;Accession: S59966

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-193 <HO2>

A;Cross-references: UNIPROT:P41025; UNIPARC:UPI0000128454; EMBL:Z33640; NID:S562273; PID

C;Genetics:

A;Start codon: TTG

C;Superfamily: signal peptidase I sips

C;Keywords: hydrolase, serine proteinase; transmembrane protein

Query Match 87.1%; Score 27; DB 2; Length 193;

Best Local Similarity 100.0%; Pred. No. 78;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5

Db 180 KPVFF 184

RESULT 19

signal peptidase I sipT - *Bacillus subtilis*

C;Species: *Bacillus subtilis*

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: G69707

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emmeron, P.F.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.

Koeter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A;Authors: Yoshikawa, H.F.; Zumatein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: G69707

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-193 <KUN>

A;Cross-references: UNIPROT:P71013; UNIPARC:UPI000006032F; GB:Z99111; GB:AL009126; NID:9

A;Experimental source: strain 168

C;Genetics:

A;Gene: sipT

C;Superfamily: signal peptidase I sips

Query Match 87.1%; Score 27; DB 2; Length 193;

Best Local Similarity 100.0%; Pred. No. 78;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5

Db 180 KPVFF 184

RESULT 20

AH0299

probable membrane protein YPO2455 [imported] - *Yersinia pestis* (strain CO92)

C;Species: *Yersinia pestis*

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AH0299

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AH0299

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-232 <KUR>

A;Cross-references: UNIPROT:Q8ZDV0; UNIPARC:UPI00000DCD3E; GB:AL590842; PIDN:CAC91260.1

C;Genetics:

A;Gene: YPO2455

Query Match 87.1%; Score 27; DB 2; Length 232;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5

Db 19 KPVFF 23

RESULT 21

E72329

hypothetical protein TM0818 - *Thermotoga maritima* (strain MS88)

C;Species: *Thermotoga maritima*

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: E72329

R;Neilson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke

Garrett, M.E.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: E72329

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-274 <ARN>

A;Cross-references: UNIPROT:Q9WZS5; UNIPARC:UPI00000D3985; GB:AE000512; NI

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM0818

Query Match 87.1%; Score 27; DB 2; Length 274;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5

Db 260 KPVFF 264

RESULT 22

T29189

hypothetical protein C55C3.2 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T29189

R;Woessene, J.; Steillyes, L.

submitted to the EMBL Data Library, April 1996

A;Description: The sequence of *C. elegans* cosmid C55C3.

A;Reference number: Z20585

A;Accession: T29189

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 1-298 <WOE>

A;Cross-references: UNIPROT:Q18868; UNIPARC:UPI0000074B15; EMBL:U53335; PIDN:AAA96172.1

A;Experimental source: strain Bristol N2; clone C55C3

C;Genetics:

A;Gene: CESP:C55C3.2

```

A;Map position: 4
A;Introns: 35/1; 64/3; 212/3; 260/1

  Query Match      87.1%; Score 27; DB 2; Length 298;
  Best Local Similarity 100.0%; Pred. No. 1.2e+02;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
DB 85 KVFVFF 89
|||||

RESULT 23
T06845
hypothetical protein ycf39 - Cyanophora paradoxa cyanelle
C:Species: Cyanelle Cyanophora paradoxa
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06845
R:Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.
submitted to the EMBL Data Library, July 1995
A:Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.
A:Reference number: Z15840
A:Accession: T06845
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-321 <STI>
A:Cross-references: UNIPROT:P48279; UNIPARC:UPI000013A4A8; EMBL:U30821; NID:g1016083; PI
A:Experimental source: cv. strain Pringsheim LB555
C:Genetics:
A:Gene: ycf39
A:Genome: cyanelle
C:Keywords: cyanelle

  Query Match      87.1%; Score 27; DB 2; Length 321;
  Best Local Similarity 66.7%; Pred. No. 1.2e+02;
  Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 6
DB 104 KFIFFS 109
|||:|

RESULT 24
S73198
hypothetical protein 349 - red alga (Porphyra purpurea) chloroplast
C:Species: chloroplast Porphyra purpurea
C>Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: S73198
R:Reith, M.; Munnholland, J.
Plant Mol. Biol. Rep. 13, 333-335, 1995
A:Title: Complete nucleotide sequence of the Porphyra purpurea chloroplast genome.
A:Reference number: S73108
A:Accession: S73198
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-349 <BEI>
A:Cross-references: UNIPROT:P51277; UNIPARC:UPI000013A78F; EMBL:U38804; NID:g1276652; PI
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C:Genetics:
A:Genome: chloroplast
C:Superfamily: leucine zipper-containing protein AT103

  Query Match      87.1%; Score 27; DB 2; Length 349;
  Best Local Similarity 66.7%; Pred. No. 1.3e+02;
  Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 6
DB 156 KFIFFA 161
|||:|

RESULT 25

```

```

S74431
hypothetical protein all1214 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S74431
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda-
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S74431
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-358 <KAN>
A:Cross-references: UNIPROT:P72584; UNIPARC:UPI00000C0957; EMBL:D30899; GB:AB001339; NI
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: leucine zipper-containing protein AT103

  Query Match      87.1%; Score 27; DB 2; Length 358;
  Best Local Similarity 66.7%; Pred. No. 1.4e+02;
  Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 6
DB 165 KFIFFA 170
|||:|

RESULT 26
AE2218
hypothetical protein alr3300 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AE2218
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi-
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2218
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <KUR>
A:Cross-references: UNIPROT:Q8YR22; UNIPARC:UPI00000CE73B; GB:BA000019; PIDN:BA874999.1,
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr3300
C:Superfamily: leucine zipper-containing protein AT103

  Query Match      87.1%; Score 27; DB 2; Length 358;
  Best Local Similarity 66.7%; Pred. No. 1.4e+02;
  Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 6
DB 165 KFIFFA 170
|||:|

RESULT 27
H90559
hypothetical protein MYPV 3840 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: H90559
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.,
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: H90559
A>Status: Preliminary
A:Molecule type: DNA

```

A;Residues: 1-370 <KUR>
A;Cross-references: UNIPROT:Q9QNH7; UNIPARC:UPI00000C807C; GB:AL445566; PID:g14089798; R
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU 3840
A;Genetic code: SGC3

Query Match 87.1%; Score 27; DB 2; Length 370;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
|:|:|:|
Db 23 KYIFFA 28

RESULT 28
T23285
hypothetical protein K03D7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23285
R;Matthews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19721
A;Accession: T23285
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-408 <WIL>
A;Cross-references: UNIPROT:O45653; UNIPARC:UPI00000610BB; EMBL:Z81562; PIDN:CAB04555.1;
A;Experimental source: clone K03D7
C;Genetics:
A;Gene: CESP:K03D7.8
A;Map position: 5
A;Introns: 117/3; 304/1

Query Match 87.1%; Score 27; DB 2; Length 408;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
|:|:|:|
Db 243 KFVFF 247

RESULT 29
T47754
leucine zipper-containing protein AT103 - Arabidopsis thaliana
N;Alternate names: PNL34 protein homolog; protein F24I3.20
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47754; S71218
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Stert, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24475
A;Accession: T47754
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-409 <NYA>
A;Cross-references: UNIPROT:Q9MIK4; UNIPARC:UPI00000A741A; EMBL:AL1138655
A;Experimental source: cultivar Columbia; BAC clone F24I3
R;Zheng, C.C.; O'Neill, S.D.
submitted to the EMBL Data Library, October 1995
A;Description: Molecular analysis of a novel phytochrome-regulated Pharbitis cDNA and its
A;Reference number: S71218
A;Accession: S71218
A;Molecule type: mRNA
A;Residues: 37-156, 'S', 158-409 <ZHE>
A;Cross-references: UNIPARC:UPI00000A9BBC; EMBL:U38232; NID:g1033194; PID:g1033195
C;Genetics:
A;Gene: AT103
A;Map position: 3
A;Introns: 158/3; 180/2; 289/3; 322/3

A;Note: F24I3.20
C;Superfamily: leucine zipper-containing protein AT103

Query Match 87.1%; Score 27; DB 2; Length 409;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
|:|:|:|
Db 210 KFIFYA 215

RESULT 30
E96635
hypothetical protein T7P1.13 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E96635
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
Chin, C.W.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E96635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-436 <STO>
A;Cross-references: UNIPROT:Q9C954; UNIPARC:UPI00000483C7; GB:AE005173; NID:g5751689; P
C;Genetics:
A;Gene: T7P1.13
A;Map position: 1

Query Match 87.1%; Score 27; DB 2; Length 436;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
|:|:|:|
Db 185 KYIFFA 190

RESULT 31
B72361
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: B72361
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72361
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-459 <ARN>
A;Cross-references: UNIPROT:Q9WZ33; UNIPARC:UPI00000C13F0; GB:AE001731; GB:AE0000512; N
C;Genetics:
A;Gene: TM0563

Query Match 87.1%; Score 27; DB 2; Length 459;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5

```

|||||
Db      210 KFVFF 214

RESULT 32
T20124
hypothetical protein C50H2.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20124
R:McMurray, A.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19226
A:Accession: T20124
A>Status: preliminary; translated from GB/EMBL/DDSV
A:Molecule type: DNA
A:Residues: 1-488 <N1>
A:CROSS-references: UNIPROT:Q18760; UNIPARC:UPI000007F0DB; EMBL:Z73971; PIDN:CAA98250.1;
A:Experimental source: clone C50H2
C:Genetics:
A:Gene: CRSP:C50H2.2
A:Map position: 5
A:Introns: 67/2; 107/3; 138/3; 180/3; 337/2; 391/3; 445/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C50H2.2

Query Match      87.1%; Score 27; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KFVFF 5
Db      203 KFVFF 207

RESULT 33
H86248
protein T23J18.22 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86248
R:Theologas, A.; Ecker, J.R.; Palm, C.J.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H86248
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-522 <STO>
A:CROSS-references: UNIPROT:Q9LPT0; UNIPARC:UPI00000A13DA; GB:AE005172; NID:g6554189; PI
C:Genetics:
A:Gene: T23J18.22
A:Map position: 1

Query Match      87.1%; Score 27; DB 2; Length 522;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KFVFF 5
Db      257 KFVFF 261

RESULT 34
S49827
probable membrane protein YDR072c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein D4405; hypothetical protein YD8554.05c

```

```

C:Species: Saccharomyces cerevisiae
C>Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C:Accession: S49827; S48758; S55820; S67889; S67888
R:Richards, C.; Harris, D.E.
submitted to the EMBL Data Library, November 1994
A:Reference number: S49823
A:Accession: S49827
A:Molecule type: DNA
A:Residues: 1-527 <RIC>
A:CROSS-references: UNIPROT:P38954; UNIPARC:UPI000012D81A; EMBL:Z46796; NID:g577794; PI
R:Coster, F.; Jonniaux, J.L.; Goffeau, A.
submitted to the EMBL Data Library, October 1994
A:Reference number: S48758
A:Accession: S48758
A:Molecule type: DNA
A:Residues: 1-524 <COS>
A:CROSS-references: UNIPARC:UPI0000168B70; EMBL:X82086; NID:g558241; PID:g558243
R:Coster, F.; Jonniaux, J.L.; Goffeau, A.
Yeast 11, 673-679, 1995
A:Title: Analysis of a 32.8 kb segment of yeast chromosome IV reveals 21 open reading f
A:Reference number: S55819; MUID:96093910; PMID:7483840
A:Accession: S55820
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-525 <COM>
A:CROSS-references: UNIPARC:UPI000017B30A; EMBL:X82086
R:Poury, P.; Jonniaux, J.L.; Purnelle, B.; Coster, F.; Goffeau, A.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67889
A:Accession: S67889
A:Molecule type: DNA
A:Residues: 1-524 <FOU>
A:CROSS-references: UNIPARC:UPI0000168B70; EMBL:Z74368; MIPS:YDR072C
A:Experimental source: strain S288C
R:Blocker, H.; Brandt, P.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67587
A:Accession: S67888
A:Molecule type: DNA
A:Residues: 417-527 <ELO>
A:CROSS-references: UNIPARC:UPI000017B30B; EMBL:Z74368; MIPS:YDR072C
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:SYR4
A:CROSS-references: SGD:S0002479; MIPS:YDR072C
A:Map position: 4R
C:Keywords: transmembrane protein
F:24-40/Domain: transmembrane #status predicted <TM1>
F:101-117/Domain: transmembrane #status predicted <TM2>
F:153-169/Domain: transmembrane #status predicted <TM3>
F:194-210/Domain: transmembrane #status predicted <TM4>
F:294-310/Domain: transmembrane #status predicted <TM5>
F:462-478/Domain: transmembrane #status predicted <TM6>

Query Match      87.1%; Score 27; DB 2; Length 527;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KFVFF 6
Db      62 KPFFFA 67

RESULT 35
B81107
exodeoxyribonuclease V, alpha chain NMB1233 [imported] - Neisseria meningitidis (strain
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81107
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.;
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizzi, M.
Science 287, 1809-1815, 2000

```


A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vezzani, A.; Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A;Reference number: A81000; MUID:20175755; PMID:10710307
 A;Accession: B81107
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-581 <TET>
 A;Cross-references: UNIPROT:Q9JZ93; UNIPARC:UPI000000C4671; GB:AE0020471; GB:AE002098; NID:184471
 A;Experimental source: serogroup B, strain MC58
 C;Genetics:
 A;Gene: NMB1233
 C;Superfamily: exodeoxyribonuclease V 67K chain

Query Match 87.1%; Score 27; DB 2; Length 581;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
 546 KFVFF 550

Db

RESULT 36

B81909
 exodeoxyribonuclease V alpha subunit NMA1401 [imported] - *Neisseria meningitidis* (strain MC58)
 C;Species: *Neisseria meningitidis*
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C;Accession: B81909
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, P.; Parkhill, J.; Jorgensen, K.; Leather, S.; Mouton, S.; Mungall, K.; Quail, M.A.; Rajandream, A.; Holroyd, S.; Jorgensen, K.; Leather, S.; Mouton, S.; Mungall, K.; Quail, M.A.; Rajandream, A.; Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
 A;Reference number: A81775; MUID:20222556; PMID:10761919
 A;Accession: B81909
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-581 <PAR>
 A;Cross-references: UNIPROT:Q9JUB8; UNIPARC:UPI000000C4BB0; GB:AL162755; GB:AL157959; NID:184471
 A;Experimental source: serogroup A, strain Z2491
 C;Genetics:
 A;Gene: recD; NMA1401
 C;Superfamily: exodeoxyribonuclease V 67K chain

Query Match 87.1%; Score 27; DB 2; Length 581;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
 546 KFVFF 550

Db

RESULT 37

I38028
 matrix metalloproteinase 14 (EC 3.4.24.-) membrane type precursor - human
 N;Alternate names: matrix metalloproteinase MMP14; membrane type matrix metalloproteinase
 C;Species: *Homo sapiens* (man)
 C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
 C;Accession: I38028; G02274; I38046; S78011; S45341; S71384
 R;Will, H.; Hinzmann, B.
 Eur. J. Biochem. 231, 602-608, 1995
 A;Title: cDNA sequence and mRNA tissue distribution of a novel human matrix metalloproteinase
 A;Reference number: I38028; MUID:95377289; PMID:7649159
 A;Accession: I38028
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-582 <WILL>
 A;Cross-references: UNIPROT:P50281; UNIPARC:UPI00000048136; EMBL:Z48481; NID:G963053; PMID:184471
 R;Luo, G.
 submitted to the EMBL Data Library, November 1995
 A;Reference number: H00963
 A;Accession: G02274
 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
 A;Residues: 1-582 <DUO>
 A;Cross-references: UNIPARC:UPI00000048136; EMBL:U41078; NID:G1127836; PIDN:AAA83770.1; I38028
 R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Bassett, P.; Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
 A;Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cells
 A;Reference number: I38046; MUID:95224014; PMID:7708715
 A;Accession: I38046
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-7,'S',9-582 <OKA>
 A;Cross-references: UNIPARC:UPI000003096F; EMBL:X83535; NID:G804993; PIDN:CAA58519.1; P; R;Seiki, M.
 submitted to the EMBL Data Library, January 1994
 A;Reference number: S78011
 A;Accession: S78011
 A;Molecule type: mRNA
 A;Residues: 1-7,'S',9-337,'K',339-582 <SEI>
 A;Cross-references: UNIPARC:UPI000003DC76; EMBL:D26512; NID:G793762; PIDN:BAA05519.1; P; R;Sato, H.; Takino, T.; Okada, Y.; Cao, J.; Shinagawa, A.; Yamamoto, E.; Seiki, M.
 Nature 370, 61-65, 1994
 A;Title: A matrix metalloproteinase expressed on the surface of invasive tumour cells.
 A;Reference number: S45341; MUID:94286011; PMID:8015608
 A;Accession: S45341
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-7,'S',9-188,'R',190,'A',192-267,'K',269-272,'HY',275,'P',277-285,'KQ',288
 A;Cross-references: UNIPARC:UPI0000157586; EMBL:D26512
 R;Sato, H.; Kinoshta, T.; Takino, T.; Nakayama, K.; Seiki, M.
 FEBS Lett. 393, 101-104, 1996
 A;Title: Activation of a recombinant membrane type 1-matrix metalloproteinase (MT1-MMP)
 A;Reference number: S71384; MUID:96397540; PMID:8804434
 A;Accession: S71384
 A;Molecule type: protein
 A;Residues: 112-116 <SAW>
 A;Cross-references: UNIPARC:UPI0000175D8E
 C;Genetics:
 A;Gene: GDB:MMP14; MT1-MMP
 A;Cross-references: GDB:375731; OMIM:600754
 A;Map position: 14q11-14q12
 C;Superfamily: Interstitial collagenase; metalloproteinase; zinc; zymogen
 C;Keywords: Glycoprotein; hydrolase; metalloproteinase; predicted <SIG>
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-97/Domain: activation peptide #status predicted <PRO>
 F;61-284/Domain: matrix metalloproteinase homology <MMP>
 F;98-582/Product: matrix metalloproteinase 14 membrane type #status predicted <MAT>
 F;285-313/Domain: hinge #status predicted <HNG>
 F;314-508/Domain: hemopexin repeat homology <PXN>
 F;539-562/Domain: transmembrane #status predicted <TMW>
 F;93,239,243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 F;130/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
 F;240/Active site: Glu #status predicted
 F;319-508/Disulfide bonds: #status predicted

Query Match 87.1%; Score 27; DB 2; Length 582;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
 378 KFVFF 382

Db

RESULT 38

I84471
 matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - rat
 N;Alternate names: membrane-type metalloproteinase
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I84471; I61946
 R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Bassett, P.; Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995

```

A:Cross-references: UNIPARC:UPI0000174EF6
C:Superfamily: hydroxymethylglutaryl-CoA (HMG-CoA) reductase
C:Keywords: coenzyme A; NADP; oxidoreductase

Query Match      87.1%; Score 27; DB 2; Length 856;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKVFF 5
DB      360 KKVFF 364

RESULT 41
S44883
ZC262.3 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S44883
R:Anderson, K.
submitted to the EMBL Data Library, September 1993
A:Description: Sequence of the C. elegans cosmid ZC262.
A:Reference number: S44818
A:Accession: S44883
A:Status: preliminary
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-857 <AND>
A:Cross-references: UNIPROT:P34595; UNIPARC:UPI0000179325; EMBL:I23647; NID:g38
C:Genetics:
A:Introns: 72/2; 145/1; 191/1; 263/3; 297/1; 363/2; 403/2; 448/2; 523/2; 563/2;
C:Superfamily: Caenorhabditis elegans ZC262.3 protein

Query Match      87.1%; Score 27; DB 2; Length 857;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKVFF 5
DB      87 KKVFF 91

RESULT 42
T31795
hypothetical protein R02F11.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31795
R:Davidson, S.; Wohldmann, P.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid R02F11.
A:Reference number: Z21087
A:Accession: T31795
A:Status: preliminary; translated from GE/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-870 <DAV>
A:Cross-references: UNIPROT:O16363; UNIPARC:UPI000016423C; EMBL:AF016439; PIDN:
A:Experimental source: strain Bristol N2; clone R02F11
C:Genetics:
A:Gene: CESP:R02F11.2
A:Map position: 5
A:Introns: 44/2; 116/2; 164/3; 265/2; 335/2; 380/1; 397/1; 419/3; 475/1; 582/2;

Query Match      87.1%; Score 27; DB 2; Length 870;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KKVFFA 6
DB      2 RPIFFA 7

RESULT 43
R556300

```

probable membrane protein YJL119c - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: hypothetical protein J0738
 C:Species: *Saccharomyces cerevisiae*
 C>Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
 C:Accession: S56900
 R:Czapluch, C.; Kordes, E.; Pujol, A.; Jauniaux, J.C.
 submitted to the Protein Sequence Database, September 1995
 A:Reference number: S56891
 A:Accession: S56900
 A:Molecule type: DNA
 A:Residues: 1-107 <CZI>
 A:Cross-references: UNIPROT:P47021; UNIPARC:UPI000013B5E8; EMBL:Z49394; NID:gl008309; P
 C:Genetics:
 A:Gene: MIPS:YJL119c
 A:Cross-references: SGD:S0003655
 A:Map position: 10L
 C:Superfamily: *Saccharomyces* probable membrane protein YJL119c
 C:Keywords: transmembrane protein

Query Match 83.9%; Score 26; DB 2; Length 107;
 Best Local Similarity 83.3%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
 Db 102 KFFVFA 107

RESULT 44
 G87731
 protein W10C8.3 [imported] - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C:Accession: G87731
 R:anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A>Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biolog
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: G87731
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-127 <STO>
 A:Cross-references: UNIPARC:UPI0000164023; GB:chr_I; PIDN:AAB97593.1; PID:g2804486; GSPD
 C:Genetics:
 A:Gene: W10C8.3
 A:Map position: 1

Query Match 83.9%; Score 26; DB 2; Length 127;
 Best Local Similarity 80.0%; Pred. No. 89;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFF 5
 Db 83 KPIFF 87

RESULT 45
 C81280
 probable periplasmic cytochrome C Cj1358c [imported] - *Campylobacter jejuni* (strain NCTC
 C:Species: *Campylobacter jejuni*
 C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
 C:Accession: C81280
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Bagham, D.; Chillin
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
 Nature 403, 665-668, 2000
 A>Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp
 A:Reference number: A81250; MUID:20150912; PMID:10688204
 A:Accession: C81280
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-171 <PAR>

A:Cross-references: UNIPROT:Q9PMU1; UNIPARC:UPI000000C1EDC; GB:AL1139078; GB:AL111168; NI
 A:Experimental source: serotype O2, strain NCTC 11168
 C:Genetics:
 A:Gene: Cj1358c
 C:Superfamily: denitrification system component NapC/NirT (membrane-bound tetraheme cyto

Query Match 83.9%; Score 26; DB 2; Length 171;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFFA 6
 Db 24 FVFFFA 28

RESULT 46
 T47707
 hypothetical protein Fli16.90 - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C:Accession: T47707
 R:Benes, V.; Wurnbach, E.; Drzonek, H.; Ansoorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.
 submitted to the Protein Sequence Database, March 2000
 A:Reference number: Z24473
 A:Accession: T47707
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-183 <BEN>
 A:Cross-references: UNIPROT:Q9M054; UNIPARC:UPI000000A218E; EMBL:AL161667
 A:Experimental source: cultivar Columbia; BAC clone Fli16
 C:Genetics:
 A:Map position: 3
 A:Introns: 70/3
 A:Note: Fli16.90

Query Match 83.9%; Score 26; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFFA 6
 Db 18 FVFFFA 22

RESULT 47
 A86806
 transcription regulator [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
 C:Species: *Lactococcus lactis* subsp. *lactis*
 C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C:Accession: A86806
 R:Boilotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrh
 Genome Res. 11, 731-753, 2001
 A>Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: A86806
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-188 <STO>
 A:Cross-references: UNIPROT:Q9CFL8; UNIPARC:UPI000000C6A3D; GB:AE005176; PID:g12724440;
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: yohC

Query Match 83.9%; Score 26; DB 2; Length 188;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFF 5
 Db 170 KPIFF 174

RESULT 48

S73449
MG028 homolog B01_orf203 - Mycoplasma pneumoniae (strain ATCC 29342)
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C:Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 05-Oct-2004
C:Accession: S73449
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A:Reference number: S73327; MUID:97105885; PMID:8948633
A:Accession: S73449
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-203 <HIM>
A:Cross-references: UNIPROT:P75083; UNIPARC:UPI000013912P; EMBL:AE000015; GB:U00089; NID
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: uncharacterized conserved protein

Query Match 83.9%; Score 26; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||||
DB 89 FVFFA 93

RESULT 49
G70437
soluble hydrogenase small subunit - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Oct-2004
C:Accession: G70437
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98156666; PMID:9537320
A:Accession: G70437
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-216 <AQF>
A:Cross-references: UNIPROT:O67529; UNIPARC:UPI0000056670; GB:AE000746; NID:g2983925; PI
A:Experimental source: strain VF5
C:Genetics:
A:Gene: shys
C:Superfamily: serine-pyruvate/aspartate aminotransferase

Query Match 83.9%; Score 26; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||||
DB 61 FVFFA 65

RESULT 50
F86844
hypothetical protein ybbD [imported] - Lactococcus lactis subsp. lactis (strain ILL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86844
R:Solotkin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: F86844
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-218 <STO>

A:Cross-references: UNIPROT:Q9CES6; UNIPARC:UPI00000C6AFC; GB:AE005176; PID:g12724779; I
A:Experimental source: strain ILL1403
C:Genetics:
A:Gene: ybbD
C:Superfamily: dedA protein

Query Match 83.9%; Score 26; DB 2; Length 218;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
|||||
DB 155 KVIFF 159

RESULT 51
T22101
hypothetical protein F42F12.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22101
R:Lloyd, C.
Submitted to the EMBL Data Library, November 1995
A:Reference number: Z19514
A:Accession: T22101
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-243 <WIL>
A:Cross-references: UNIPROT:Q20344; UNIPARC:UPI000007AEF3; EMBL:Z68116; PIDN:CAA92173.1;
A:Experimental source: clone F42F12
C:Genetics:
A:Gene: CESP:F42F12.3
A:Map position: X
A:Introns: 85/2; 138/1; 222/2
C:Superfamily: Caenorhabditis elegans hypothetical protein ZK1251.3

Query Match 83.9%; Score 26; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||||
DB 18 FVFFA 22

RESULT 52
B81693
conserved hypothetical protein TC0525 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81693
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: B81693
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-255 <TET>
A:Cross-references: UNIPROT:Q9PKE0; UNIPARC:UPI0000057969; GB:AE002321; GB:AE002160; NIT
A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0525
C:Superfamily: Chlamydia trachomatis hypothetical protein CT254

Query Match 83.9%; Score 26; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||||
DB 68 FVFFA 72

```

D81085
Htrb/MebB family protein NMB1418 [imported] - Neisseria meningitidis (strain MC58 serog
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C;Accession: D81085
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: D81085
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-289 <TET>
A;Cross-references: UNIPROT:Q9JYV2; UNIPARC:UPI00000C46E0; GB:AE002491; GB:AE002098; NI
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1418
C;Superfamily: lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase

Query Match      83.9%; Score 26; DB 2; Length 289;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
Db 2 KFIFP 6

RESULT 56
A27692
sarcotoxin IIA precursor - flesh fly (Sarcophaga peregrina)
C;Species: Sarcophaga peregrina
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C;Accession: A27692
R;Ando, K.; Natori, S.
Biochemistry 27, 1715-1721, 1988
A;Title: Molecular cloning, sequencing, and characterization of cDNA for sarcotoxin IIA
A;Reference number: A27692; MUID:88209545; PMID:2452654
A;Accession: A27692
A;Molecule type: mRNA
A;Residues: 1-294 <AND>
A;Cross-references: UNIPROT:P14667; UNIPARC:UPI0000135ECC; GB:M18873; NID:g161272; PID
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-294/Product: sarcotoxin IIA #status predicted <MAT>

Query Match      83.9%; Score 26; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFPA 6
Db 4 FVFPA 8

RESULT 57
B36351
sarcotoxin II-2 - flesh fly (Sarcophaga peregrina)
C;Species: Sarcophaga peregrina
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Accession: B36351
R;Kanai, A.; Natori, S.
Mol. Cell. Biol. 10, 6114-6122, 1990
A;Title: Analysis of a gene cluster for sarcotoxin II, a group of antibacterial protein
A;Reference number: A36351; MUID:91061717; PMID:2247051
A;Accession: B36351
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <KAN>
A;Cross-references: UNIPROT:P24489; UNIPARC:UPI0000135EC9; GB:D90153; NID:g217388; PID

```

```

T44414
hypothetical protein BH0166 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44414; F83670
R;Takami, H.; Takaki, Y.; Nakasone, K.; Hirama, C.; Inoue, A.; Horikoshi, K.
Biosci. Biotechnol. Biochem. 63, 452-455, 1999
A;Title: Sequence analysis of a 32-kb region including the major ribosomal protein gene
A;Reference number: Z22756; MUID:99209008; PMID:10192928
A;Accession: T44414
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-265 <TAK>
A;Cross-references: UNIPROT:Q929J1; UNIPARC:UPI00000D4117; EMBL:AB017508; NID:g4512395;
A;Experimental source: strain C-125
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83670
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-265 <STO>
A;Cross-references: UNIPARC:UPI00000D4117; GB:AP001507; GB:BA000004; NID:g10172612; PIDN
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0166
A;Note: ybar
C;Superfamily: cobalt transport protein Q homolog

Query Match      83.9%; Score 26; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFPA 6
Db 35 FVFPA 39

RESULT 54
B81857
probable acetyltransferase NMA1630 [imported] - Neisseria meningitidis (strain Z2491 ser
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-Oct-2004
C;Accession: B81857
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20225556; PMID:10761919
A;Accession: B81857
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-289 <PAR>
A;Cross-references: UNIPROT:Q9JUT4; UNIPARC:UPI00000C4C38; GB:AL162756; GB:AL157959; NID
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA1630
C;Superfamily: lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase

Query Match      83.9%; Score 26; DB 2; Length 289;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
Db 2 KFIFP 6

RESULT 55

```

```

Query Match      83.9%; Score 26; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
DB      4 FVFFA 8

RESULT 58
S75656
hypothetical protein slr1980 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S75656
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75656
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-297 <KAN>
A:Cross-references: UNIPROT:P74131; UNIPARC:UPI00000C100A; EMBL:D90912; GB:AB001339; NID
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match      83.9%; Score 26; DB 2; Length 297;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KFVFF 5
DB     104 KFIFP 108

RESULT 59
D86216
protein T23G18.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86216
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizier, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86216
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-323 <STO>
A:Cross-references: UNIPROT:Q9SGD8; UNIPARC:UPI000009EE07; GB:AE005172; NID:G6579209; PI
C:Genetics:
A:Gene: T23G18.8
A:Map position: 1

Query Match      83.9%; Score 26; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
DB     99 FVFFA 103

```

```

RESULT 60
T24424
hypothetical protein T04A8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24424
R:Palmer, S.
submitted to the EMBL Data Library, August 1994
A:Reference number: Z19889
A:Accession: T24424
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-324 <WIL>
A:Cross-references: UNIPROT:P46568; UNIPARC:UPI000006112C; EMBL:Z35663; PIDN:CAA84725.1
C:Genetics:
A:Experimental source: clone T04A8
A:Gene: CESP:T04A8.1
A:Map position: 3
A:Introns: 77/3; 150/3; 198/3; 259/3

Query Match      83.9%; Score 26; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
DB     262 FVFFA 266

RESULT 61
S08459
hypothetical protein 2 - Spiroplasma virus 1
C:Species: Spiroplasma virus 1, SpV1
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 02-Mar-2001
C:Accession: S08459; S08447
R:Renaudin, J.; Aulio, P.; Vignault, J.C.; Bove, J.M.
Nucleic Acids Res. 18, 1293, 1990
A:Title: Complete nucleotide sequence of the genome of Spiroplasma citri virus SpV1-R8A2
A:Reference number: S08447; MUID:90206799; PMID:2320423
A:Accession: S08459
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-337 <REN>
A:Cross-references: UNIPARC:UPI0000138546; EMBL:X51344
A:Accession: S08447
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 262-337 <RE2>
A:Cross-references: UNIPARC:UPI0000161B8D; EMBL:X51344; NID:g61993; PIDN:CAA35725.1; PID
C:Genetics:
A:Genetic code: SGC3

Query Match      83.9%; Score 26; DB 2; Length 337;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KFVFF 5
DB      3 KFIFP 7

RESULT 62
E90564
potassium channel protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: E90564
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: E90564
A:Status: preliminary

```

A:Molecule type: DNA
A:Residues: 1-344 <KUR>
A:Cross-references: UNIPROT:Q99QES; UNIPARC:UPI00000D45DF; GB:AL445566; PID:gl4089835; R
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYP4 4210
A:Genetic code: SGC3

Query Match 83.9%; Score 26; DB 2; Length 344;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
|||:
315 KPIFF 319

Db

RESULT 63
T34333
hypothetical protein K06A1.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34333
R:Fulton, L.
submitted to the EMBL Data Library, July 1995
A:Description: The sequence of C. elegans cosmid K06A1.
A:Reference number: Z21507
A:Accession: T34333
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-381 <FUL>
A:Cross-references: UNIPROT:Q09585; UNIPARC:UPI000007A4D5; EMBL:U23449; PIDN:AAC24296.1;
A:Experimental source: strain Bristol N2; clone K06A1
C:Genetics:
A:Gene: CESP:K06A1.1
A:Map position: 2
A:Introns: 142/1; 214/2; 254/1; 343/3

Query Match 83.9%; Score 26; DB 2; Length 381;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
|||:
152 FVFFA 156

Db

RESULT 64
S68155
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - slime mold (Dictyostelium
C:Species: Dictyostelium discoideum
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68155; T43757
R:Angata, K.; Kuroe, K.; Yanagisawa, K.; Tanaka, Y.
Curr. Genet. 27, 249-256, 1995
A:Title: Codon usage, genetic code and phylogeny of Dictyostelium discoideum mitochondria
A:Reference number: S68155; MUID:95254668; PMID:7736610
A:Accession: S68155
A:Molecule type: DNA
A:Residues: 1-389 <ANG>
A:Cross-references: UNIPROT:Q37311; UNIPARC:UPI00001289A6; EMBL:D16466; NID:g6959590; PID
A:Experimental source: strain AX3
R:Ogawa, S.; Yoshino, R.; Angata, K.; Pi, M.; Iwamoto, M.; Kuroe, K.; Matsuo, K.; Morio,
submitted to the EMBL Data Library, December 1996
A:Description: The mitochondrial DNA of Dictyostelium discoideum. Complete sequence, gen
A:Reference number: Z22666
A:Accession: T43757
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-389 <OGA>
A:Cross-references: UNIPARC:UPI00001289A6; EMBL:AB000109; PIDN:BAA78061.1
C:Genetics:
A:Gene: cytb

A:Genome: mitochondrion
C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinone
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; mitochondrion
F:10-340/Domain: cytochrome b6 homology <CBH>
F:35-51/Domain: transmembrane #status predicted <TM1>
F:80-98/Domain: transmembrane #status predicted <TM2>
F:118-134/Domain: transmembrane #status predicted <TM3>
F:179-201/Domain: transmembrane #status predicted <TM4>
F:222-340/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>
F:230-246/Domain: transmembrane #status predicted <TM5>
F:289-305/Domain: transmembrane #status predicted <TM6>
F:324-344/Domain: transmembrane #status predicted <TM7>
F:354-370/Domain: transmembrane #status predicted <TM8>
F:82,183/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F:96,197/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted

Query Match 83.9%; Score 26; DB 2; Length 389;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
|||:
243 FVFFA 247

Db

RESULT 65
T22810
hypothetical protein F56H9.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22810
R:Burton, J.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19618
A:Accession: T22810
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-390 <WIL>
A:Cross-references: UNIPROT:Q20910; UNIPARC:UPI000007F97A; EMBL:Z74473; PIDN:CAA98953.1
A:Experimental source: clone F56H9
C:Genetics:
A:Gene: CESP:F56H9.4
A:Map position: 5
A:Introns: 51/1; 65/2; 112/3; 229/2; 247/3; 278/3; 330/1; 370/3
C:Superfamily: GTP-binding regulatory protein Gs alpha chain

Query Match 83.9%; Score 26; DB 2; Length 390;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
|||:
229 KPIFF 233

Db

RESULT 66
T00516
hypothetical protein At2g23160 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T20D16.21
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 31-Dec-2004
C:Accession: T00516; C84621
R:Roundley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau
submitted to the EMBL Data Library, November 1997
A:Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.
A:Reference number: Z14164
A:Accession: T00516
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-395 <ROU>
A:Cross-references: UNIPROT:O22191; UNIPARC:UPI00000AAAFDA; EMBL:AC002391; NID:g2642427;
A:Experimental source: cultivar Columbia

R.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: C84621

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-395 <STO>

A:Cross-references: UNIPARC:UPI00000AAPDA; GB:AE002093; NID:g2642447; PIDN:AB87115.1; C:Genetics:

A:Gene: AC2923160; T20D16.21

A:Map position: 2

A:Introns: 295/3

A>Note: T20D16.21

C:Superfamily: hypothetical protein containing F-box domain

Query Match 83.9%; Score 26; DB 2; Length 395;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5

Db 245 KFIFP 249

RESULT 67

D81040

Cytochrome c-type biogenesis protein, probable NMB1803 [imported] - Neisseria meningitidis

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: D81040

R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V. A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: D81040

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-395 <TET>

A:Cross-references: UNIPROT:Q9JY05; UNIPARC:UPI00000C47CE; GB:AE002530; GB:AE002098; NID

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB1803

Query Match 83.9%; Score 26; DB 2; Length 395;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6

Db 120 FVFFA 124

RESULT 68

B81986

Probable membrane protein NMA0660 [imported] - Neisseria meningitidis (strain Z2491 sero

C:Species: Neisseria meningitidis

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C:Accession: B81986

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel i; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; MUID:20222556; PMID:10761919

A:Accession: B81986

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-395 <PAR>

A:Cross-references: UNIPROT:Q9JVV9; UNIPARC:UPI00000C4A09; GB:AL162753; GB:AL157959; NID

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMA0660

Query Match 83.9%; Score 26; DB 2; Length 395;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6

Db 120 FVFFA 124

RESULT 69

T46710

multidrug resistance transporter [imported] - Listeria monocytogenes

C:Species: Listeria monocytogenes

C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004

C:Accession: T46710

R;Huillet, E.E.H.; Larpin, S.; Pardon, P.; Berche, P.

FEMS Microbiol. Lett. 174, 265-272, 1999

A>Title: Identification of a new locus in Listeria monocytogenes involved in cellobiose-

A:Reference number: Z23136; MUID:99271176; PMID:10339818

A:Accession: T46710

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-397 <HUI>

A:Cross-references: UNIPROT:Q9X769; UNIPARC:UPI0000055470; EMBL:AJ009627; NID:g4914621;

C:Genetics:

A:Gene: lltB

Query Match 83.9%; Score 26; DB 2; Length 397;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6

Db 245 FVFFA 249

RESULT 70

AE1613

multidrug-efflux transporter homolog lin1446 [imported] - Listeria innocua (strain Clip1

C:Species: Listeria innocua

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AE1613

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A>Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AE1613

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-397 <GLA>

A:Cross-references: UNIPROT:Q92B08; UNIPARC:UPI00000CC57B; GB:AL592022; PIDN:CAC96677.1;

A:Experimental source: strain Clip11262

C:Genetics:

A:Gene: lin1446

Query Match 83.9%; Score 26; DB 2; Length 397;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6

Db 245 FVFFA 249

RESULT 71
A11250
multidrug-efflux transporter homolog lmo1409 [imported] - Listeria monocytogenes (strain
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: A11250
R;Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Krest, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluster, T.; Smoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: A11250
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <GLA>
A;Cross-references: UNIPROT:Q9X769; UNIPARC:UPI0000055470; GB:NC_003210; PIDN:CAC99487.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1409

Query Match 83.9%; Score 26; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||||
DB 245 FVFFA 249

RESULT 72
T44331
hypothetical protein wb1d [imported] - Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44331
R;Yamaseki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y.
Gene 237, 321-332, 1999
A;Title: The genes responsible for O-antigen synthesis of Vibrio cholerae O139 are close
A;Reference number: 222749; MUID:99453293; PMID:10521656
A;Accession: T44331
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-398 <YAM>
A;Cross-references: UNIPROT:O87160; UNIPARC:UPI00000B5419; EMBL:AB012957; NID:g4115688;
A;Experimental source: strain O22
C;Genetics:
A;Note: wb1d

Query Match 83.9%; Score 26; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||||
DB 263 FVFFA 267

RESULT 73
H69833
conserved hypothetical protein yhjI - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: H69833
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardin
ois,

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: H69833

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-401 <KUN>

A;Cross-references: UNIPROT:O07563; UNIPARC:UPI00000601AF; GB:Z99109; GB:AL009126; NID:
A;Experimental source: strain 168
C;Genetics:
A;Gene: yhjI

Query Match 83.9%; Score 26; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||||
DB 215 FVFFA 219

RESULT 74
C95990
probable sugar uptake ABC transporter permease protein ggub [imported] - Sinorhizobium
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95990
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna
Proc. Natl. Acad. Sci. U.S.A. 98, 9899-9894, 2001
A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing end
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: C95990
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <KUR>
A;Cross-references: UNIPROT:Q92UE4; UNIPARC:UPI00000CB7A2; GB:AL591985; PIDN:CAC49587.1
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, I
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
C;Genetics:
A;Gene: ggub; SM520893
A;Genome: plasmid
C;Superfamily: 1-arabinose transport system permease araH

Query Match 83.9%; Score 26; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||||
DB 223 FVFFA 227

RESULT 75
CBQFR
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Rhodospirillum rubrum
C;Species: Rhodospirillum rubrum
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: S12257; A38814
R;Majewski, C.; Trebat, A.

Mol. Gen. Genet. 224, 373-382, 1990
A;Title: The pet genes of Rhodospirillum rubrum: cloning and sequencing of the genes for
A;Reference number: S12255; MUID:91094774; PMID:2176269
A;Accession: S12257
A;Molecule type: DNA
A;Residues: 1-405 <MA1>
A;Cross-references: UNIPROT:P231134; UNIPARC:UPI0000128ACD; EMBL:X55387; NID:g45382; PIDN
A;Note: the authors translated the codon AAT for residue 161 as Leu and CTG for residue
A;Accession: A38814
A;Molecule type: protein
A;Residues: 1-26, 'E', <MA2>
A;Cross-references: UNIPARC:UPI0000171D0F
C;Genetics:
A;Gene: petB
C;Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; oxidoreductase
F;1-405/Product: cytochrome b #status experimental <MAT>
F;22-354/Domain: cytochrome b homology <CBH>
F;22-222/Domain: cytochrome b6 homology <CH6>
F;47-63/Domain: transmembrane #status predicted <TM1>
F;92-110/Domain: transmembrane #status predicted <TM2>
F;130-146/Domain: transmembrane #status predicted <TM3>
F;191-213/Domain: transmembrane #status predicted <TM4>
F;236-354/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>
F;244-260/Domain: transmembrane #status predicted <TM5>
F;303-319/Domain: transmembrane #status predicted <TM6>
F;338-356/Domain: transmembrane #status predicted <TM7>
F;368-384/Domain: transmembrane #status predicted <TM8>
F;94,195/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F;108,209/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted

Query Match 83.9%; Score 26; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||||
Db 257 FVFFA 261

Search completed: December 29, 2005, 17:49:11
Job time : 17.9677 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.29032 Seconds
(without alignments)
13.656 Million cell updates/sec

Title: US-10-009-122-4

Perfect score: 31

Sequence: 1 KPVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA New:*

1: /cgn2_6/ptodata/2/pubaa/US08_NEW_PUB.pep.*

2: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB.pep.*

3: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB.pep.*

4: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB.pep.*

5: /cgn2_6/ptodata/2/pubaa/US03_NEW_PUB.pep.*

6: /cgn2_6/ptodata/2/pubaa/US10_NEW_PUB.pep.*

7: /cgn2_6/ptodata/2/pubaa/US11_NEW_PUB.pep.*

8: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	27	87.1	582	7 US-11-090-439-58	Sequence 58, Appl
2	27	87.1	592	6 US-10-467-657-4888	Sequence 4888, Ap
3	27	87.1	738	7 US-11-147-047-48	Sequence 48, Appl
4	27	87.1	1070	7 US-11-147-047-49	Sequence 49, Appl
5	26	83.9	19	6 US-10-467-657-8712	Sequence 8712, Ap
6	26	83.9	220	6 US-10-467-657-3154	Sequence 3154, Ap
7	26	83.9	299	6 US-10-467-657-2190	Sequence 2190, Ap
8	26	83.9	395	6 US-10-467-657-1950	Sequence 1950, Ap
9	26	83.9	418	6 US-10-467-657-5788	Sequence 5788, Ap
10	25	80.6	19	6 US-10-923-605-5	Sequence 5, Appli
11	25	80.6	19	6 US-10-934-818-5	Sequence 5, Appli
12	25	80.6	40	7 US-11-016-706-36	Sequence 36, Appl
13	25	80.6	40	7 US-11-098-674-12	Sequence 12, Appl
14	25	80.6	42	6 US-10-923-605-1	Sequence 1, Appli
15	25	80.6	42	6 US-10-934-818-1	Sequence 1, Appli
16	25	80.6	42	7 US-11-016-706-37	Sequence 37, Appl
17	25	80.6	43	6 US-10-934-818-6	Sequence 6, Appli
18	25	80.6	43	6 US-10-250-581-1	Sequence 1, Appli
19	25	80.6	43	6 US-10-250-581-1	Sequence 1, Appli
20	25	80.6	184	6 US-10-467-657-7560	Sequence 7560, Ap
21	25	80.6	525	7 US-11-082-389-350	Sequence 350, App
22	25	80.6	770	6 US-10-982-545-15	Sequence 15, Appl
23	25	80.6	770	6 US-10-789-273-38	Sequence 38, Appl
24	24	77.4	194	6 US-10-467-657-3978	Sequence 3978, Ap
25	24	77.4	229	6 US-10-793-626-62	Sequence 62, Appl

26	24	77.4	443	6	US-10-793-626-1860	Sequence 1860, Ap
27	24	77.4	533	6	US-10-467-657-4566	Sequence 4566, Ap
28	24	77.4	657	7	US-11-080-591-48	Sequence 48, Appl
29	24	77.4	4384	6	US-10-467-657-4242	Sequence 4242, Ap
30	24	77.4	4384	6	US-10-821-234-1120	Sequence 1120, Ap
31	24	74.2	49	6	US-10-467-657-1370	Sequence 1370, Ap
32	24	74.2	49	6	US-10-467-657-2308	Sequence 2308, Ap
33	24	74.2	49	6	US-10-467-657-5610	Sequence 5610, Ap
34	24	74.2	49	6	US-10-467-657-7516	Sequence 7516, Ap
35	24	74.2	49	6	US-10-467-657-8322	Sequence 8322, Ap
36	24	74.2	54	6	US-10-467-657-4324	Sequence 4324, Ap
37	24	74.2	56	6	US-10-467-657-8286	Sequence 8286, Ap
38	24	74.2	126	6	US-10-793-626-2766	Sequence 2766, Ap
39	24	74.2	209	6	US-10-793-626-304	Sequence 304, App
40	24	74.2	234	6	US-10-793-626-1034	Sequence 1034, Ap
41	24	74.2	288	6	US-10-467-657-4456	Sequence 4456, Ap
42	24	74.2	391	6	US-10-613-744-13	Sequence 13, Appl
43	24	74.2	410	6	US-10-467-657-4858	Sequence 4858, Ap
44	24	74.2	432	7	US-11-055-822-1096	Sequence 1096, Ap
45	24	74.2	432	7	US-11-113-424-186	Sequence 186, App
46	24	74.2	449	6	US-10-467-657-678	Sequence 678, App
47	24	74.2	534	7	US-11-082-389-348	Sequence 348, App
48	24	74.2	633	6	US-10-467-657-3440	Sequence 3440, Ap
49	24	74.2	633	6	US-10-467-657-4632	Sequence 4632, Ap
50	24	74.2	660	7	US-11-186-284-125	Sequence 125, App
51	24	74.2	708	6	US-10-821-234-917	Sequence 917, App
52	24	74.2	766	6	US-10-793-626-420	Sequence 420, App
53	24	74.2	1012	6	US-10-995-561-908	Sequence 908, App
54	24	74.2	2323	6	US-10-793-626-760	Sequence 760, App
55	24	71.0	30	6	US-10-467-657-8998	Sequence 8998, Ap
56	24	71.0	72	7	US-11-000-463-378	Sequence 378, App
57	24	71.0	72	7	US-11-000-463-850	Sequence 850, App
58	24	71.0	77	6	US-10-467-657-360	Sequence 360, App
59	24	71.0	79	6	US-10-467-657-2026	Sequence 2026, Ap
60	24	71.0	101	6	US-10-485-517-286	Sequence 286, App
61	24	71.0	101	6	US-10-467-657-6824	Sequence 6824, Appl
62	24	71.0	139	7	US-11-125-837-24	Sequence 24, Appl
63	24	71.0	149	6	US-10-467-657-6110	Sequence 6110, Ap
64	24	71.0	149	6	US-10-467-657-7550	Sequence 7550, Ap
65	24	71.0	154	6	US-10-467-657-6130	Sequence 6130, Ap
66	24	71.0	180	6	US-10-485-517-346	Sequence 346, App
67	24	71.0	187	6	US-10-980-388-65	Sequence 65, Appl
68	24	71.0	210	6	US-10-467-657-4386	Sequence 4386, Ap
69	24	71.0	222	6	US-10-467-657-3000	Sequence 3000, Ap
70	24	71.0	238	6	US-10-467-657-6248	Sequence 6248, Ap
71	24	71.0	240	7	US-11-054-515-1391	Sequence 1391, Ap
72	24	71.0	241	7	US-11-074-176-66	Sequence 66, Appl
73	24	71.0	250	6	US-10-793-626-1124	Sequence 1124, Ap
74	24	71.0	254	6	US-10-467-657-6144	Sequence 6144, Ap
75	24	71.0	268	6	US-10-467-657-1178	Sequence 1178, Ap
76	24	71.0	268	6	US-10-467-657-5704	Sequence 5704, Ap
77	24	71.0	277	6	US-10-667-295-85	Sequence 85, Appl
78	24	71.0	326	6	US-10-873-528-33	Sequence 33, Appl
79	24	71.0	328	6	US-10-848-375-1	Sequence 1, Appli
80	24	71.0	331	6	US-10-873-528-147	Sequence 147, App
81	24	71.0	341	6	US-10-858-730-124	Sequence 124, App
82	24	71.0	346	6	US-10-793-626-504	Sequence 504, App
83	24	71.0	347	6	US-10-821-234-1379	Sequence 1379, Ap
84	24	71.0	353	7	US-11-067-984-6	Sequence 6, Appli
85	24	71.0	362	6	US-10-467-657-2872	Sequence 2872, Ap
86	24	71.0	365	6	US-10-875-716-9	Sequence 9, Appli
87	24	71.0	366	7	US-11-055-822-400	Sequence 400, App
88	24	71.0	366	7	US-11-055-822-492	Sequence 492, App
89	24	71.0	376	6	US-10-793-626-490	Sequence 490, App
90	24	71.0	376	6	US-10-793-626-2260	Sequence 2260, Ap
91	24	71.0	383	6	US-10-793-626-2026	Sequence 2026, Ap
92	24	71.0	436	6	US-10-467-657-7578	Sequence 7578, Ap
93	24	71.0	445	6	US-10-821-234-1606	Sequence 1606, Ap
94	24	71.0	465	6	US-10-793-626-1676	Sequence 1676, Ap
95	24	71.0	481	6	US-10-995-561-959	Sequence 959, App
96	24	71.0	494	6	US-10-467-657-592	Sequence 592, App
97	24	71.0	505	6	US-10-873-528-120	Sequence 120, App
98	24	71.0	522	6	US-10-793-626-604	Sequence 604, App

99	22	71.0	528	6	US-10-864-758-7	Sequence 7, Appli	172	21	67.7	652	6	US-10-873-528-26	Sequence 26, Appl
100	22	71.0	541	7	US-11-000-463-238	Sequence 238, App	173	21	67.7	658	6	US-10-873-528-17	Sequence 17, Appl
101	22	71.0	566	6	US-10-467-657-8046	Sequence 8046, Ap	174	21	67.7	676	6	US-10-510-947-1	Sequence 1, Appli
102	22	71.0	578	6	US-11-083-800-2	Sequence 2, Appli	175	21	67.7	677	6	US-10-873-528-155	Sequence 155, App
103	22	71.0	607	7	US-11-080-991-88	Sequence 88, Appl	176	21	67.7	697	6	US-10-485-517-202	Sequence 202, App
104	22	71.0	709	6	US-10-131-826A-202	Sequence 202, App	177	21	67.7	756	6	US-10-467-657-8694	Sequence 8694, Ap
105	22	71.0	786	6	US-10-467-962B-103	Sequence 103, App	178	21	67.7	801	6	US-10-793-626-2020	Sequence 2020, Ap
106	22	71.0	790	6	US-10-131-826A-204	Sequence 204, App	179	21	67.7	837	7	US-11-094-519A-43	Sequence 43, Appl
107	22	71.0	943	6	US-10-821-234-1012	Sequence 1012, Ap	180	21	67.7	845	7	US-11-094-519A-42	Sequence 42, Appl
108	22	71.0	1062	6	US-10-821-234-1079	Sequence 1079, Ap	181	21	67.7	1052	6	US-10-467-657-3992	Sequence 3992, Ap
109	22	71.0	1070	7	US-11-000-463-721	Sequence 721, App	182	21	67.7	1076	6	US-10-467-657-5708	Sequence 5708, Ap
110	22	71.0	1194	7	US-11-000-463-249	Sequence 249, App	183	21	67.7	1170	7	US-11-080-026-2	Sequence 2, Appli
111	21	67.7	5	7	US-11-098-674-1	Sequence 1, Appli	184	21	67.7	1170	7	US-11-107-028-4	Sequence 4, Appli
112	21	67.7	39	6	US-10-467-657-4630	Sequence 4630, Ap	185	21	67.7	1751	7	US-11-103-957-45	Sequence 45, Appl
113	21	67.7	40	6	US-10-467-657-4616	Sequence 4616, Ap	186	20	64.5	16	7	US-11-089-764-65	Sequence 65, Appl
114	21	67.7	43	6	US-10-467-657-8642	Sequence 8642, Ap	187	20	64.5	16	7	US-11-089-764-66	Sequence 66, Appl
115	21	67.7	47	6	US-10-467-657-5436	Sequence 5436, Ap	188	20	64.5	23	7	US-11-085-812-16	Sequence 16, Appl
116	21	67.7	55	6	US-10-485-517-387	Sequence 387, App	189	20	64.5	28	6	US-10-250-581-14	Sequence 14, Appl
117	21	67.7	57	7	US-11-000-463-770	Sequence 770, App	190	20	64.5	28	6	US-10-250-581-17	Sequence 17, Appl
118	21	67.7	63	7	US-11-000-463-353	Sequence 353, App	191	20	64.5	28	6	US-10-250-581-14	Sequence 14, Appl
119	21	67.7	63	7	US-11-000-463-825	Sequence 825, App	192	20	64.5	28	6	US-10-250-581-17	Sequence 17, Appl
120	21	67.7	72	6	US-10-467-657-5578	Sequence 5578, Ap	193	20	64.5	40	6	US-10-250-581-15	Sequence 15, Appl
121	21	67.7	72	6	US-11-000-463-298	Sequence 298, App	194	20	64.5	40	6	US-10-250-581-18	Sequence 18, Appl
122	21	67.7	75	6	US-10-467-657-8472	Sequence 8472, Ap	195	20	64.5	40	6	US-10-250-581-15	Sequence 15, Appl
123	21	67.7	79	7	US-11-123-896-134	Sequence 134, App	196	20	64.5	40	6	US-10-250-581-18	Sequence 18, Appl
124	21	67.7	90	6	US-10-467-657-4374	Sequence 4374, Ap	197	20	64.5	42	6	US-10-250-581-16	Sequence 16, Appl
125	21	67.7	91	6	US-10-821-234-1238	Sequence 1238, Ap	198	20	64.5	42	6	US-10-250-581-19	Sequence 19, Appl
126	21	67.7	94	6	US-10-467-657-4730	Sequence 4730, Ap	199	20	64.5	42	6	US-10-250-581-16	Sequence 16, Appl
127	21	67.7	102	6	US-10-467-657-5604	Sequence 5604, Ap	200	20	64.5	42	6	US-10-250-581-19	Sequence 19, Appl
128	21	67.7	113	6	US-10-793-626-1848	Sequence 1848, Ap	201	20	64.5	44	6	US-10-467-657-1118	Sequence 1118, Ap
129	21	67.7	120	6	US-10-793-626-2376	Sequence 2376, Ap	202	20	64.5	45	6	US-10-467-657-8968	Sequence 8968, Ap
130	21	67.7	140	6	US-10-982-145-66	Sequence 66, Appl	203	20	64.5	50	6	US-10-467-657-7892	Sequence 7892, Ap
131	21	67.7	141	6	US-10-982-145-67	Sequence 67, Appl	204	20	64.5	54	6	US-10-467-657-2264	Sequence 2264, Ap
132	21	67.7	164	6	US-10-467-657-1450	Sequence 1450, Ap	205	20	64.5	54	6	US-10-467-657-4978	Sequence 4978, Ap
133	21	67.7	168	6	US-10-927-641-69	Sequence 69, Appl	206	20	64.5	56	6	US-10-467-657-1050	Sequence 1050, Ap
134	21	67.7	182	6	US-10-793-626-724	Sequence 724, App	207	20	64.5	66	6	US-10-467-657-766	Sequence 766, App
135	21	67.7	183	6	US-10-467-657-8302	Sequence 8302, Ap	208	20	64.5	79	7	US-11-080-991-10	Sequence 10, Appl
136	21	67.7	183	7	US-11-069-642-125	Sequence 125, App	209	20	64.5	92	6	US-10-467-657-5952	Sequence 5952, Ap
137	21	67.7	198	6	US-10-467-657-5440	Sequence 5440, Ap	210	20	64.5	105	6	US-10-467-657-9209	Sequence 9209, Ap
138	21	67.7	220	6	US-10-793-626-1822	Sequence 1822, Ap	211	20	64.5	115	6	US-10-793-626-1554	Sequence 1554, Ap
139	21	67.7	227	6	US-10-793-626-2396	Sequence 2396, Ap	212	20	64.5	120	6	US-10-467-657-6982	Sequence 6982, Ap
140	21	67.7	227	6	US-10-793-626-2396	Sequence 2396, Ap	213	20	64.5	120	6	US-10-467-657-7938	Sequence 7938, Ap
141	21	67.7	233	6	US-10-467-657-8268	Sequence 8268, Ap	214	20	64.5	123	6	US-10-821-234-988	Sequence 988, App
142	21	67.7	235	7	US-11-188-473-2	Sequence 2, Appli	215	20	64.5	123	6	US-10-467-657-6378	Sequence 6378, Ap
143	21	67.7	246	7	US-11-092-140-111	Sequence 111, App	216	20	64.5	127	7	US-11-106-796-10	Sequence 10, Appl
144	21	67.7	247	7	US-11-103-957-69	Sequence 69, Appl	217	20	64.5	129	6	US-10-501-039-8	Sequence 8, Appli
145	21	67.7	248	7	US-11-076-164-9	Sequence 9, Appli	218	20	64.5	135	6	US-10-793-626-2284	Sequence 2284, Ap
146	21	67.7	269	6	US-10-467-657-330	Sequence 330, App	219	20	64.5	138	6	US-10-793-626-1254	Sequence 1254, Ap
147	21	67.7	286	6	US-10-793-626-2192	Sequence 2192, Ap	220	20	64.5	150	6	US-10-793-626-2324	Sequence 2324, Ap
148	21	67.7	294	7	US-11-055-822-480	Sequence 480, App	221	20	64.5	154	7	US-11-082-389-424	Sequence 424, App
149	21	67.7	294	7	US-11-055-822-880	Sequence 880, App	222	20	64.5	155	6	US-10-467-657-2420	Sequence 2420, Ap
150	21	67.7	298	6	US-10-454-437-384	Sequence 384, App	223	20	64.5	160	7	US-11-009-939-44	Sequence 44, Appl
151	21	67.7	298	7	US-11-055-822-478	Sequence 478, App	224	20	64.5	166	6	US-10-821-234-1293	Sequence 1293, Ap
152	21	67.7	298	7	US-11-055-822-878	Sequence 878, App	225	20	64.5	166	6	US-10-878-556A-20	Sequence 20, Appl
153	21	67.7	301	6	US-10-793-626-206	Sequence 206, App	226	20	64.5	174	6	US-10-793-626-1520	Sequence 1520, Ap
154	21	67.7	355	6	US-10-467-657-7996	Sequence 7996, Ap	227	20	64.5	183	6	US-10-467-657-6906	Sequence 6906, Ap
155	21	67.7	400	6	US-10-793-626-1056	Sequence 1056, Ap	228	20	64.5	188	7	US-11-100-183-27	Sequence 27, Appl
156	21	67.7	403	7	US-11-109-156-29	Sequence 29, Appl	229	20	64.5	190	6	US-10-467-657-3436	Sequence 3436, Ap
157	21	67.7	407	6	US-10-821-234-1389	Sequence 1389, Ap	230	20	64.5	193	6	US-10-793-626-1340	Sequence 1340, Ap
158	21	67.7	419	7	US-11-084-624-18	Sequence 18, Appl	231	20	64.5	196	6	US-10-131-826A-168	Sequence 168, App
159	21	67.7	452	6	US-10-793-626-3092	Sequence 3092, Ap	232	20	64.5	196	6	US-10-793-626-2584	Sequence 2584, Ap
160	21	67.7	464	6	US-10-689-742-164	Sequence 164, App	233	20	64.5	201	5	US-09-940-308-5	Sequence 5, Appli
161	21	67.7	490	7	US-11-074-176-316	Sequence 316, App	234	20	64.5	211	6	US-10-821-234-1372	Sequence 1372, Ap
162	21	67.7	495	7	US-11-074-176-60	Sequence 60, Appl	235	20	64.5	211	6	US-10-467-657-6932	Sequence 6932, Ap
163	21	67.7	502	6	US-10-821-234-1554	Sequence 1554, Ap	236	20	64.5	215	6	US-10-131-826A-4	Sequence 4, Appli
164	21	67.7	514	6	US-10-467-657-2664	Sequence 2664, Ap	237	20	64.5	215	6	US-10-131-826A-488	Sequence 488, App
165	21	67.7	514	7	US-11-103-037-3	Sequence 3, Appli	238	20	64.5	215	7	US-11-080-991-112	Sequence 112, App
166	21	67.7	515	6	US-10-630-203-6	Sequence 6, Appli	239	20	64.5	221	6	US-10-793-626-1392	Sequence 1392, Ap
167	21	67.7	521	6	US-10-793-626-532	Sequence 532, App	240	20	64.5	221	6	US-10-793-626-2420	Sequence 2420, Ap
168	21	67.7	526	6	US-10-606-302-5	Sequence 5, Appli	241	20	64.5	228	6	US-10-793-626-360	Sequence 360, App
169	21	67.7	526	6	US-10-606-302-5	Sequence 5, Appli	242	20	64.5	228	6	US-10-793-626-488	Sequence 488, App
170	21	67.7	528	6	US-10-793-626-1930	Sequence 1930, Ap	243	20	64.5	228	6	US-10-467-657-568	Sequence 568, App
171	21	67.7	537	6	US-10-467-657-6958	Sequence 6958, Ap	244	20	64.5	228	6	US-10-467-657-4838	Sequence 4838, Ap

245 20 64.5 233 6 US-10-821-234-1322
246 20 64.5 234 6 US-10-793-626-132
247 20 64.5 245 6 US-10-467-657-7884
248 20 64.5 263 6 US-10-510-386-234
249 20 64.5 275 7 US-11-110-977-4
250 20 64.5 276 7 US-11-112-882-86
251 20 64.5 277 6 US-10-454-437-8
252 20 64.5 277 6 US-11-055-822-608
253 20 64.5 281 6 US-10-821-234-1080
254 20 64.5 288 6 US-10-467-657-1272
255 20 64.5 291 7 US-11-102-883-22
256 20 64.5 292 7 US-11-102-883-24
257 20 64.5 294 6 US-10-467-657-7686
258 20 64.5 294 7 US-11-112-882-85
259 20 64.5 295 7 US-11-091-100-2
260 20 64.5 298 7 US-11-085-812-4
261 20 64.5 304 7 US-11-112-882-3
262 20 64.5 306 6 US-10-467-657-7222
263 20 64.5 311 6 US-10-793-626-2450
264 20 64.5 319 6 US-10-131-826A-134
265 20 64.5 321 6 US-10-467-657-2504
266 20 64.5 323 6 US-10-467-657-556
267 20 64.5 324 6 US-10-793-626-1262
268 20 64.5 324 6 US-10-467-657-7692
269 20 64.5 324 6 US-10-467-657-8440
270 20 64.5 325 5 US-09-940-308-8
271 20 64.5 325 6 US-10-454-437-142
272 20 64.5 330 7 US-11-085-812-2
273 20 64.5 335 6 US-10-467-657-3818
274 20 64.5 337 6 US-10-875-716-2
275 20 64.5 338 6 US-10-467-657-136
276 20 64.5 338 6 US-10-467-657-6798
277 20 64.5 338 6 US-10-878-556A-19
278 20 64.5 344 6 US-10-131-826A-376
279 20 64.5 347 6 US-10-467-657-2014
280 20 64.5 350 6 US-10-485-517-288
281 20 64.5 350 7 US-11-095-624-2
282 20 64.5 350 7 US-11-095-624-3
283 20 64.5 350 7 US-11-095-624-4
284 20 64.5 351 7 US-11-095-624-5
285 20 64.5 353 7 US-11-060-023-2
286 20 64.5 353 7 US-11-060-023-4
287 20 64.5 353 7 US-11-060-023-6
288 20 64.5 353 7 US-11-060-023-8
289 20 64.5 353 7 US-11-060-023-12
290 20 64.5 353 7 US-11-060-023-14
291 20 64.5 353 7 US-11-060-023-15
292 20 64.5 353 7 US-11-060-023-16
293 20 64.5 355 6 US-10-454-437-102
294 20 64.5 356 7 US-11-055-822-972
295 20 64.5 356 7 US-11-055-822-1052
296 20 64.5 359 7 US-11-060-023-11
297 20 64.5 359 7 US-11-060-023-13
298 20 64.5 360 7 US-11-060-023-17
299 20 64.5 378 7 US-11-080-091-3
300 20 64.5 378 7 US-11-080-091-11

ALIGNMENTS

RESULT 1
US-11-090-439-58
; Sequence 58, Application US/11090439
; Publication No. US20050266442A1
; GENERAL INFORMATION:
; APPLICANT: Squillace, Rachel
; APPLICANT: Weiner, Michael P.
; TITLE OF INVENTION: Immortalized Human Tuberos Sclerosis Null
; TITLE OF INVENTION: Angiomyolipoma Cell and Method of Use Thereof
; FILE REFERENCE: 24318-502
; CURRENT APPLICATION NUMBER: US/11/090,439
; CURRENT FILING DATE: 2005-03-25

; PRIOR APPLICATION NUMBER: 60/556,344
; PRIOR FILING DATE: 2004-03-25
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-439-58

Query Match 87.1%; Score 27; DB 7; Length 582;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 KVFPP 5
Db 378 KVFPP 382

RESULT 2
US-10-467-657-4888
; Sequence 4888, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4888
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4888

Query Match 87.1%; Score 27; DB 6; Length 592;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 KVFPP 5
Db 557 KVFPP 561

RESULT 3
US-11-147-047-48
; Sequence 48, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; CURRENT APPLICATION NUMBER: 60/236,874

```
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-48
```

```
Query Match      87.1%; Score 27; DB 7; Length 738;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVFVF 5
Db      184 KVFVF 188
```

```
RESULT 4
US-11-147-047-49
; Sequence 49, Application US/11147047
; Publication No. US20050260668A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 1070
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-49
```

```
Query Match      87.1%; Score 27; DB 7; Length 1070;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVFVF 5
Db      244 KVFVF 248
```

```
RESULT 5
US-10-467-657-8712
; Sequence 8712, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
```

```
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8712
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8712
```

```
Query Match      83.9%; Score 26; DB 6; Length 19;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVFVF 5
Db      15 KVFVF 19
```

```
RESULT 6
US-10-467-657-3154
; Sequence 3154, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3154
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3154
```

```
Query Match      83.9%; Score 26; DB 6; Length 220;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 FVFVF 6
Db      204 FVFVF 208
```

```
RESULT 7
US-10-467-657-2190
; Sequence 2190, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
```

; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 2190
 ; LENGTH: 299
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-2190

Query Match 83.9%; Score 26; DB 6; Length 299;
 Best Local Similarity 80.0%; Pred. No. 64;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5
 Db 12 KFIFF 16

RESULT 8
 US-10-467-657-1950
 ; Sequence 1950, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON Spa
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASNANI Vega
 ; APPLICANT: MASNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 1950
 ; LENGTH: 395
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-1950

Query Match 83.9%; Score 26; DB 6; Length 395;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFPA 6
 Db 120 FVFPA 124

RESULT 9
 US-10-467-657-5788
 ; Sequence 5788, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON Spa
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 5788
 ; LENGTH: 418
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-5788

Query Match 83.9%; Score 26; DB 6; Length 418;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFPA 6
 Db 337 FVFPA 341

RESULT 10
 US-10-923-605-5
 ; Sequence 5, Application US/10923605
 ; Publication No. US20050249727A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schenk, Dale B.
 ; APPLICANT: Neuralab Limited
 ; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
 ; FILE REFERENCE: 152703-004740US
 ; CURRENT APPLICATION NUMBER: US/10/923,605
 ; CURRENT FILING DATE: 2004-08-20
 ; PRIOR APPLICATION NUMBER: US/09/322,289
 ; PRIOR FILING DATE: 1999-05-28
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28
 ; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
 ; OTHER INFORMATION: inserted and two added Gly residues
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)
 ; OTHER INFORMATION: Xaa = acetyl histidine
 US-10-923-605-5

Query Match 80.6%; Score 25; DB 6; Length 19;
 Best Local Similarity 83.3%; Pred. No. 8;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
 Db 4 KLVFPA 9

RESULT 11
 US-10-934-818-5
 ; Sequence 5, Application US/10934818
 ; Publication No. US20050255122A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schenk, Dale B.
 ; APPLICANT: Neuralab Limited
 ; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
 ; FILE REFERENCE: 152703-472000US
 ; CURRENT APPLICATION NUMBER: US/10/934,818
 ; CURRENT FILING DATE: 2004-09-02
 ; PRIOR APPLICATION NUMBER: US 60/067,740
 ; PRIOR FILING DATE: 1997-12-02
 ; PRIOR APPLICATION NUMBER: US 60/080,970
 ; PRIOR FILING DATE: 1998-04-07
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28
 ; OTHER INFORMATION: peptide with carboxyl terminal Cys residue

; OTHER INFORMATION: inserted and two added Gly residues
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)
 ; OTHER INFORMATION: Xaa = acetyl histidine
 US-10-934-818-5

Query Match 80.6%; Score 25; DB 6; Length 19;
 Best Local Similarity 83.3%; Pred. No. 8;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 | | | | |
 Db 4 KLVFFA 9

RESULT 12
 US-11-016-706-36
 ; Sequence 36, Application US/11016706
 ; Publication No. US20050244334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CASTILLO, GERARDO
 ; APPLICANT: LAKE, THOMAS P.
 ; APPLICANT: NGUYEN, BETH P.
 ; APPLICANT: SANDERS, VIRGINIA J.
 ; APPLICANT: SNOW, ALAN D.
 ; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
 ; FILE REFERENCE: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
 ; CURRENT APPLICATION NUMBER: US/11/016,706
 ; CURRENT FILING DATE: 2004-12-16
 ; PRIOR APPLICATION NUMBER: 09/962,955
 ; PRIOR FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: 09/938,275
 ; PRIOR FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: 08/947,057
 ; PRIOR FILING DATE: 1997-10-08
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 36
 ; LENGTH: 40
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-11-016-706-36

Query Match 80.6%; Score 25; DB 7; Length 40;
 Best Local Similarity 83.3%; Pred. No. 16;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 | | | | |
 Db 16 KLVFFA 21

RESULT 13
 US-11-098-674-12
 ; Sequence 12, Application US/11098674
 ; Publication No. US20050267029A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ancsin, John B.
 ; APPLICANT: Elmova, Elena
 ; APPLICANT: Kisilevsky, Robert
 ; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
 ; IDENTIFICATION AND USE
 ; FILE REFERENCE: PTO-0066
 ; CURRENT APPLICATION NUMBER: US/11/098,674
 ; CURRENT FILING DATE: 2005-04-04
 ; PRIOR APPLICATION NUMBER: US 60/559,122
 ; PRIOR FILING DATE: 2004-04-02
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 12
 ; LENGTH: 40

; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-098-674-12

Query Match 80.6%; Score 25; DB 7; Length 40;
 Best Local Similarity 83.3%; Pred. No. 16;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 | | | | |
 Db 16 KLVFFA 21

RESULT 14
 US-10-923-605-1
 ; Sequence 1, Application US/10923605
 ; Publication No. US20050249727A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schenk, Dale B.
 ; APPLICANT: Neuralab Limited
 ; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
 ; FILE REFERENCE: 15270J-004740US
 ; CURRENT APPLICATION NUMBER: US/10/923,605
 ; CURRENT FILING DATE: 2004-08-20
 ; PRIOR APPLICATION NUMBER: US/09/322,289
 ; PRIOR FILING DATE: 1999-05-28
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 42
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
 US-10-923-605-1

Query Match 80.6%; Score 25; DB 6; Length 42;
 Best Local Similarity 83.3%; Pred. No. 17;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 | | | | |
 Db 16 KLVFFA 21

RESULT 15
 US-10-934-818-1
 ; Sequence 1, Application US/10934818
 ; Publication No. US20050255122A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schenk, Dale B.
 ; APPLICANT: Neuralab Limited
 ; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
 ; FILE REFERENCE: 15270J-472000US
 ; CURRENT APPLICATION NUMBER: US/10/934,818
 ; CURRENT FILING DATE: 2004-09-02
 ; PRIOR APPLICATION NUMBER: US 60/067,740
 ; PRIOR FILING DATE: 1997-12-02
 ; PRIOR APPLICATION NUMBER: US 60/080,970
 ; PRIOR FILING DATE: 1998-04-07
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 42
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
 US-10-934-818-1

Query Match 80.6%; Score 25; DB 6; Length 42;
 Best Local Similarity 83.3%; Pred. No. 17;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
| | | | |
Db 16 KLVFFA 21

RESULT 16

US-11-016-706-37
; Sequence 37, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTO.F03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-37

Query Match 80.6%; Score 25; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
| | | | |
Db 16 KLVFFA 21

RESULT 17

US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match 80.6%; Score 25; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
| | | | |
Db 16 KLVFFA 21

RESULT 18

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 80.6%; Score 25; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
| | | | |
Db 16 KLVFFA 21

RESULT 19

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 80.6%; Score 25; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
| | | | |
Db 16 KLVFFA 21

RESULT 20

US-10-467-657-7560
; Sequence 7560, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11

```
; PRIOR APPLICATION NUMBER: CB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7560
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7560
```

```
Query Match      80.6%; Score 25; DB 6; Length 184;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 KVFVFA 6
      |||||
Db      91 KVFVFA 96
```

```
RESULT 21
US-11-082-389-350
; Sequence 350, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/441031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 350
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-350
```

```
Query Match      80.6%; Score 25; DB 7; Length 525;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVFVFA 6
      |:|:|
Db      230 KVFVFA 235
```

RESULT 22

```
US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease
; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; OTHER INFORMATION: Alzheimer's disease amyloid protein
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1) .. (17)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1) .. (40)
; OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40
; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18) .. (687)
; OTHER INFORMATION: soluble APP-alpha
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18) .. (671)
; OTHER INFORMATION: soluble APP-beta
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672) .. (770)
; OTHER INFORMATION: C99
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672) .. (713)
; OTHER INFORMATION: beta-amyloid protein 42
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672) .. (711)
; OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
; OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688) .. (770)
; OTHER INFORMATION: C83
```

```

; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(713)
; OTHER INFORMATION: P3(42)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(711)
; OTHER INFORMATION: P3(40)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (712)..(770)
; OTHER INFORMATION: gamma-CTF(59)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (714)..(770)
; OTHER INFORMATION: gamma-CTF(57)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (721)..(770)
; OTHER INFORMATION: gamma-CTF(50)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (740)..(770)
; OTHER INFORMATION: C31
; US-10-982-545-15

Query Match      80.6%; Score 25; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 687 KLVFFA 692

RESULT 23
US-10-789-273-38
; Sequence 38, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-273-38

Query Match      80.6%; Score 25; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 687 KLVFFA 692

RESULT 24
US-10-467-657-3978
; Sequence 3978, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3978
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3978

Query Match      77.4%; Score 24; DB 6; Length 194;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 13 RPAPFA 18

RESULT 25
US-10-793-626-62
; Sequence 62, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-62

Query Match      77.4%; Score 24; DB 6; Length 229;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5
Db 59 KVFVF 63

RESULT 26
US-10-793-626-1860
; Sequence 1860, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04

```

```

; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1860
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1860

```

```

Query Match      77.4%; Score 24; DB 6; Length 443;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KVVFF 5
      |||||
Db      168 KVVFF 172

```

```

RESULT 27
US-10-467-657-4566
; Sequence 4566, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4566
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4566

```

```

Query Match      77.4%; Score 24; DB 6; Length 533;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 KVVFFA 6
      |||||
Db      165 KVVFFA 170

```

```

RESULT 28
US-11-080-991-48
; Sequence 48, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Velby, Pette Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 657

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-48

```

```

Query Match      77.4%; Score 24; DB 7; Length 657;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KVVFF 5
      |||||
Db      90 KVVFF 94

```

```

RESULT 29
US-10-467-657-4242
; Sequence 4242, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4242
; LENGTH: 916
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4242

```

```

Query Match      77.4%; Score 24; DB 6; Length 916;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KVVFFA 6
      |||||
Db      655 KVVFFA 660

```

```

RESULT 30
US-10-821-234-1120
; Sequence 1120, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1120
; LENGTH: 4384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1120

```

```

Query Match      77.4%; Score 24; DB 6; Length 4384;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```
Qy      1 KFVFFA 6
Db      1320 KFVFFA 1325

RESULT 31
US-10-467-657-1370
; Sequence 1370, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1370
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1370

Query Match      74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFPPA 6
Db      23 FVFPS 27

RESULT 32
US-10-467-657-2308
; Sequence 2308, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2308
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2308

Query Match      74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFPPA 6
Db      23 FVFPS 27

RESULT 33
US-10-467-657-5610
; Sequence 5610, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5610
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5610

Query Match      74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFPPA 6
Db      23 FVFPS 27

RESULT 34
US-10-467-657-7516
; Sequence 7516, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7516
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7516

Query Match      74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFPPA 6
Db      23 FVFPS 27

RESULT 35
US-10-467-657-8322
; Sequence 8322, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
```

```
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8322
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8322
```

```
Query Match 74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 FVFFA 6
Db 23 FVFFS 27
|||||
```

```
RESULT 36
US-10-467-657-4324
; Sequence 4324, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4324
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4324
```

```
Query Match 74.2%; Score 23; DB 6; Length 54;
Best Local Similarity 80.0%; Pred. No. 53;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 FVFFA 6
Db 44 FVFFS 48
|||||
```

```
RESULT 37
US-10-467-657-8286
; Sequence 8286, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
```

```
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8286
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8286
```

```
Query Match 74.2%; Score 23; DB 6; Length 56;
Best Local Similarity 80.0%; Pred. No. 55;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 FVFFA 6
Db 30 FVFFS 34
|||||
```

```
RESULT 38
US-10-793-626-2766
; Sequence 2766, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2766
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2766
```

```
Query Match 74.2%; Score 23; DB 6; Length 126;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 FVFFA 6
Db 10 YVFFA 14
|||||
```

```
RESULT 39
US-10-793-626-304
; Sequence 304, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 304
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-304
```

```
Query Match 74.2%; Score 23; DB 6; Length 209;
```

Best Local Similarity 60.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 0;

Qy 1 KVFVF 5
Db 145 RFIFV 149

RESULT 40

US-10-793-626-1034
; Sequence 1034, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1034
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1034

Query Match 74.2%; Score 23; DB 6; Length 234;

Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
Db 124 FMFFA 128

RESULT 41

US-10-467-657-4456
; Sequence 4456, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4456
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4456

Query Match 74.2%; Score 23; DB 6; Length 288;

Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVF 5
Db 61 KPFF 65

RESULT 42

US-10-613-744-13
; Sequence 13, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-613-744-13

Query Match 74.2%; Score 23; DB 6; Length 391;

Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5
Db 61 RFIFV 65

RESULT 43

US-10-467-657-4858
; Sequence 4858, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4858
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4858

Query Match 74.2%; Score 23; DB 6; Length 410;

Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
Db 207 FLFFA 211

RESULT 44

US-11-055-822-1096

; Sequence 1096, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 1096
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-1096

Query Match 74.2%; Score 23; DB 7; Length 432;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
||:|
Db 329 FVFFA 333

RESULT 45
US-11-113-424-186
; Sequence 186, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358

; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 186
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-11-113-424-186

Query Match 74.2%; Score 23; DB 7; Length 432;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
||:|
Db 399 FVFFA 403

RESULT 46
US-10-467-657-678
; Sequence 678, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWing99, version 1.04
; SEQ ID NO 678
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-678

Query Match 74.2%; Score 23; DB 6; Length 449;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
||:|
Db 395 FVFFA 399

RESULT 47
US-11-082-389-348
; Sequence 348, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389


```

; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 348
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-348

```

```

Query Match      74.2%; Score 23; DB 7; Length 534;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KPVFF 5
Db      239 KFIFY 243

```

```

RESULT 48
US-10-467-657-3440
; Sequence 3440, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3440
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3440

```

```

Query Match      74.2%; Score 23; DB 6; Length 633;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 KPVFF 5
Db      367 KPAPP 371

```

```

RESULT 49
US-10-467-657-4632

```

```

; Sequence 4632, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4632
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4632

```

```

Query Match      74.2%; Score 23; DB 6; Length 633;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 KPVFF 5
Db      367 KPAPP 371

```

```

RESULT 50
US-11-186-284-125
; Sequence 125, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: BURGART, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP001-029P2ENM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-125

```

```

Query Match      74.2%; Score 23; DB 7; Length 660;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 KPVFF 6
Db      531 KAVFFA 536

```

```

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 908
; LENGTH: 1012
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-995-561-908

Query Match      74.2%; Score 23; DB 6; Length 1012;
Best Local Similarity 80.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |:|
Db      988 FLFFA 992

RESULT 54
US-10-793-626-760
; Sequence 760, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 760
; LENGTH: 2323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-760

Query Match      74.2%; Score 23; DB 6; Length 2323;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |:|
Db      1210 FMFFA 1214

RESULT 55
US-10-467-657-8998
; Sequence 8998, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8998

; TITLE OF INVENTION: METHODS for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 917
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-917

Query Match      74.2%; Score 23; DB 6; Length 708;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KPVFFA 6
      |:|
Db      579 KAVFFA 584

RESULT 52
US-10-793-626-420
; Sequence 420, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 420
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-420

Query Match      74.2%; Score 23; DB 6; Length 766;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |:|
Db      357 FMFFA 361

RESULT 53
US-10-995-561-908
; Sequence 908, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
```

; LENGTH: 30
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8998

Query Match 71.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFF 5
Db 7 FVFF 10

RESULT 56

US-11-000-463-378
; Sequence 378, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:

; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000.463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 378
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-000-463-850

US-11-000-463-850
; Sequence 850, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:

; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000.463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 378
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-000-463-378

US-11-000-463-378
; Sequence 378, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:

; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod

Query Match 71.0%; Score 22; DB 7; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFF 5
Db 8 FVFF 11

RESULT 57

US-11-000-463-850
; Sequence 850, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:

; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod

; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000.463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 850
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-000-463-850

US-11-000-463-850
; Sequence 850, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:

; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.

US-11-000-463-850
; Sequence 850, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:

; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.

US-11-000-463-850
; Sequence 850, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:

; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.

US-11-000-463-850
; Sequence 850, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:

; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

US-11-000-463-850

```
Db          32 FVFF 35

RESULT 59
US-10-467-657-2026
; Sequence 2026, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2026
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2026

Query Match          71.0%; Score 22; DB 6; Length 79;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
   :|||
Db 10 QPIFF 14

RESULT 60
US-10-485-517-286
; Sequence 286, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629W0
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 286
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-286

Query Match          71.0%; Score 22; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
   ||||
Db 83 FVFF 86

RESULT 61
US-10-467-657-6824
; Sequence 6824, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6824
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6824

Query Match          71.0%; Score 22; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
   ||||
Db 62 FVFF 65

RESULT 62
US-11-125-837-24
; Sequence 24, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-24

Query Match          71.0%; Score 22; DB 7; Length 139;
Best Local Similarity 80.0%; Pred. NO. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
   |:|||
Db 6 KVVFF 10

RESULT 63
US-10-467-657-6110
; Sequence 6110, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
```

; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6110
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6110

Query Match 71.0%; Score 22; DB 6; Length 149;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPVFFA 6
:|||||
Db 88 EFFFFA 93

RESULT 64
US-10-467-657-7550
; Sequence 7550, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7550
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7550

Query Match 71.0%; Score 22; DB 6; Length 149;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPVFFA 6
:|||||
Db 88 EFFFFA 93

RESULT 65
US-10-467-657-6130
; Sequence 6130, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 6130
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6130

Query Match 71.0%; Score 22; DB 6; Length 154;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPVFFA 6
:|||||
Db 93 EFFFFA 98

RESULT 66
US-10-485-517-346
; Sequence 346, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: F100629WC
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 346
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-346

Query Match 71.0%; Score 22; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
:|||||
Db 134 FVFF 137

RESULT 67
US-10-980-388-65
; Sequence 65, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogell, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Huff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303

```

; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-65

Query Match          71.0%; Score 22; DB 6; Length 187;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db 179 RYVFFA 184

RESULT 68
US-10-467-657-4386
; Sequence 4386, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4386
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4386

Query Match          71.0%; Score 22; DB 6; Length 210;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 72 FVFF 75

RESULT 69
US-10-467-657-3000
; Sequence 3000, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

```

```

; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3000
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3000

Query Match          71.0%; Score 22; DB 6; Length 222;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 143 FVFF 146

RESULT 70
US-10-467-657-6248
; Sequence 6248, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6248
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6248

Query Match          71.0%; Score 22; DB 6; Length 238;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 218 FVFF 221

RESULT 71
US-11-054-515-1391
; Sequence 1391, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14

```

```
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1391
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1391

Query Match      71.0%; Score 22; DB 7; Length 240;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFA 6
Db      56 RFVYVA 61

RESULT 72
US-11-074-176-66
; Sequence 66, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klienhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Arcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-66

Query Match      71.0%; Score 22; DB 7; Length 241;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KVFVFA 6
Db      229 KFDVFA 234

RESULT 73
US-10-793-626-1124
; Sequence 1124, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US

; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1124
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1124

Query Match      71.0%; Score 22; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFF 5
Db      65 FVFF 68

RESULT 74
US-10-467-657-6144
; Sequence 6144, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6144
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6144

Query Match      71.0%; Score 22; DB 6; Length 254;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FVFF 5
Db      197 FVFF 200

RESULT 75
US-10-467-657-1178
; Sequence 1178, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
```

```
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1178
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1178
```

```
Query Match      71.0%; Score 22; DB 6; Length 268;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 FVFFA 6
Db      25 FAFFA 29
```

```
Search completed: December 29, 2005, 18:50:15
Job time : 4.29032 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78.1936 Seconds
(without alignments)
54.137 Million cell updates/sec

Title: US-10-009-122-9

Perfect score: 29

Sequence: 1 KVVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	186	1	P9835 oryza sativ
2	29	100.0	186	2	P93414 oryza sativ
3	29	100.0	231	2	Q8C6Y8 mus musculus
4	29	100.0	372	2	Q6D7U3 ERWCT
5	29	100.0	373	2	Q7M9N5 WOLST
6	29	100.0	387	2	Q9K110 BACCE
7	29	100.0	387	2	Q4MT39 BACCZ
8	29	100.0	387	2	Q63DD4 BACCZ
9	29	100.0	387	2	Q6HKU6 BACHK
10	29	100.0	387	2	Q73AP3 BACCL
11	29	100.0	387	2	Q81SK9 BACAN
12	29	100.0	410	2	Q8C5I3 MOUSE
13	29	100.0	442	2	Q9PHV5 CAMJE
14	29	100.0	703	2	Q5HYE1 HUMAN
15	29	100.0	721	2	Q6AG35 LEIXX
16	29	100.0	925	2	Q95786 HUMAN
17	29	100.0	925	2	Q5VY71 HUMAN
18	29	100.0	926	2	Q8Q899 MOUSE
19	29	100.0	940	2	Q9GLV6 FIG
20	29	100.0	1144	1	NOS2 MOUSE
21	29	100.0	1144	2	Q5SXT3 MOUSE
22	29	100.0	1145	2	Q8R410 MOUSE
23	29	100.0	1145	2	Q6P6A0 MOUSE
24	28	96.6	164	2	Q73N39 TREDE
25	28	96.6	203	2	Q6AKS9 DESPS
26	28	96.6	380	2	Q67225 AQUAE
27	28	96.6	387	2	Q81FH5 BACCR
28	28	96.6	399	2	Q5WPU9 LUTLO
29	28	96.6	450	2	Q4TRF8 SPHN
30	28	96.6	464	2	Q4S415 TETNG
31	28	96.6	606	2	Q91VU5 MOUSE

32	28	96.6	623	2	Q4WBU2 ASPFU
33	28	96.6	630	2	Q5K7E5 CRYNE
34	28	96.6	663	2	Q6RUU2 MOUSE
35	28	96.6	690	2	Q831B2 TROW8
36	28	96.6	698	2	Q83GW3 TROWT
37	28	96.6	760	2	Q55HW1 CRYNE
38	28	96.6	1265	2	Q6ZQ91 MOUSE
39	28	96.6	1412	2	Q5E3M1 CHICK
40	28	96.6	1655	2	Q4Q5Q4 LEIMA
41	27	93.1	88	2	Q4LBQ8 SODGL
42	27	93.1	183	2	Q9RQ09 BACTN
43	27	93.1	315	2	Q61C67 CABER
44	27	93.1	362	2	Q4HSJ7 CAMUP
45	27	93.1	382	2	Q9V7J0 DROME
46	27	93.1	410	2	Q6L2B4 PICTO
47	27	93.1	447	2	Q59243 PYRHO
48	27	93.1	556	2	Q95S93 DROME
49	27	93.1	556	2	Q9V7I9 DROME
50	27	93.1	785	2	Q9GQ82 DROME
51	27	93.1	1384	2	Q68X27 CHLRE
52	27	93.1	1408	2	Q7QEF0 ANOGR
53	27	93.1	1443	2	Q9VPR0 DROME
54	27	93.1	1458	2	Q5BI64 DROME
55	27	93.1	1503	2	Q7KTZ4 DROME
56	27	93.1	1676	2	Q8A6R7 BACTN
57	26	89.7	33	2	Q9UC33 HUMAN
58	26	89.7	42	2	Q5EJU6 GRAGR
59	26	89.7	42	2	Q5GJJ7 TURTR
60	26	89.7	42	2	Q7M088 CAVPO
61	26	89.7	52	2	Q8WZ99 HUMAN
62	26	89.7	55	2	Q82VG8 NITEU
63	26	89.7	57	1	A4_URSHA
64	26	89.7	58	1	A4_CANFA
65	26	89.7	58	1	A4_RABIT
66	26	89.7	58	1	A4_SHEEP
67	26	89.7	59	1	A4_BOVIN
68	26	89.7	79	2	Q5WJL8 BACSK
69	26	89.7	79	2	Q35463 CRIGR
70	26	89.7	81	1	MOAD_ECOLI
71	26	89.7	81	2	Q9APP7 9BACT
72	26	89.7	81	2	Q57RF2 SALCH
73	26	89.7	81	2	Q65TT0 MANSCH
74	26	89.7	81	2	Q7NGP4 PHOLL
75	26	89.7	81	2	Q8D977 VIBVU
76	26	89.7	81	2	Q9KT78 VIBCH
77	26	89.7	81	2	Q83S38 SHIFL
78	26	89.7	81	2	Q7MM72 VIBVU
79	26	89.7	81	2	Q8X807 ECOS7
80	26	89.7	83	2	Q5PGA0 SALPA
81	26	89.7	83	2	Q8Z886 SALT1
82	26	89.7	83	2	Q8ZQO0 SALT1
83	26	89.7	85	2	Q87MY3 VIBPA
84	26	89.7	109	2	Q6YVX4 ORYSA
85	26	89.7	113	2	Q8JH58 CHESE
86	26	89.7	137	2	Q7UPR1 RHORA
87	26	89.7	141	2	Q5LGT9 BACFR
88	26	89.7	141	2	Q64XP1 BACFR
89	26	89.7	143	2	Q8EMC6 OCEIH
90	26	89.7	152	2	Q9STZ9 ARATH
91	26	89.7	163	2	Q5PGG6 ANAMM
92	26	89.7	193	2	Q98OV9 SULSO
93	26	89.7	195	2	Q7N3A0 PHOLL
94	26	89.7	207	1	HIS2 CAMJE
95	26	89.7	207	2	Q4HDT2 CAMCO
96	26	89.7	207	2	Q5HSI7 CAMJR
97	26	89.7	218	2	Q8BPV5 MOUSE
98	26	89.7	221	2	Q6AMY5 DESPS
99	26	89.7	229	2	Q8V576 ARATH
100	26	89.7	231	2	Q9SV79 ARATH
101	26	89.7	252	2	Q73M22 TREDE
102	26	89.7	264	2	Q9FGJ8 ARATH
103	26	89.7	265	2	Q4SV83 TETNG
104	26	89.7	293	1	Y844_ARCFU

Q4WBU2	aspergillus
Q5K7E5	cryptococcus
Q6RUU2	mus musculus
Q831B2	tropheryma
Q83GW3	cryptococcus
Q55HW1	mus musculus
Q6ZQ91	mus musculus
Q5F3M1	gallus gall
Q4Q5Q4	leishmania
Q4LBQ8	sodalis glo
Q9RQ09	bacteroides
Q61C67	caenorhabdi
Q4HSJ7	campylobact
Q9V7J0	drosophila
Q6L2B4	microphilus
Q59243	pyrococcus
Q95S93	drosophila
Q9V7I9	drosophila
Q9GQ82	drosophila
Q68X27	chlamydomon
Q7QEF0	anopheles 9
Q5BI64	drosophila
Q7KTZ4	drosophila
Q8A6R7	bacteroides
Q9UC33	homo sapien
Q5EJU6	grampus gri
Q5GJJ7	tursiops tr
Q7M088	cavia porce
Q8WZ99	homo sapien
Q82VG8	nitrosomona
Q29149	u alzheimer
Q28280	c alzheimer
Q28748	o alzheimer
Q28757	o alzheimer
Q28053	b alzheimer
Q5WJL8	bacillus cl
Q35463	cricetulus
P30748	escherichia
Q9APP7	uncultured
Q57RF2	salmonella
Q65TT0	mannheimia
Q7NGP4	photorhabdu
Q8D977	vibrio vuln
Q9KT78	vibrio chol
Q83S38	shigella fl
Q7MM72	vibrio vuln
Q8X807	escherichia
Q5PGA0	salmonella
Q8Z886	salmonella
Q8ZQO0	salmonella
Q87MY3	vibrio para
Q6YVX4	oryza sativ
Q8JH58	chelydra se
Q7UPR1	rhodopirell
Q5LGT9	bacteroides
Q4XP1	bacteroides
Q8EMC6	oceanobacil
Q9STZ9	arabidopsis
Q5PGG6	anaplasma m
Q98OV9	sulfolobus
Q7N3A0	photorhabdu
Q9PM71	campylobact
Q4HDT2	campylobact
Q5HSI7	campylobact
Q8BPV5	mus musculu
Q6AMY5	desulfotale
Q8V576	arabidopsis
Q9SV79	arabidopsis
Q73M22	treponema d
Q9FGJ8	arabidopsis
Q4SV83	tetradon n
Y844	archaeoglob

105	26	89.7	294	2	Q97XW2_SULSO	Q97xw2 sulfolobus
106	26	89.7	294	2	Q62HR5_BURMA	Q62hrs burkholderi
107	26	89.7	300	2	Q9XU61_CANEL	Q9xu61 caenorhabdi
108	26	89.7	314	2	Q7S8K9_NEUCR	Q7s8k9 neurospora
109	26	89.7	330	2	Q9PGI8_XYLFA	Q9pgi8 xyella fas
110	26	89.7	339	1	MURG_THEME	Q9wy74 thermotoga
111	26	89.7	349	2	Q9XU59_CANEL	Q9xu59 caenorhabdi
112	26	89.7	352	2	Q9XGY6_XYLFT	Q9xgy6 simmondsia
113	26	89.7	352	2	Q87EP8_XYLFT	Q87ep8 xyella fas
114	26	89.7	357	2	Q8U460_PYRFU	Q8u460 pyrococcus
115	26	89.7	357	2	Q8UUI8_BRARE	Q8uii8 brachydanio
116	26	89.7	366	2	Q8EPLI_XANAC	Q8epil xanthomonas
117	26	89.7	370	2	Q6SSJ1_MANSU	Q6ssj1 manheimia
118	26	89.7	374	2	Q7MAT1_WOLSU	Q7mat1 wolinnella s
119	26	89.7	384	2	Q8BPC7_MOUSE	Q8bpc7 mus musculus
120	26	89.7	391	2	Q4N5U7_THERPA	Q4n5u7 theileria p
121	26	89.7	395	2	Q9SWD9_9DIPT	Q9swd9 phlebotomus
122	26	89.7	403	2	Q5LIL7_GROKA	Q5lil7 geobacillus
123	26	89.7	404	2	Q4UY85_XANCP	Q4uy85 xanthomonas
124	26	89.7	404	2	Q8P597_XANCP	Q8p597 xanthomonas
125	26	89.7	428	2	Q9M1Q8_ARATH	Q9m1q8 arabidopsis
126	26	89.7	443	2	Q4HHQ1_CAMCO	Q4hha1 campylobact
127	26	89.7	461	2	Q89329_9POTV	Q89329 zucchini ye
128	26	89.7	467	2	Q4L3I9_STAHL	Q4l3i9 staphylococ
129	26	89.7	469	2	Q4Y3I8_PLACH	Q4y3i8 plasmodium
130	26	89.7	470	2	Q7T9I0_9POTV	Q7t9i0 zucchini ye
131	26	89.7	472	2	Q7T9I0_9POTV	Q7t9i0 zucchini ye
132	26	89.7	477	1	YPUM_RHOCA	Q8uuu0 brachydanio
133	26	89.7	488	2	Q52NV6_9POTV	P26176 rhodobacter
134	26	89.7	490	2	Q7T9I1_9POTV	Q52nv6 zucchini ye
135	26	89.7	490	2	Q7T9I2_9POTV	Q7t9i1 zucchini ye
136	26	89.7	493	2	Q5K4D5_9POTV	Q7t9i2 zucchini ye
137	26	89.7	493	2	Q5K4D5_9POTV	Q5k4d5 soybean mos
138	26	89.7	496	2	Q5K4D0_9POTV	Q5k4d5 soybean mos
139	26	89.7	508	2	Q5GV85_XANOR	Q5k4d0 daebeen mos
140	26	89.7	520	2	Q9K207_CHLPN	Q5gv85 xanthomonas
141	26	89.7	534	2	Q93296_CHICK	Q9k207 chlamydia p
142	26	89.7	554	2	Q7P7T7_FUSNV	Q93296 gallus gall
143	26	89.7	569	2	Q9PVL1_CHICK	Q7p7t7 fusobacteri
144	26	89.7	594	2	Q9JSK0_CHLPN	Q9pvl1 gallus gall
145	26	89.7	603	2	Q9XIQ9_THEME	Q9jsk0 chlamydia p
146	26	89.7	609	2	Q6CFJ3_YARLI	Q9xliq9 thermotoga
147	26	89.7	612	2	Q919E7_BRARE	Q6cfj3 yarowia li
148	26	89.7	613	2	Q8HML1_9TELE	Q919e7 brachydanio
149	26	89.7	614	2	Q94YP6_9TELE	Q8hml1 hiodon alos
150	26	89.7	615	2	Q5OZ85_ENTHI	Q94yp6 osteoglossu
151	26	89.7	617	2	Q929B2_CHLPN	Q5oz85 entamoeba h
152	26	89.7	624	2	Q8RDN8_FUSNN	Q929b2 chlamydia p
153	26	89.7	624	2	Q7SD58_NEUCR	Q8rdn8 fusobacteri
154	26	89.7	638	2	Q5B2V4_EMENI	Q7sd58 neurospora
155	26	89.7	670	2	Q8KGX2_RHIL0	Q5b2v4 aspergillus
156	26	89.7	678	2	Q7Z2T1_BRARE	Q8kgx2 rhizobium l
157	26	89.7	682	2	Q64DY0_9ARCH	Q7z2t1 brachydanio
158	26	89.7	693	2	Q98SG0_XENLA	Q64dy0 uncultured
159	26	89.7	695	2	Q648X4_9ARCH	Q98sg0 xenopus lae
160	26	89.7	695	2	Q5R477_PONPY	Q648x4 uncultured
161	26	89.7	695	2	Q6RH29_CANFA	Q5r477 pongo pygma
162	26	89.7	695	2	Q56JK3_CANFA	Q6rh29 canis famli
163	26	89.7	695	2	Q6GR78_MOUSE	Q56jk3 canis famli
164	26	89.7	695	2	Q9DGJ8_CHICK	Q6gr78 mus musculus
165	26	89.7	695	2	Q98SF9_XENLA	Q9dgj8 gallus gall
166	26	89.7	695	2	Q7ZXQ0_XENLA	Q98sf9 xenopus lae
167	26	89.7	714	2	Q56JK4_CANFA	Q7zxq0 xenopus lae
168	26	89.7	733	2	Q6P6Q5_RAT	Q56jk4 canis famli
169	26	89.7	737	1	A4_FUREU	Q6p6q5 rattus norv
170	26	89.7	738	2	Q6NUZ1_BRARE	Q93279 fugu rubrip
171	26	89.7	738	2	Q90W28_BRARE	Q6nuz1 brachydanio
172	26	89.7	747	2	Q91963_9PIPI	Q90w28 brachydanio
173	26	89.7	749	2	Q56JK2_STEPC	Q91963 xenopus. ap
174	26	89.7	749	2	Q6NRR1_XENLA	Q56jk2 stenella co
175	26	89.7	750	2	Q6DJB6_XENTR	Q6nrr1 xenopus lae
176	26	89.7	751	1	A4_SARSC	Q6djb6 xenopus tro
177	26	89.7	751	2	Q6GSC0_HUMAN	Q95241 s amyloid b
						Q6gsc0 homo sapten

26	89.7	751	2	Q6RH28_CANFA	Q6rh28 canis famli
26	89.7	751	2	Q56JK5_CANFA	Q56jk5 canis famli
26	89.7	751	2	Q4R4R8_MACFA	Q4r4r8 macaca faec
26	89.7	751	2	Q9DGJ7_CHICK	Q9dgj7 gallus gall
26	89.7	754	2	Q4RY33_TETNG	Q4ry33 tetraodon n
26	89.7	759	2	Q4S0J4_TETNG	Q4s0j4 tetraodon n
26	89.7	770	1	A4_CAVFO	Q60495 c amyloid b
26	89.7	770	1	A4_HUMAN	P05067 h amyloid b
26	89.7	770	1	A4_MOUSE	P53601 m amyloid b
26	89.7	770	1	A4_MOUSE	P12023 m amyloid b
26	89.7	770	1	A4_PANTR	Q51e80 p amyloid b
26	89.7	770	1	A4_PIG	P79307 s amyloid b
26	89.7	770	1	A4_RAT	P08592 r amyloid b
26	89.7	770	2	Q6RH30_CANFA	Q6rh30 canis famli
26	89.7	770	2	Q56JK6_CANFA	Q56jk6 canis famli
26	89.7	770	2	Q53ZT3_MOUSE	Q53ztc3 mus musculu
26	89.7	770	2	Q547B7_RAT	Q547b7 rattus norv
26	89.7	780	1	A4_TETFL	Q73683 tetraodon f
26	89.7	817	2	Q6QQP9_VIBVU	Q6qqp9 vibrio vuln
26	89.7	817	2	Q87FQ8_VIBVU	Q87fq8 vibrio para
26	89.7	817	2	Q8D4P2_VIBVU	Q8d4p2 vibrio vuln
26	89.7	817	2	Q9KNF1_VIBCH	Q9knf1 vibrio chol
26	89.7	840	2	Q7MG92_VIBVU	Q7mg92 vibrio vuln
26	89.7	939	2	Q6CETO_YARLI	Q6ceto yarowia li
26	89.7	952	2	Q40RZ2_9POTV	Q40rz2 calla lily
26	89.7	962	2	Q4NTK2_9DELT	Q4ntk2 anaeromyxob
26	89.7	1016	2	Q05912_9POTV	Q05912 zucchini ye
26	89.7	1056	2	Q6FKH6_CANGA	Q6fkh6 candida gla
26	89.7	1083	2	Q81311_PLAP7	Q81311 plasmodium
26	89.7	1497	2	Q95YH6_DROME	Q95yh6 drosophila
26	89.7	1571	2	Q95YH7_DROME	Q95yh7 drosophila
26	89.7	1571	2	Q8MSO4_DROME	Q8maq4 drosophila
26	89.7	1612	2	Q9VE37_DROME	Q9ve37 drosophila
26	89.7	1916	2	Q8QKU4_9POTV	Q8qku4 zucchini ye
26	89.7	3080	1	POLG_ZYMVC	P19479 z genome po
26	89.7	3080	2	Q6WN47_9POTV	Q6wn47 zucchini ye
26	89.7	3080	2	Q6WN48_9POTV	Q6wn48 zucchini ye
26	89.7	3080	2	Q6WN49_9POTV	Q6wn49 zucchini ye
26	89.7	3080	2	Q6Y2U7_9POTV	Q6y2u7 zucchini ye
26	89.7	3080	2	Q7T908_9POTV	Q7t908 zucchini ye
26	89.7	3080	2	Q7T914_9POTV	Q7t914 zucchini ye
26	89.7	3083	1	POLG_ZYMVS	Q03979 z genome po
26	89.7	3105	2	Q70XR2_9POTV	Q70xr2 soybean mos
25	86.2	40	2	Q91FF3_IRSV6	Q91ff3 chilo iride
25	86.2	66	2	Q728F0_DRSVH	Q728f0 desulfovibr
25	86.2	74	1	Y1J31_MYCGE	P47377 mycoplasma
25	86.2	81	2	Q6D3D0_ERWCT	Q6d3d0 erwinia car
25	86.2	89	2	Q83VF2_LACLC	Q83vf2 lactococcus
25	86.2	104	2	Q5LXX2_STRT1	Q5lxx2 streptococ
25	86.2	104	2	Q5M2H4_STRT2	Q5m2h4 streptococ
25	86.2	105	2	Q64CV5_9ARCH	Q64cv5 uncultured
25	86.2	107	2	Q59MN1_CANAL	Q59mnl candida alb
25	86.2	107	2	Q8E222_STRAS	Q8e222 streptococ
25	86.2	107	2	Q8E7H9_STRAS	Q8e7h9 streptococ
25	86.2	109	2	Q9X292_THEME	Q9x292 thermotoga
25	86.2	122	2	Q4Y0Z7_PLACH	Q4y0z7 plasmodium
25	86.2	124	2	Q61N30_CAEBR	Q61n30 caenorhabdi
25	86.2	125	2	Q6U9U2_9CAUD	Q6u9u2 bacterioph
25	86.2	125	2	Q56F01_9CAUD	Q56f01 aeromonas p
25	86.2	128	2	Q6LGS9_PROPR	Q6lgs9 photobacter
25	86.2	136	2	Q18208_CABEL	Q18208 caenorhabdi
25	86.2	141	2	Q8U3A1_PYRFU	Q8u3a1 pyrococcus
25	86.2	143	2	Q91Y69_MESSAU	Q91y69 mesocricetu
25	86.2	145	2	Q5USA9_9PEZI	Q5usa9 monacrosop
25	86.2	146	2	Q9V0B4_PYRAB	Q9v0b4 pyrococcus
25	86.2	148	2	Q17202_CAEEL	Q17202 caenorhabdi
25	86.2	156	2	Q8DN20_STRR6	Q8dn20 streptococ
25	86.2	157	2	Q97N92_STRPN	Q97n92 streptococ
25	86.2	157	2	Q8XNL2_CLOPE	Q8xnl2 clostridium
25	86.2	159	2	Q58626_PYRHO	Q58626 pyrococcus
25	86.2	161	2	Q32197_9LILI	Q32197 eichhornia
25	86.2	162	2	Q9N284_BOVIN	Q9n284 bos taurus
25	86.2	163	2	Q32164_9LILI	Q32164 eichhornia

251 25 86.2 163 2 Q32179_9LILI
 252 25 86.2 163 2 Q32190_9LILI
 253 25 86.2 163 2 Q32201_9LILI
 254 25 86.2 163 2 Q32202_9LILI
 255 25 86.2 163 2 Q32210_9LILI
 256 25 86.2 163 2 Q32390_9LILI
 257 25 86.2 163 2 Q32419_9LILI
 258 25 86.2 163 2 Q32424_9LILI
 259 25 86.2 163 2 Q32430_9LILI
 260 25 86.2 163 2 Q32441_9LILI
 261 25 86.2 163 2 Q32556_9LILI
 262 25 86.2 163 2 Q32579_9LILI
 263 25 86.2 163 2 Q32648_9LILI
 264 25 86.2 163 2 Q32802_PONCO
 265 25 86.2 163 2 Q32892_9LILI
 266 25 86.2 163 2 Q32915_PONCO
 267 25 86.2 164 2 Q32915_PONCO
 268 25 86.2 165 2 Q32915_PONCO
 269 25 86.2 172 2 Q32915_PONCO
 270 25 86.2 180 2 Q32915_PONCO
 271 25 86.2 188 2 Q32915_PONCO
 272 25 86.2 188 2 Q32915_PONCO
 273 25 86.2 188 2 Q32915_PONCO
 274 25 86.2 190 2 Q32915_PONCO
 275 25 86.2 194 2 Q32915_PONCO
 276 25 86.2 196 2 Q32915_PONCO
 277 25 86.2 196 2 Q32915_PONCO
 278 25 86.2 196 2 Q32915_PONCO
 279 25 86.2 198 2 Q32915_PONCO
 280 25 86.2 198 2 Q32915_PONCO
 281 25 86.2 198 2 Q32915_PONCO
 282 25 86.2 198 2 Q32915_PONCO
 283 25 86.2 199 2 Q32915_PONCO
 284 25 86.2 200 2 Q32915_PONCO
 285 25 86.2 200 2 Q32915_PONCO
 286 25 86.2 202 2 Q32915_PONCO
 287 25 86.2 202 2 Q32915_PONCO
 288 25 86.2 208 2 Q32915_PONCO
 289 25 86.2 210 2 Q32915_PONCO
 290 25 86.2 217 2 Q32915_PONCO
 291 25 86.2 218 2 Q32915_PONCO
 292 25 86.2 218 2 Q32915_PONCO
 293 25 86.2 220 2 Q32915_PONCO
 294 25 86.2 228 2 Q32915_PONCO
 295 25 86.2 229 2 Q32915_PONCO
 296 25 86.2 229 2 Q32915_PONCO
 297 25 86.2 229 2 Q32915_PONCO
 298 25 86.2 230 2 Q32915_PONCO
 299 25 86.2 231 2 Q32915_PONCO
 300 25 86.2 232 2 Q32915_PONCO

ALIGNMENTS

RESULT 1
 GL19_ORYSA STANDARD; PRT; 186 AA.

AC P29835;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE 19 kDa globulin precursor (Alpha-globulin).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 ON NCBI_TaxID=4530;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
 RC STRAIN=cv. Japonica / Nipponbare; TISSUE=Endosperm;
 RX MEDLINE=92119226; PubMed=1731968;
 RA Shorrosh B.S., Wen L., Zen K.C., Huang J.K., Pan J.S., Hermodson M.A.,

RA Tanaka K., Muthukrishnan S., Reeck G.R.;
 RT "A novel cereal storage protein: molecular genetics of the 19 kDa
 RL Globulin of rice.";
 RL Plant Mol. Biol. 18:151-154 (1992).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 5-186.
 RC STRAIN=cv. Japonica / Lemont; TISSUE=Endosperm;
 RX MEDLINE=93277591; PubMed=8503935;
 RA Krishnan H.B., Puppe S.G.;
 RT "Nucleotide sequence of an abundant rice seed globulin: homology with
 RT the high molecular weight glutelins of wheat, rye and triticale.";
 RL Biochem. Biophys. Res. Commun. 193:460-466 (1993).
 CC -1- FUNCTION: Seed storage protein.
 CC -1- SIMILARITY: Belongs to the 2S seed storage albumins family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; X63990; CAA45400.1; -; mRNA.
 DR EMBL; L12252; AAA72362.1; ALT_INIT; mRNA.
 DR PIR; S20024; WNR219.
 DR HSSP; P24565; LPNB.
 DR Gramene; P29835; -.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001419; Glutenin.
 DR PANTHER; PTHR14054; Glutenin; 1.
 DR Pfam; PF00234; Tryp_alpha_aml; 1.
 DR PRINTS; PR00210; GLUTENIN.
 DR SMART; SM00499; AAI; 1.
 DR Direct protein sequencing; Seed storage protein; Signal;
 KW Storage protein.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 186 19 kDa Globulin.
 SQ SEQUENCE 186 AA; 21050 MW; 9E09BA74CB0B6810 CRC64;
 Query Match 100.0%; Score 29; DB 1; Length 186;
 Best Local Similarity 100.0%; Pred. No. 1.1e-02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 DB 4 KVVFFA 9
 RESULT 2
 P93414_ORYSA PRELIMINARY; PRT; 186 AA.
 ID P93414_ORYSA PRELIMINARY;
 AC P93414;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE 26 kDa globulin (Alpha-globulin).
 GN Names=P0010D04.16; Synonyms=OUI057_B02.5;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 ON NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Endosperm;
 RX MEDLINE=96235139; PubMed=8666249; DOI=10.1016/0378-1119(95)00887-X;
 RA Nakase M., Hotta H., Adachi T., Aoki N., Nakamura R., Masumura T.,
 RA Tanaka K., Matsuda T.;
 RT "Cloning of the rice seed alpha-globulin-encoding gene: sequence
 RT similarity of the 5'-flanking region to those of the genes encoding
 RT wheat high molecular-weight glutenin and barley D hordein.";
 RL Gene 170:223-226 (1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RT "Oryza sativa BAC OJ1057 B02 genomic sequence.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; D50643; BAA09308.1; -; Genomic DNA.
DR EMBL; AC130605; AAT44292.1; -; Genomic DNA.
DR EMBL; AC113332; AAT93857.1; -; Genomic DNA.
DR PIR; JC4784; JC4784.
DR HSP; P24565; LPNB.
DR Gramene; P93414; -.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutinin.
DR Pfam; PF00234; Tryp alpha amyl; 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 186 AA; 21055 MW; AE2B8F1107C8BC94 CRC64;
Query Match 100.0%; Score 29; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFFFA 6
DB 4 KVFFFA 9
|||||
RESULT 3
ID Q8C6Y8 MOUSE PRELIMINARY; PRT; 231 AA.
AC Q8C6Y8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched
DE library, clone:ID830015B12 product:hypothetical DEAD/DEAH box helicase
DE containing protein, full insert sequence. (fragment).
GN Name=Ddx58;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eumetazoa; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner T., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
RA Fukuda S., Furuno M., Hanagaki T., Hiraoka T., Hirozane T.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Kasukawa T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK052871; BAC35183.1; -; mRNA.
DR MGI; MGI:2442858; Ddx58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR Pfam; PF00270; DEAD; 1.
DR SMART; SM00487; DEXDC; 1.
KW Helicase; Hypothetical protein.
FT NON_TER 231 231
SQ SEQUENCE 231 AA; 25524 MW; 1D191607390D7FBB CRC64;
Query Match 100.0%; Score 29; DB 2; Length 231;

```
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy 1 KWVFFA 6
Db 145 KWVFFA 150

RESULT 4
Q6D7U3 ERWCT PRELIMINARY; PRT; 372 AA.
AC Q6D7U3;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Hydrogenase isoenzymes formation protein.
GN Name=hypD; OrderedLocusNames=ECA1232;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCEI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holleva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors."
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
DR EMBL; BX950851; CAG74142.1; -, Genomic_DNA.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR TIGRFAMs; TIGR005622; Hydrn_mat_hypD; 1.
DR TIGRFAMs; TIGR00075; hypD; 1.
KW Complete proteome.
SQ SEQUENCE 372 AA; 41130 MW; A001A18AC015B620 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KWVFFA 6
Db 139 KWVFFA 144

RESULT 5
Q7M9N5 WOLSU PRELIMINARY; PRT; 373 AA.
AC Q7M9N5;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE HYDROGENASE PROTEIN.
GN Name=HYPD; OrderedLocusNames=WS0793;
OS Wolinella succinogenes.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Wolinella.
OX NCBI_TaxID=844;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DSMZ 1740;
RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
RA Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
RA Meyer P., Lederer H., Schuster S.C.;
RT "Complete genome sequence and analysis of Wolinella succinogenes.";
```

```
RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
DR EMBL; BX571659; CAE09906.1; -, Genomic_DNA.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR TIGRFAMs; TIGR005622; Hydrn_mat_hypD; 1.
DR TIGRFAMs; TIGR00075; hypD; 1.
KW Complete proteome.
SQ SEQUENCE 373 AA; 41793 MW; 3B7815EDB25790A6 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 373;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KWVFFA 6
Db 138 KWVFFA 143

RESULT 6
Q9KI10 BACCE PRELIMINARY; PRT; 387 AA.
AC Q9KI10;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE GerN.
GN Name=gerN;
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1396;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC10876;
RX MEDLINE=20576148; PubMed=11133940; DOI=10.1128/JB.183.2.476-482.2001;
RA Thackray P.D., Behravan J., Southworth T.W., Moir A.;
RT "GerN, an antiporter homologue important in germination of Bacillus
RT cereus endospores."
RL J. Bacteriol. 183:476-482(2001).
DR EMBL; AF246294; AAF91326.1; -, Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41093 MW; 40DE45B71B715D01 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KWVFFA 6
Db 184 KWVFFA 189

RESULT 7
Q4MT39 BACCE PRELIMINARY; PRT; 387 AA.
AC Q4MT39;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Na+/H+ antiporter.
GN ORFNames=BCE_G9241.1647;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
```

```

OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241; DOI=10.1073/pnas.0402414101;
RX PubMed=15155910; Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Hoffmaster A.R., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Marston C.K., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Maiden M.C.J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAEK01000008; RA15336.1; -, Genomic DNA.
SQ SEQUENCE 387 AA; 41122 MW; 15CC136E79B12C38 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFFFA 6
Db 184 KVFFFA 189

RESULT 8
Q63DD4 BACCZ
ID Q63DD4 BACCZ PRELIMINARY; PRT; 387 AA.
AC Q63DD4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18770.1; -, Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41090 MW; DBA5991F6DD63F33 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFFFA 6
Db 184 KVFFFA 189

RESULT 9
Q63DD4 BACCZ
ID Q63DD4 BACCZ PRELIMINARY; PRT; 387 AA.
AC Q63DD4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18770.1; -, Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41090 MW; DBA5991F6DD63F33 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFFFA 6
Db 184 KVFFFA 189

```

```

Q6HKU6 BACHK
ID Q6HKU6 BACHK PRELIMINARY; PRT; 387 AA.
AC Q6HKU6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN; OrderedLocNames=B79727_1493;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=97-27;
RC Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017355; AAT63168.1; -, Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41076 MW; DFFECAD90985F951 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFFFA 6
Db 184 KVFFFA 189

RESULT 10
Q73AP3 BACCI
ID Q73AP3 BACCI PRELIMINARY; PRT; 387 AA.
AC Q73AP3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Germination protein gerN.
GN OrderedLocNames=BCE1729;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017269; AAS40658.1; -, Genomic DNA.
DR TIGR; BCE1729; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.

```

DR InterPro; IPR004771; K_eff.
 DR InterPro; IPR006153; Na_H_porter.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 DR TIGRFAMs; TIGR00932; 2a37; 1.
 KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 387 AA; 41104 MW; DC7CD48C609FEB3A3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
 Best Local Similarity 100.0%; Pred. NO. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 DB 184 KVVFFA 189

RESULT 11

Q81SK9 BACAN
 ID Q81SK9 BACAN PRELIMINARY; PRT; 387 AA.
 AC Q81SK9; Q610J3; Q6KUP8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Germination protein GenN.
 DE OrderedLocusNames=BA1639; BAS1521; GBAA1639;
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=1392;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ames / isolate Porton;
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
 RA Nelson K.E., Tettelin H., Fouts D.E., Bisen J.A., Gill S.R.,
 RA Holtzapple E.K., Okstad O.A., Helgason E., Rikstene J., Wu M.,
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
 RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
 RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
 RA "The genome sequence of *Bacillus anthracis* Ames and comparison to
 RT closely related bacteria";
 RL Nature 423:81-86(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ames / isolate 0581;
 RX Ravel J., Raeko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RT "Bacillus anthracis comparative genomics";
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Storne;
 RX Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Rice H.;
 RT "Complete genome sequence of *Bacillus anthracis* Sterne";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017029; AAP25572.1; -; Genomic DNA.
 DR EMBL; AE017334; AAT30749.1; -; Genomic DNA.
 DR EMBL; AE017225; AAT53839.1; -; Genomic DNA.
 DR TIGR; BA1639; -;
 DR TIGR; GBAA1639; -;
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0008324; F: cation transporter activity; IEA.
 DR GO; GO:0015299; F: solute:hydrogen antiporter activity; IEA.
 DR GO; GO:0006812; P: cation transport; IEA.
 DR GO; GO:0006885; P: regulation of pH; IEA.

DR GO; GO:0006810; P: transport; IEA.
 DR InterPro; IPR004771; K_eff.
 DR InterPro; IPR006153; Na_H_porter.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 DR TIGRFAMs; TIGR00932; 2a37; 1.
 KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 387 AA; 40932 MW; D59F6A08A283BCA3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
 Best Local Similarity 100.0%; Pred. NO. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 DB 184 KVVFFA 189

RESULT 12

Q8C513 MOUSE
 ID Q8C513 MOUSE PRELIMINARY; PRT; 410 AA.
 AC Q8C513;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
 DE enriched library, clone:6430573D20 product:hypothetical DEAD/DEAH box
 DE helicase containing protein, full insert sequence.
 DE Names=DDX58;
 GN Mus musculus (Mouse).
 OS Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RX MEDLINE=21085660; PubMed=1217851; DOI=10.1038/35055500;
 RA Kawai J., Shinsgawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Offido T., Furuno M., Aono H., Baldarelli R., Bash G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohteki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RA the FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RL 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]

```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RN Genome Res. 10:1617-1630(2000).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki R., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akai H., Tanaka Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AK078287; BAC37205.1; -; mRNA.
DR Ensembl; ENSMUSG0000040296; Mus musculus.
DR MGI; MGI:2442858; Ddx58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR Pfam; PF00270; DEAD; 1.
DR SMART; SM00487; DEXDC; 1.
KW Helicase, Hypothetical protein, Nuclear protein.
SQ SEQUENCE 410 AA; 46841 MW; ECC9E3D2D28C5FE0 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 293 KVVFFA 298

RESULT 13
Q9PHV5_CAMJ6
ID Q9PHV5_CAMJ6 PRELIMINARY; PRT; 442 AA.
AC Q9PHV5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative integral membrane protein.
GN OrderedLocusNames=Cj0560;
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCB1_TaxID=197;
RN [1]

```

```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCCTC 11168;
RX MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
RA Parkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagsels K., Kariyeh A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL; AL139075; CAB75196.1; -; Genomic_DNA.
DR PIR; H81402; H81402.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; P:antipporter activity; IEA.
DR GO; GO:0015238; P:drug transporter activity; IEA.
DR GO; GO:0006855; P:multidrug transport; IEA.
DR InterPro; IPR002114; HPr_Serp_S.
DR InterPro; IPR002528; MatE.
DR Pfam; PF01554; MatE; 1.
DR TIGRFAMs; TIGR00797; matE; 1.
DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 442 AA; 49452 MW; 38EA04E7AB1A8F3E CRC64;

Query Match 100.0%; Score 29; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 313 KVVFFA 318

RESULT 14
QSHYE1_HUMAN
ID QSHYE1_HUMAN PRELIMINARY; PRT; 703 AA.
AC QSHYE1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein DKFP686N19181 (fragment).
GN Name=DKFP686N19181;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCB1_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin endothel;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Newes H.W., Weil B., Amd C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX647917; CA146068.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Hypothetical protein.
FT NON_TER 703
SQ SEQUENCE 703 AA; 80308 MW; 3CF7500F4F955586 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 703;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



```

Qy 1 KVVFPA 6
Db 247 KVVFPA 252

RESULT 15
Q6AG25 LEIXX
ID Q6AG25_LEIXX PRELIMINARY; PRT; 721 AA.
AC Q6AG25;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE ATP-dependent RNA helicase.
GN OrderedLocusNames=Lxx07490;
OS Leifsonia xyl (subsp. xyl).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Microbacteriaceae; Leifsonia.
OX NCBI_TaxID=59736;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CTCB07;
RX PubMed=15305603;
RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
RA Almeida N.F. Jr., Carrier H., Coutinho L.L., El-Dorri H.A.,
RA Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumley S.M., Secubal J.C.;
RA "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
RT xyl subsp. xyl."
RL Mol. Plant Microbe Interact. 17:827-836(2004).
DR EMBL; AE016822; AAY88670.1; -; Genomic_DNA.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Complete proteome; DNA-binding; Helicase; Hydrolase.
SQ SEQUENCE 721 AA; 78860 MW; 73F5D2A8435BADE3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 721;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 564 KVVFPA 569

RESULT 16
Q95786 HUMAN
ID Q95786_HUMAN PRELIMINARY; PRT; 925 AA.
AC Q95786;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNA helicase.
GN Name=DDX58; Synonym=RIG-I;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OX Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

Sun Y.W.;
"RIG-I, a human homolog gene of RNA helicase, is induced by retinoic
acid during the differentiation of acute promyelocytic leukemia
cell.";
Thesis (1997), Shanghai Institute of Hematology, Rui-Jin Hospital,
Shanghai Second Medical University.
RL NUCLEOTIDE SEQUENCE.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Yi-Wu S.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF038963; AAD19826.1; -; mRNA.
DR Ensembl; ENSG00000107201; Homo sapiens.
DR HGNC; HGNC:19102; DDX58.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Helicase.
SQ SEQUENCE 925 AA; 106613 MW; 5922B4F3DD0F00D4 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 925;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 292 KVVFPA 297

RESULT 17
Q5VYTI HUMAN
ID Q5VYTI_HUMAN PRELIMINARY; PRT; 925 AA.
AC Q5VYTI;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE OTTHUMP00000021185.
GN Name=RP11-334P12.2; ORFNames=RP11-334P12.2-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OX Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Doggett S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sehra H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AL353671; CAH71251.1; -; Genomic_DNA.
DR EMBL; AL161783; CAH72600.1; -; Genomic_DNA.
DR EMBL; AL161783; CAH71251.1; JOINED; Genomic_DNA.
DR EMBL; AL353671; CAH72600.1; JOINED; Genomic_DNA.
DR Ensembl; ENSG00000107201; Homo sapiens.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.

```

"An RNA helicase, RHIV -1, induced by porcine reproductive and respiratory syndrome virus (PRRSV) is mapped on porcine chromosome 10q13.";

RT RT Microb. Pathog. 28:267-278(2000).

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

DR EMBL: AF181119; MAG09428.1; -; mRNA.

DR GO: 0005524; F:ATP binding; IEA.

DR GO: 0004386; F:Helicase activity; IEA.

DR GO: 0003676; F:nucleic acid binding; IEA.

DR InterPro: IPR011545; DEAD/DEAH N.

DR InterPro: IPR001650; Helicase_C.

DR Pfam: PF00270; DEAD; 1.

DR Pfam: PF00271; Helicase_C; 1.

DR SMART: SM00487; DEXDC; 1.

DR SMART: SM00490; HELICG; 1.

KW Helicase; Hydrolase; Nuclear protein; Repeat.

SQ SEQUENCE 940 AA; 107584 MW; 118CA910B0AF7821 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 940;

Best Local Similarity 100.0%; Pred. NO. 4.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

DB 290 KVVFFA 295

RESULT 20

NOS2_MOUSE STANDARD; PRT; 1144 AA.

ID -NOS2_MOUSE 070515; 070516;

AC P29477; 070515; 070516;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)

DE (Inducible NOS) (INOS) (Macrophage NOS) (MAC-NOS).

GN Name=Nos2; Synonyms=Inos1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridea; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

RP NUCLEOTIDE SEQUENCE.

RP MEDLINE=92229444; PubMed=1373522;

RA Xie Q.-W., Cho H.J., Calaycay J., Mumford R.A., Swiderek K.M.,

RA Lee T.D., Ding A., Trogo F., Nathan C.;

RT "Cloning and characterization of inducible nitric oxide synthase from

RT mouse macrophages.";

RL Science 256:225-228(1992).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RP MEDLINE=92357701; PubMed=1379716;

RA Lowenstein C.J., Glatt C.S., Bredt D.S., Snyder S.H.;

RT "Cloned and expressed macrophage nitric oxide synthase contrasts with

RT the brain enzyme.";

RL Proc. Natl. Acad. Sci. U.S.A. 89:6711-6715(1992).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RP MEDLINE=92210618; PubMed=1372907;

RA Lyons C.R., Orloff G.J., Cunningham J.M.;

RT "Molecular cloning and functional expression of an inducible nitric

RT oxide synthase from a murine macrophage cell line.";

RL J. Biol. Chem. 267:6370-6374(1992).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RP MEDLINE=96088781; PubMed=7503239;

RA Kone B.C., Schwoebel J., Turner P., Mohaupt M.G., Cangro C.B.;

RT "Role of NF-kappa B in the regulation of inducible nitric oxide

RT synthase in an MTL cell line.";

RL Am. J. Physiol. 269:F718-F729(1995).

RN [5]

RP NUCLEOTIDE SEQUENCE, AND VARIANTS ARG-211; LEU-967 AND PHE-968.

RC STRAIN-B10.S/J, BALB/cBYJ, DBA/2J, NOD/LtJ, and SJL/J; TISSUE-Spleen;
 RX MEDLINE=99370037; PubMed=10438970;
 RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
 RA Blankenhorn E.P.;
 RT "Sequence polymorphisms in the chemokines Sclav (TCA-3), Scya2
 RT (monocyte chemoattractant protein (MCP)-1), and Scya12 (MCP-5) are
 RT candidates for eae7, a locus controlling susceptibility to monophasic
 RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
 RL J. Immunol. 163:2262-2266(1999).
 RN [6]
 RN EFFECT OF ASPIRIN.
 RC TISSUE=Macrophage;
 RX MEDLINE=95372392; PubMed=7544010;
 RA Amin A.R., Vyas P., Attur M., Leszczynska-Piziak J., Patel I.R.,
 RA Weismann G., Abramson S.B.;
 RT "The mode of action of aspirin-like drugs: effect on inducible nitric
 RT oxide synthase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).
 RN [7]
 RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 116-496.
 RX MEDLINE=97477482; PubMed=9334294; DOI=10.1126/science.278.5337.425;
 RA Crane B.R., Arvai A.S., Gachhui R., Wu C., Ghosh D.K., Getzoff E.D.,
 RA Stuehr D.J., Tainer J.A.;
 RT "The structure of nitric oxide synthase oxygenase domain and inhibitor
 RT complexes.";
 RL Science 278:425-431(1997).
 RN [8]
 RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.
 RX MEDLINE=98182450; PubMed=9516116; DOI=10.1126/science.279.5359.2121;
 RA Crane B.R., Arvai A.S., Ghosh D.K., Wu C., Getzoff E.D., Stuehr D.J.,
 RA Tainer J.A.;
 RT "Structure of nitric oxide synthase oxygenase dimer with pterin and
 RT substrate.";
 RL Science 279:2121-2126(1998).
 RN [9]
 RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
 RX MEDLINE=20031637; PubMed=10562538; DOI=10.1093/emboj/18.22.6260;
 RA Ghosh D.K., Crane B.R., Ghosh S., Wolan D., Gachhui R., Crooks C.,
 RA Presta A., Tainer J.A., Getzoff E.D., Stuehr D.J.;
 RT "Inducible nitric oxide synthase: role of the N-terminal beta-hairpin
 RT hook and pterin-binding segment in dimerization and
 RT tetrahydropterin interaction.";
 RL EMBO J. 18:6260-6270(1999).
 RN [10]
 RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499.
 RX MEDLINE=20031638; PubMed=10562539; DOI=10.1093/emboj/18.22.6271;
 RA Crane B.R., Rosenfeld R.J., Arvai A.S., Ghosh D.K., Ghosh S.,
 RA Tainer J.A., Stuehr D.J., Getzoff E.D.;
 RT "N-terminal domain swapping and metal ion binding in nitric oxide
 RT synthase dimerization.";
 RL EMBO J. 18:6271-6281(1999).
 RN [11]
 RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
 RX MEDLINE=20233702; PubMed=10769116; DOI=10.1021/b1992409a;
 RA Crane B.R., Arvai A.S., Ghosh S., Getzoff E.D., Stuehr D.J.,
 RA Tainer J.A.;
 RT "Structures of the N(omega)-hydroxy-L-arginine complex of inducible
 RT nitric oxide synthase oxygenase dimer with active and inactive
 RT pterins.";
 RL Biochemistry 39:4608-4621(2000).
 RN [12]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF TRP-457 MUTANTS.
 RX MEDLINE=21526413; PubMed=11669619; DOI=10.1021/bi011183k;
 RA Aoyagi M., Arvai A.S., Ghosh S., Stuehr D.J., Tainer J.A.,
 RA Getzoff E.D.;
 RT "Structures of tetrahydropterin binding-site mutants of inducible
 RT nitric oxide synthase oxygenase dimer and implicated roles of
 RT Trp457.";
 RL Biochemistry 40:12826-12832(2001).
 RN [13]
 RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
 RX MEDLINE=22325496; PubMed=12437348; DOI=10.1021/bi026313j;
 RA Rosenfeld R.J., Garcin E.D., Panda K., Andersson G., Aberg A.,

RA Wallace A.V., Morris G.M., Olson A.J., Stuehr D.J., Tainer J.A.,
 RA Getzoff E.D.;
 RT "Conformational changes in nitric oxide synthases induced by
 RT chlorzoxazone and nitroindazoles: crystallographic and computational
 RT analyses of inhibitor potency.";
 RL Biochemistry 41:13915-13925(2002).
 RN [14]
 RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 77-495.
 RX MEDLINE=2251717; PubMed=12464241; DOI=10.1016/S0003-9861(02)00555-6;
 RA Fedorov R., Ghosh D.K., Schlichting I.;
 RT "Crystal structures of cyanide complexes of p450cam and the oxygenase
 RT domain of inducible nitric oxide synthase - structural models of the
 RT short-lived oxygen complexes.";
 RL Arch. Biochem. Biophys. 409:25-31(2003).
 CC -I- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule
 CC with diverse functions throughout the body. In macrophages, NO
 CC mediates tumoricidal and bactericidal actions.
 CC -I- CATALYTIC ACTIVITY: L-arginine + n NADPH + m O(2) = citrulline +
 CC nitric oxide + n NADP(+).
 CC -I- COFACTOR: Heme.
 CC -I- COFACTOR: FAD. Binds 1 mole of FAD.
 CC -I- COFACTOR: FMN. Binds 1 mole of FMN.
 CC -I- COFACTOR: Tetrahydrobiopterin (BH4). May stabilize the dimeric
 CC form of the enzyme.
 CC -I- ENZYME REGULATION: Not stimulated by calcium/calmodulin. Aspirin
 CC inhibits expression and function of this enzyme and effects may be
 CC exerted at the level of translational/posttranslational
 CC modification and directly on the catalytic activity.
 CC -I- SUBUNIT: Homodimer. Binds SLC9A3R1 (By similarity).
 CC -I- TISSUE SPECIFICITY: Macrophages.
 CC -I- INDUCTION: By treatment with endotoxins or cytokines.
 CC -I- SIMILARITY: Belongs to the NOS family.
 CC -I- SIMILARITY: Contains 1 flavodoxin-like domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; M87039; AAA39315.1; -; mRNA.
 CC EMBL; M92649; -; NOT ANNOTATED CDS; mRNA.
 CC EMBL; M84373; AAA39834.1; -; mRNA.
 CC EMBL; U43428; AAC52356.1; -; mRNA.
 CC EMBL; AF065919; AAC17914.1; -; mRNA.
 CC EMBL; AF065920; AAC17915.1; -; mRNA.
 CC EMBL; AF065921; AAC17916.2; -; mRNA.
 CC EMBL; AF065922; AAC17917.2; -; mRNA.
 CC EMBL; AF065923; AAC17918.2; -; mRNA.
 CC PIR; A43271; A43271.
 CC DR PDB; 1DD7; X-ray; A=114-498.
 CC DR PDB; 1DF1; X-ray; A/B=77-499.
 CC DR PDB; 1DWV; X-ray; A/B=77-496.
 CC DR PDB; 1DWX; X-ray; A/B=77-496.
 CC DR PDB; 1DWX; X-ray; A/B=77-496.
 CC DR PDB; 1JWJ; X-ray; A/B=66-498.
 CC DR PDB; 1JWK; X-ray; A/B=66-498.
 CC DR PDB; 1M8D; X-ray; A/B=65-498.
 CC DR PDB; 1M8E; X-ray; A/B=65-498.
 CC DR PDB; 1M8H; X-ray; A/B=65-498.
 CC DR PDB; 1M8I; X-ray; A/B=65-498.
 CC DR PDB; 1M9T; X-ray; A/B=65-498.
 CC DR PDB; 1N2N; X-ray; A/B=77-495.
 CC DR PDB; 1NOC; X-ray; A=115-498.
 CC DR PDB; 1NOD; X-ray; A/B=77-499.
 CC DR PDB; 1NOS; X-ray; @=115-498.
 CC DR PDB; 1QOM; X-ray; A/B=65-498.
 CC DR PDB; 1QW4; X-ray; A/B=77-495.
 CC DR PDB; 1QW5; X-ray; A/B=77-495.
 CC DR PDB; 1R35; X-ray; A/B=66-498.
 CC DR PDB; 1VAR; X-ray; A/B=77-495.
 CC DR PDB; 2BRJ; X-ray; A=77-498.
 CC DR PDB; 2NOD; X-ray; A/B=77-499.

```
DR PDB; 2NOS; X-ray; @=115-498.
DR PDB; 3NOD; X-ray; A/B=77-499.
DR IntAct; P29477; -.
DR Ensembl; ENSMUSG0000020826; Mus musculus.
DR MGI; MGI:97361; Nos2.
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR GO; GO:0005829; C:cytosol; TAS.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0005516; F:calmodulin binding; TAS.
DR GO; GO:0020037; F:heme binding; NAS.
DR GO; GO:0042803; F:protein homodimerization activity; ISS.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0001542; P:ovulation (sensu Mammalia); IMP.
DR GO; GO:0045585; P:positive regulation of cytotoxic T-cell dif. .; ISS.
DR GO; GO:0001666; P:response to hypoxia; IDA.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001709; FPN cyt_redctse.
DR InterPro; IPR012144; NOS_
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO_synthase_1; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS50902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN 1.
SQ SEQUENCE 1145 AA; 130685 MW; DAD5AAF53680B005 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1144;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6
Db 514 KVVFPA 519

RESULT 21
Q5SXT3 MOUSE
ID Q5SXT3_MOUSE PRELIMINARY; PRT; 1144 AA.
AC Q5SXT3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Nitric oxide synthase 2, inducible, macrophage (Inducible nitric oxide synthase).
GN Name=Nos2; ORFNames=RP23-341J22.2-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Coxe F., Levacher B., Rique H., Leopold O., Boutin J.A.,
RA Galizzi J.-P.;
RT "Genomic structure of the murine inducible nitric oxide synthase (i-
RT NOS) gene."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL592185; CAI25275.1; -; Genomic DNA.
DR EMBL; AF427516; AAL24076.1; -; Genomic DNA.
SQ SEQUENCE 1144 AA; 130574 MW; 0735BE676113457F CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1144;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6
Db 514 KVVFPA 519

RESULT 22
Q8R410 MOUSE
ID Q8R410_MOUSE PRELIMINARY; PRT; 1145 AA.
AC Q8R410;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inducible nitric oxide synthase.
GN Name=Nos2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

NCBI_TaxID=10090;
[1]
NUCLEOTIDE SEQUENCE.
STRAIN=ICR;
Hagiwara K., Endo Y., Xin H., Takahashi M., Hugin, Nukiwa T.;
Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AY090567; AAM11887.1; -; mRNA.
HSSP; P29477; 1DWV.
MGI; MGI:97361; Nos2.
GO; GO:0030863; C:cortical cytoskeleton; IDA.
GO; GO:0005829; C:cytosol; ISS.
GO; GO:0048471; C:perinuclear region; IDA.
GO; GO:0005516; F:calmodulin binding; ISS.
GO; GO:0020037; F:heme binding; ISS.
GO; GO:0042803; F:nitric-oxide synthase activity; ISS.
GO; GO:0042742; P:defense response to bacteria; ISS.
GO; GO:0006954; P:inflammatory response; ISS.
GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
GO; GO:0001542; P:ovulation (sensu Mammalia); IMP.
GO; GO:0045585; P:positive regulation of cytotoxic T-cell dif. .; ISS.
GO; GO:0001666; P:response to hypoxia; IDA.
GO; GO:0006801; P:superoxide metabolism; ISS.
InterPro; IPR003097; FAD_binding.
InterPro; IPR001094; Flavodoxin like.
InterPro; IPR008254; Flav nitox synth.
InterPro; IPR001709; FPN cyt_redctse.
InterPro; IPR012144; NOS_
InterPro; IPR004030; NO synthase.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00667; FAD_binding_1; 1.
Pfam; PF00258; Flavodoxin_1; 1.
Pfam; PF00175; NAD_binding_1; 1.
Pfam; PF02898; NO_synthase_1; 1.
PIRSF; PIRSF000333; NOS; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
PROSITE; PS50902; FLAVODOXIN LIKE; 1.
PROSITE; PS60001; NOS; UNKNOWN 1.
SQ SEQUENCE 1145 AA; 130685 MW; DAD5AAF53680B005 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1145;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6
Db 515 KVVFPA 520

RESULT 23
Q6P6A0 MOUSE
ID Q6P6A0_MOUSE PRELIMINARY; PRT; 1145 AA.
AC Q6P6A0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Nos2 protein.
GN Name=Nos2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Hopkins R.F., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L.,
```

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., LeVean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RA Strausberg R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC062378; AAH62378.1; -; mRNA.
 DR HSSP; P29477; 1JWK.
 DR MGI; MGI:97361; Nos2.
 DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
 DR GO; GO:0048471; C:perinuclear region; IDA.
 DR GO; GO:0004517; F:nitric-oxide synthase activity; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0042803; F:protein homodimerization activity; IDA.
 DR GO; GO:0042742; P:defense response to bacteria; IMP.
 DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
 DR GO; GO:0001666; P:response to hypoxia; IDA.
 DR GO; GO:0006801; P:superoxide metabolism; IMP.
 DR InterPro; IPR003097; FAD binding.
 DR InterPro; IPR001094; Flavodoxin like.
 DR InterPro; IPR008254; Flavodoxin synth.
 DR InterPro; IPR001709; PPN_Cyt_redctse.
 DR InterPro; IPR012144; NOS.
 DR InterPro; IPR004030; NO synthase.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00667; FAD binding 1; 1.
 DR Pfam; PF00258; Flavodoxin 1; 1.
 DR Pfam; PF00175; NAD binding 1; 1.
 DR Pfam; PF02898; NO synthase 1; 1.
 DR PIRSP; PIRSF000333; NOS; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 DR PROSITE; PS0902; FLAVODOXIN LIKE; 1.
 DR PROSITE; PS60001; NOS; UNKNOWN 1.
 SQ SEQUENCE 1145 AA; 130671 MW; C26E09F536923295 CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 1145;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 DB 515 KVVFFA 520
 |||||
 RESULT 24
 ID Q73N39 TREDE PRELIMINARY; PRT; 164 AA.
 AC Q73N39;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Membrane protein, putative.
 GN OrderedLocusNames=TDE1317;
 OS Treponema denticola.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=158;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 35405 / DSM 14222;
 RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
 RA Sedhadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
 RA Seshadri R., Vaidyan T.M., DeBoy R.T., Fouts D.E., Hatt D.H.,
 RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
 RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
 RA Gebregeorgis E., Geer K., Teagave G., Malek J.A., Ayodeji B.,
 RA Shatman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
 RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
 RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
 RT "Comparison of the genome of the oral pathogen Treponema denticola
 RT with other spirochete genomes";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).
 DR EMBL; AR017250; AAS11834.1; -; Genomic_DNA.
 DR TIGR; TDE1317; -.
 KW Complete proteome.
 SQ SEQUENCE 164 AA; 18968 MW; 27E92778DDA9117C CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 164;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 DB 50 KVVFFA 55
 |||||
 RESULT 25
 Q6AKE9 DESPS
 ID Q6AKE9 DESPS PRELIMINARY; PRT; 203 AA.
 AC Q6AKE9;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Related to McbG protein.
 GN OrderedLocusNames=DP2447;
 OS Desulfotalea psychrophila.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
 OC Desulfobulbaceae; Desulfotalea.
 OX NCBI_TaxID=84980;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=LSv54 / DSM 12343;
 RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
 RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
 RA Teeling H., Leuschner W.D., Gloeckner P.-O., Lupas A.N., Amann R.,
 RA Klenk H.-P.;
 RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
 RT from permanently cold Arctic sediments";
 RL Environ. Microbiol. 6:887-902 (2004).
 DR EMBL; CR522870; CAG37176.1; -; Genomic_DNA.
 DR InterPro; IPR001646; 5peptide repeat.
 DR Pfam; PF00805; Pentapeptide; 3.
 KW Complete proteome.
 SQ SEQUENCE 203 AA; 23270 MW; 2EA1CD022861292D CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 203;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 DB 52 KVVFFA 57
 |||||
 RESULT 26
 O67225 AQUAE
 ID O67225 AQUAE PRELIMINARY; PRT; 380 AA.
 AC O67225;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```

DE Hydrogenase expression/formation protein HypD.
GN Name=hypD; OrderedLocNames=AQ_1157;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Shead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
RL EMBL; AS000726; AAC07185.1; -; Genomic_DNA.
DR PIR; F70399; F70399.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR PIRSF; PIRSF005622; Hydrgn_mat_hypD; 1.
DR TIGRFAMs; TIGR00075; hypD; 1.
KW Complete proteome.
SQ SEQUENCE 380 AA; 42791 MW; 49C0E52BA655A5F5 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 380;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 141 KVIFFA 146

RESULT 27
Q81FH5_BACCR PRELIMINARY; PRT; 387 AA.
ID Q81FH5;
AC Q81FH5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Na+/H+ antiporter Napa (inosine-dependent germination).
GN OrderedLocNames=BC1612;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,
RA Kapural V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Rusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
RL EMBL; AE017003; AAP08591.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41037 MW; 907C03B6BA150B4A CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DE Hydrogenase expression/formation protein HypD.
GN Name=hypD; OrderedLocNames=AQ_1157;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Shead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
RL EMBL; AS000726; AAC07185.1; -; Genomic_DNA.
DR PIR; F70399; F70399.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR PIRSF; PIRSF005622; Hydrgn_mat_hypD; 1.
DR TIGRFAMs; TIGR00075; hypD; 1.
KW Complete proteome.
SQ SEQUENCE 380 AA; 42791 MW; 49C0E52BA655A5F5 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 380;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 141 KVIFFA 146

RESULT 27
Q81FH5_BACCR PRELIMINARY; PRT; 387 AA.
ID Q81FH5;
AC Q81FH5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Na+/H+ antiporter Napa (inosine-dependent germination).
GN OrderedLocNames=BC1612;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,
RA Kapural V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Rusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
RL EMBL; AE017003; AAP08591.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41037 MW; 907C03B6BA150B4A CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 184 KIVFFA 189

RESULT 28
Q5WPU9_LUTLO PRELIMINARY; PRT; 399 AA.
ID Q5WPU9;
AC Q5WPU9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 43.2 kDa salivary protein.
GN ORFNames=LJMI1_Clu9;
OS Lutzomyia longipalpis (Sand fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea;
OC Psychodidae; Lutzomyia; Lutzomyia.
OX NCBI_TaxID=7200;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Salivary gland;
RX PubMed=15371479; DOI=10.1242/jeb.01185;
RA Valenzuela J.G., Garfield M., Rowton E.D., Pham V.M.;
RT "Identification of the most abundant secreted proteins from the
RT salivary glands of the sand fly Lutzomyia longipalpis, vector of
RT Leishmania chagasi.";
RL J. Exp. Biol. 207:3717-3729(2004).
DR EMBL; AY445935; AAS05318.1; -; mRNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
SQ SEQUENCE 399 AA; 45277 MW; F4E19F115794AAE8 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 399;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
DB 305 KVIFFA 310

RESULT 29
Q4TRF8_9SPHN PRELIMINARY; PRT; 450 AA.
ID Q4TRF8;
AC Q4TRF8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Membrane protein.
GN ORFNames=ELI0568;
OS Erythrobacter litoralis HTCC2594.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=314225;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTCC2594;
RA Giannopoulou S.J., Cho J.-C., Ferrera S., Johnson J., Kravitz S.,
RA Halpern A., Remington K., Beeson K., Tran B., Rogers Y.-H.,
RA Friedman R., Venter J.C.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBSJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAG0100001; EAL76762.1; -; Genomic DNA.
SQ SEQUENCE 450 AA; 50280 MW; 077F448E75ADF977 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 450;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 KVVFPA 6
Db 116 KIVFFA 121

RESULT 30
Q4S4T5_TETNG
ID Q4S4T5_TETNG PRELIMINARY; PRT; 464 AA.
AC Q4S4T5;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome 2 SCAF14738, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=STENG0024047001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Telostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN NUCLEOTIDE SEQUENCE.
RA Jallou O., Aury J.M., Brunet P., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Crenaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McSwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]

RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014738; CAG04347.1; -; Genomic_DNA.
FT NON_TER 464 464
SQ SEQUENCE 464 AA; 53213 MW; 0F9FF01DB193CE5C CRC64;

Query Match 96.6%; Score 28; DB 2; Length 464;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 304 KIVFFA 309

RESULT 31
Q91VU5_MOUSE
ID Q91VU5_MOUSE PRELIMINARY; PRT; 606 AA.
AC Q91VU5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Wtcc2 protein.
GN Name=Wtcc2; Synonyms=Wtcc2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

```

RN NUCLEOTIDE SEQUENCE.
RP STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RG NUCLEOTIDE SEQUENCE.
RP STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RX NIH MGC Project;
RG Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009019; AA09019.1; -; mRNA.
DR Ensembl; ENSMUSG0000024169; Mus musculus.
DR MGI; MGI:2146906; A1661311.
DR GO; GO:0005488; F.biding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
SQ SEQUENCE 606 AA; 70992 MW; 4BB6057E07ADA16C CRC64;

Query Match 96.6%; Score 28; DB 2; Length 606;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 376 KIVFFA 381

RESULT 32
Q4WB22_ASFPF
ID Q4WB22_ASFPF PRELIMINARY; PRT; 623 AA.
AC Q4WB22;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Afug06810;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]

RG NUCLEOTIDE SEQUENCE.
RP STRAIN=AF293;
RA Nierman W., Pain A., Anderson M.J., Mortman J., Kim H.Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins K., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kmagai T., Laton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majors W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
RA Penalba M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,

```

RA Rabinowitch E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Roming C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.,
RA "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAH01000013; BAI85442.1; -; Genomic_DNA.
SQ SEQUENCE 623 AA; 72379 MW; 08795F0DEF6C18E2 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 623;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 96 KVFVFA 101
||:||||

RESULT 33
Q5K7E5 CRYNE PRELIMINARY; PRT; 630 AA.
AC Q5K7E5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CN00130;
OS Cryptococcus neoformans var. neoformans JEC21.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
ON NCBI_TaxID=214684;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JEC21;
RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,
RA Van Aken S., Fraser C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=JEC21;
RX PubMed=15653466; DOI=10.1126/science.1103773;
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
RA Kwon-Chung K.J., Lengler K.B., Maiti R., Marra M.A., Marra R.E.,
RA Mathewson C.A., Mitchell T.G., Perlea M., Riggs F.R., Salzberg S.L.,
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
RA Fraser C.M., Hyman R.W.;
RL "The genome of the basidiomycetous yeast and human pathogen
RT Cryptococcus neoformans";
RL Science 307:1321-1324(2005).
DR EMBL; AS017356; AAW47004.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR007219; Fungal trans.
DR InterPro; IPR001138; Fungi_Trcsrp_N.
DR Pfam; PF04082; Fungal_trans; 1.

DR Pfam; PF00172; Zn clus; 1.
DR PRINTS; PR00054; FUNGALZNCYS.
DR SMART; SM00066; GAL4; 1.
DR PROSITE; PS00463; ZN2_CV6_FUNGAL_1; 1.
DR PROSITE; PS00463; ZN2_CV6_FUNGAL_2; 1.
KW Complete proteome; DNA-binding; Hypothetical protein; Metal-binding;
KW Nuclear protein; Transcription; Transcription regulation; Zinc.
SQ SEQUENCE 630 AA; 68912 MW; 730A7C02A87D6B9B CRC64;

Query Match 96.6%; Score 28; DB 2; Length 630;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 572 KVFVFA 577
||:||||

RESULT 34
Q6RUU2 MOUSE PRELIMINARY; PRT; 663 AA.
AC Q6RUU2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Brathwaite M., Waelitz P., Dudekula D., Nagaraja R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY491413; AAS21643.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 663 AA; 77192 MW; CEB02E3EBD356F1C CRC64;

Query Match 96.6%; Score 28; DB 2; Length 663;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 433 KVFVFA 438
||:||||

RESULT 35
Q83IB2 TROM8 PRELIMINARY; PRT; 690 AA.
AC Q83IB2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative helicase regulator.
GN OrderedLocNames=TW130;
OS Tropheryma whipplei (strain TW08/27) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcaceae; Cellulomonadaceae; Tropheryma.
ON NCBI_TaxID=218496;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22495039; PubMed=12606174; DOI=10.1016/S0140-6736(03)12597-4;
RA Bentley S.D., Maitwald M., Murphy L.D., Fallon M.J., Yeats C.A.,
RA Dover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.E.,
RA von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
RA Barrell B.G., Parkhill J., Reiman D.A.;
RL "Sequencing and analysis of the genome of the Whipple's disease
RT bacterium Tropheryma whipplei";
RL Lancet 361:637-644(2003).
DR EMBL; BX251410; CAD66810.1; -; Genomic_DNA.

DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0004386; F:Helicase activity; IEA.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR000330; SNF2_N.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF00176; SNF2_N; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICC; 1.
 KW Complete proteome.
 SQ SEQUENCE 690 AA; 76266 MW; CD3633B948669E32 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 690;
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 :|||
 Db 526 KIVFFA 531

RESULT 36

Q83GW3 TROWT
 ID Q83GW3 TROWT PRELIMINARY; PRT; 698 AA.
 AC Q83GW3;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE DNA helicase
 GN OrderedLocustNames=TW118;
 OS Tropheryma whippiei (strain Twist) (Whipple's bacillus).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcineae; Cellulomonadaceae; Tropheryma.
 OX NCBI_TaxID=203267;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Twist;
 RX MEDLINE=22784088; PubMed=12902375;
 RA Raoult D., Ogata H., Audic S., Robert C., Suhre K., Drancourt M.,
 RA Claverie J.-M.;
 RT "Tropheryma whippiei Twist: a human pathogenic Actinobacteria with a
 RT reduced genome.";
 RL Genome Res. 13:1800-1809 (2003).
 DR EMBL; AE016850; AAO44215.1; -; Genomic_DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0004386; F:Helicase activity; IEA.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR000330; SNF2_N.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF00176; SNF2_N; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICC; 1.
 KW Complete proteome;
 SQ SEQUENCE 698 AA; 77193 MW; 6D104BF533CDD72 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 698;
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 :|||
 Db 534 KIVFFA 539

RESULT 37

Q55HW1 CRYNE
 ID Q55HW1 CRYNE PRELIMINARY; PRT; 760 AA.
 AC Q55HW1;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=CNEN0110;
 OS Cryptococcus neoformans var. neoformans B-3501A.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=283643;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B-3501A;
 RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
 RA Wickes B.L., Fu J., Davis R.W.;
 RT "Cryptococcus neoformans serotype D sequencing."
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAEY01000066; EAL17182.1; -; Genomic_DNA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 KW DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;
 KW Transcription; Transcription regulation; Zinc.
 SQ SEQUENCE 760 AA; 84062 MW; 735C53C64A854619 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 760;
 Best Local Similarity 83.3%; Pred. No. 6.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 :|||
 Db 702 KIVFFA 707

RESULT 38

Q6ZQ91 MOUSE
 ID Q6ZQ91 MOUSE PRELIMINARY; PRT; 1265 AA.
 AC Q6ZQ91;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE MKIAA0590 protein (fragment).
 GN Name=MKIAA0590;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX PubMed=14621295;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
 RA Suga Y., Nagase T., Ohara O., Koga H.;
 RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
 RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
 RT cDNAs identified by screening of terminal sequences of cDNA clones
 RT randomly sampled from size-fractionated libraries.";
 RL DNA Res. 10:167-180 (2003).
 DR EMBL; AK129167; BAC97977.1; -; mRNA.
 DR NON TER 1
 FT SEQUENCE 1265 AA; 143403 MW; C9C157ABE80FF928 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1265;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 :|||
 Db 1081 KIVFFA 1086

```
RESULT 39
Q5F3M1 CHICK PRELIMINARY; PRT; 1412 AA.
AC Q5F3M1;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=RCJMB04.13m2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA Fiedler P., Kutter S., Biagodatecki A., Kostovska D., Kotter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT genefunction analysis."
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; AJ851629; CAH65263.1; -; mRNA.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein.
SQ SEQUENCE 1412 AA; 158448 MW; FA005085B274747 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1412;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6
Db 1225 KIVFPA 1230

RESULT 40
Q4Q5Q4 LEIMA PRELIMINARY; PRT; 1655 AA.
AC Q4Q5Q4;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Lmjf32.0310;
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neil S.,
RA Saunders D., Seeger K., Warren F., Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CTO05269; CAJ08491.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1655 AA; 181249 MW; 2B5317E9BD469A55 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1655;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6
Db 1397 KIVFPA 1402
```

```
RESULT 41
Q4LBQ8 SODGL PRELIMINARY; PRT; 88 AA.
AC Q4LBQ8;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE CheY protein.
GN Name=cheY;
OS Sodalis glossinidius.
OC Plasmid pSG4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=63612;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PLASMID=pSG4;
RA Darby A.C., Lagnel J., Matthew C.Z., Bourtzis K., Maudlin I.,
RA Welburn S.C.;
RT "Extrachromosomal DNA of the symbiont Sodalis glossinidius."
RL J. Bacteriol. 187:5003-5007(2005).
DR EMBL; AJ868439; CAI59440.1; -; Genomic_DNA.
DR EMBL; AJ868438; CAI59427.1; -; Genomic_DNA.
KW Plasmid.
SQ SEQUENCE 88 AA; 10177 MW; F4168F2A56B8D0AC CRC64;

Query Match 93.1%; Score 27; DB 2; Length 88;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6
Db 42 KIIFPA 47

RESULT 42
Q9RQ09 BACTN PRELIMINARY; PRT; 183 AA.
AC Q9RQ09; Q7C422;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE RNA polymerase sigma factor SigZ-like protein (RNA polymerase ECF-type
DE sigma factor).
GN Name=sigZ; OrderedLocusNames=BT1278;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482;
RX MEDLINE=93980805; PubMed=10449780; DOI=10.1073/pnas.96.17.9833;
RA Hooper L.V., Xu J., Falk P.G., Midtvedt T., Gordon J.I.;
RT "A molecular sensor that allows a gut commensal to control its
RT nutrient foundation in a competitive ecosystem."
RL Proc. Natl. Acad. Sci. U.S.A. 96:9833-9838(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076(2003).
DR EMBL; AF137263; AAF01488.1; -; Genomic_DNA.
DR EMBL; AB016931; AAO76385.1; -; Genomic_DNA.
DR GO; GO:0016987; F:sigma factor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006352; P:transcription initiation; IEA.
DR InterPro; IPR007627; Sigma70_r2.
```

DR InterPro; IPR011991; Wing_hlx_DNA_bd.
 DR Pfam; PF04542; Sigma70_r2; 1.
 KW Complete proteome; DNA-binding; DNA-directed RNA polymerase;
 KW Nucleotidyltransferase; Sigma factor; Transcription;
 KW Transcription regulation; Transferase.
 SQ SEQUENCE 183 AA; 22042 MW; 6B24DABC99BEC643 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 183;
 Best Local Similarity 66.7%; Pred. No. 3.3e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
 |::|||
 Db 172 KIIFPA 177

RESULT 43

Q61C67 CABER
 ID Q61C67_CABER PRELIMINARY; PRT; 315 AA.
 AC Q61C67;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein CBG13055 (Fragment).
 GN Name=CBG13055;
 OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6238;
 RN [1]

NUCLEOTIDE SEQUENCE.

RG The C.briggsae Sequencing Consortium;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CAAC0100061; CA567532.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.

DR PROSITE; PS0262; G-PROTEIN_RSCFP_F1_2; 1.
 DR G-protein coupled receptor; Hypothetical protein; Receptor;
 KW Transducer; Transmembrane.
 FT NON_TER 1
 FT TER 315
 SQ SEQUENCE 315 AA; 35855 MW; 579B590D01874512 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 315;
 Best Local Similarity 66.7%; Pred. No. 5.4e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
 |::|||
 Db 117 KIIFPA 122

RESULT 44

Q4HSJ7 CAMUP
 ID Q4HSJ7_CAMUP PRELIMINARY; PRT; 362 AA.
 AC Q4HSJ7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hydrogenase expression/formation protein HypD.
 GN Name=hypD; ORFNames=CUP0294;
 OS Campylobacter upsaliensis RM3195.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=306264;
 RN [1]

NUCLEOTIDE SEQUENCE.

RC STRAIN=RM3195;
 RA Routs D.E., Mongodin E.P., Mandrell R.E., Miller W.G., Raeko D.A.,
 RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
 RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
 RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
 RA Nelson K.E.;
 RT "Major structural and novel potential virulence mechanisms from the
 RT genomes of multiple Campylobacter species."
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

DR EMBL; AAFJ01000002; RAL53713.1; -; Genomic DNA.
 SQ SEQUENCE 362 AA; 40365 MW; 15B0A8B12D60CAED CRC64;

Query Match 93.1%; Score 27; DB 2; Length 362;
 Best Local Similarity 66.7%; Pred. No. 6.1e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
 |::|||
 Db 132 KIIFPA 137

RESULT 45

Q9V7J0 DROME
 ID Q9V7J0_DROME PRELIMINARY; PRT; 382 AA.
 AC Q9V7J0; Q9GQ81;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE C84421-PB, isoform B (Aspartyl beta-hydroxylase variant 2).
 GN Name=Asph; ORFNames=C84421;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

NUCLEOTIDE SEQUENCE.

RA MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrer J., Fleischmann W.,
 RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hoeltin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mounet S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclab J.M., P.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weisenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-E., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celisner S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacifler J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirkas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirkas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celisner S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby P.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kinkiner J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley *Drosophila* Genome Project;
 RA Celisner S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacle J., Park S., Svirkas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20564328; PubMed=10956665; DOI=10.1074/jbc.M006753200;
 RA Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
 RA O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
 RA Friedman P.A.;
 RT "Aspartyl beta-hydroxylase (Asph) and an evolutionarily conserved
 RT isoform of Asph missing the catalytic domain share exons with
 RT junction.";
 RL J. Biol. Chem. 275:39543-39554(2000).
 RL EMBL; AF003808; AAF58063.2; -; Genomic_DNA.
 DR EMBL; AF289494; AAG40807.1; -; mRNA.
 DR Ensembl; CG8421; *Drosophila melanogaster*.
 DR FlyBase; FBgn0034075; Asph.
 DR FlyBase; FBgn0034075; CG8421.
 SQ SEQUENCE 382 AA; 43287 MW; 60E5C03AEBFC6E8B CRC64;

Query Match 93.1%; Score 27; DB 2; Length 382;
 Best Local Similarity 66.7%; Pred. No. 6.4e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFFFA 6
 Db 53 KIIFFA 58
 ID Q6L2B4_PICCTO PRELIMINARY; PRT; 410 AA.
 AC Q6L2B4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Lipopolysaccharide N-acetylglucosaminyltransferase.
 OS OrderedLocustNames=PTC0303;
 OS *Picrophilus torridus*.
 OC Archaea; Euryarchaeota; Thermoplasmatales;
 OC Picrophilaceae; Picrophilus.
 OX NCBI_TaxID=82076;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=DSM 9790 / ATCC 700027;
 RX PubMed=15184674; DOI=10.1073/pnas.0401356101;
 RA Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
 RA Schepers B., Dock C., Antranikian G., Liebl W.;
 RT "Genome sequence of *Picrophilus torridus* and its implications for life
 RT around pH 0.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
 DR EMBL; AE017261; AAT42888.1; -; Genomic_DNA.
 DR GO; GO:0016757; P:transferase activity, transferring glycosyl. . .; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR InterPro; IPR001296; Glyco trans 1.
 DR Pfam; PF00534; Glycosyltransferase.
 KW Complete proteome; Glycosyltransferase; Transferase.
 SQ SEQUENCE 410 AA; 48120 MW; C192F0152E66E9B0 CRC64;
 Query Match 93.1%; Score 27; DB 2; Length 410;
 Best Local Similarity 66.7%; Pred. No. 6.8e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFFFA 6
 Db 235 KIIFFA 240
 ID O59243_PVRHO PRELIMINARY; PRT; 447 AA.
 AC O59243;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein PH1606.
 GN OrderedLocustNames=PH1606;
 OS *Pyrococcus horikoshii*.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=53953;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kuchida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, *Pyrococcus horikoshii* OT3.";
 RL DNA Res. 5:55-76(1998).
 RL EMBL; BA000001; BAA30718.1; -; Genomic_DNA.
 DR PIR; F71039; F71039.
 DR GO; GO:0016020; C:membrane; IEA.

```

DR GO: GO:0005355; P:glucose transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000803; GlucTransporter.
DR PRINTS: PR00172; GLUCTRNSP.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 447 AA; 51173 MW; 509F45A302D3B059 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 447;
Best Local Similarity 66.7%; Pred. No. 7.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVPFFA 6
Db 207 KIIFFA 212

RESULT 48
Q95893 DROME PRELIMINARY; PRT; 556 AA.
ID Q95893
AC Q95893
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE GM05229p.
GN Name=Aeph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY060905; AAL28453.1; -, mRNA.
DR FlyBase; FBgn0034075; Aeph.
DR FlyBase; FBgn0034075; CG8421.
SQ SEQUENCE 556 AA; 63089 MW; 95D82EAC57D11FB8 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 556;
Best Local Similarity 66.7%; Pred. No. 8.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVPFFA 6
Db 53 KIIFFA 58

RESULT 49
Q9V719 DROME PRELIMINARY; PRT; 556 AA.
ID Q9V719
AC Q9V719
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG8421-PD, isoform D (CG8421-pe, isoform e).
GN Name=Aeph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sueton G.G., Wortman J.R., Yeandle M.D., Zhang Q., Chen L.X.,

```

```

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Adrell J.F., Agbayani A., An H.-J., Andrews-Franckoch C., Baldwin D.,
RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari P., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gar N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
[2]
NUCLEOTIDE SEQUENCE.
MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
NUCLEOTIDE SEQUENCE.
MEDLINE=22426070; PubMed=12537573;
RA Kaminiker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
[4]
NUCLEOTIDE SEQUENCE.
MEDLINE=22426069; PubMed=12537572;
RA Milera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[5]
NUCLEOTIDE SEQUENCE.
RA Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,

```

RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- INTERACTION:
 CC O46085;EG:63B12.5; NbExp=1; IntAct=EBI-123244, EBI-151469;
 CC EMBL; AE003808; AAF58064.2; -; Genomic_DNA.
 DR IntAct; Q9V719; -;
 DR Ensembl; CG8421; Drosophila melanogaster.
 DR FlyBase; FBgn0034075; Asph.
 DR FlyBase; FBgn0034075; CG8421.
 SQ SEQUENCE 556 AA; 63144 MW; B420980CDB6C357A CRC64;

Query Match 93.1%; Score 27; DB 2; Length 556;
 Best Local Similarity 66.7%; Pred. No. 8.9e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPPA 6

Db 53 KLIFFA 58

RESULT 50

O9Q82 DROME PRELIMINARY; PRT; 785 AA.
 AC Q9G82;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Aspartyl beta-hydroxylase variant 1 (CG8421-PA, isoform A).
 GN Name:Asph; ORFNames=CG8421;
 GN Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20564328; PubMed=10956665; DOI=10.1074/jbc.M006753200;
 RA Dinchuk J.E., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Anatolides P.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA O'Neil K.T., Pocht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
 RA Friedman P.A.;
 RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G.G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dunz C., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok C., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Laako P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289493; AAG40806.1; -; mRNA.
 DR EMBL; AE003808; AAM70947.1; -; Genomic_DNA.
 DR Ensembl; CG8421; Drosophila melanogaster.
 DR FlyBase; FBgn0034075; Asph.
 DR FlyBase; FBgn0034075; CG8421.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IEA.
 DR GO; GO:0015022; C:integral to membrane; IEA.
 DR GO; GO:0005486; F:binding; IEA.
 DR GO; GO:0004597; F:peptide-aspartate beta-dioxygenase activity; IEA.
 DR GO; GO:0018193; P:peptidyl-amino acid modification; IEA.

```

DR InterPro; IPR007803; Asp Arg Hydrex.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR011990; TPR-like helical.
DR Pfam; PF05118; Asp Arg Hydrex; 1.
DR PROSITE; PS50293; TPR_REGION; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 785 AA; 89843 MW; 30A8DFCD8636F7F1 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 785;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 53 KIIFFA 58

RESULT 51
Q68K27 CHLRE
ID Q68K27 CHLRE PRELIMINARY; PRT; 1384 AA.
AC Q68K27;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 26, Last annotation update)
DE Intracellular transport particle protein 140.
GN Name=IFT140;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
OC Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
OC NCBI_TaxID=3055;
[1]
RP NUCLEOTIDE SEQUENCE.
Walker B.L., Hou Y., Dentler W.L., Witman G.B., Pazour G.J.;
"Intracellular transport protein IFT140."
Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY686103; AAT95430.1; -; mRNA.
DR GO; GO:0019861; C:flagellum; IEA.
DR InterPro; IPR002885; PPR.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 5.
DR TIGRFAMs; TIGR00756; PPR; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Flagellum.
SQ SEQUENCE 1384 AA; 154603 MW; 5D3E70C8440DABCD CRC64;

Query Match 93.1%; Score 27; DB 2; Length 1384;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1154 KIIFFA 1159

RESULT 52
Q7QEF0 ANOFA
ID Q7QEF0 ANOFA PRELIMINARY; PRT; 1408 AA.
AC Q7QEF0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000001545 (Fragment).
GN ORFNames=ENSANG000000001308;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;
OC Anophelinae; Anopheles.
OC NCBI_TaxID=180454;
[1]
RP NUCLEOTIDE SEQUENCE.

DR InterPro; IPR007803; Asp Arg Hydrex.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR011990; TPR-like helical.
DR Pfam; PF05118; Asp Arg Hydrex; 1.
DR PROSITE; PS50293; TPR_REGION; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 785 AA; 89843 MW; 30A8DFCD8636F7F1 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 785;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 53 KIIFFA 58

RESULT 51
Q68K27 CHLRE
ID Q68K27 CHLRE PRELIMINARY; PRT; 1384 AA.
AC Q68K27;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 26, Last annotation update)
DE Intracellular transport particle protein 140.
GN Name=IFT140;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
OC Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
OC NCBI_TaxID=3055;
[1]
RP NUCLEOTIDE SEQUENCE.
Walker B.L., Hou Y., Dentler W.L., Witman G.B., Pazour G.J.;
"Intracellular transport protein IFT140."
Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY686103; AAT95430.1; -; mRNA.
DR GO; GO:0019861; C:flagellum; IEA.
DR InterPro; IPR002885; PPR.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 5.
DR TIGRFAMs; TIGR00756; PPR; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Flagellum.
SQ SEQUENCE 1384 AA; 154603 MW; 5D3E70C8440DABCD CRC64;

Query Match 93.1%; Score 27; DB 2; Length 1384;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1154 KIIFFA 1159

RESULT 52
Q7QEF0 ANOFA
ID Q7QEF0 ANOFA PRELIMINARY; PRT; 1408 AA.
AC Q7QEF0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000001545 (Fragment).
GN ORFNames=ENSANG000000001308;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;
OC Anophelinae; Anopheles.
OC NCBI_TaxID=180454;
[1]
RP NUCLEOTIDE SEQUENCE.

STRAIN=PEST;
The Anopheles gambiae Sequence Committee;
"Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
STRAIN=PEST;
The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
-!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAAB0100847; EAA06855.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
FT NON_TER 1408 1408
SQ SEQUENCE 1408 AA; 157382 MW; FF63317DAB976DB2 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 1408;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1212 KIIFFA 1217

RESULT 53
Q9VPR0 DROME
ID Q9VPR0 DROME PRELIMINARY; PRT; 1443 AA.
AC Q9VPR0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG11838-PA; isoform A.
GN Names=Oseeg3; ORFNames=CG11838;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
[1]
RP NUCLEOTIDE SEQUENCE.
MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

```

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupeki M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong Y., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celnik S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Celnik S.E., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA Patel S., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnik S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnik S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RG Berkeley *Drosophila* Genome Project;
RA Celnik S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RN NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AR003589; AAF51483.1; -; Genomic_DNA.
DR FlyBase; FBgn0031262; Ose93.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR SMART; SM00320; WD40; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat.
SQ SEQUENCE 1443 AA; 161316 MW; A8C5997678040B88 CRC64;
Query Match 93.1%; Score 27; DB 2; Length 1443;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
|::|||

Db 1204 KIIFFA 1209
RESULT 54
Q5BI64 DROME PRELIMINARY; PRT; 1458 AA.
AC Q5BI64;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE LPI4662p.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; *Drosophila*.
OX NCBI_TaxID=7227;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkeley;
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Celnik S.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; E021360; AAX33508.1; -; mRNA.
DR InterPro; IPR001990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat.
SQ SEQUENCE 1458 AA; 161313 MW; 2D704C8970E541EC CRC64;
Query Match 93.1%; Score 27; DB 2; Length 1458;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
|::|||

Db 1219 KIIFFA 1224
RESULT 55
Q7KTZ4 DROME PRELIMINARY; PRT; 1503 AA.
AC Q7KTZ4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG11838-PB, isoform B.
GN Name=Ose93; ORFNames=CG11838;
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; *Drosophila*.
OX NCBI_TaxID=7227;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George K.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sidman-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster";
RA Science 287:2183-2195 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537569;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Hsara S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield G.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.B., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003589; AAS4635.1; -; Genomic DNA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
RW Repeat.

SQ SEQUENCE 1503 AA; 167957 MW; A0DD3F532590486 CRC64;
Query Match 93.1%; Score 27; DB 2; Length 1503;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
DB 1264 KIIFFA 1269
RESULT 56
Q8A6R7_BACTN PRELIMINARY; PRT; 1676 AA.
ID Q8A6R7;
AC Q8A6R7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Conserved protein, with weak BamHI domain.
GN Ordered locus names=BT1809;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=VPI-5482 / ATCC 29148;
RC MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis";
RL Science 299:2074-2076 (2003).
RL EMBL; AE016933; AA076916.1; -; Genomic DNA.
DR InterPro; IPR002048; EF-hand.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
RW Complete proteome.
SQ SEQUENCE 1676 AA; 193673 MW; 28065878C0F6C961 CRC64;
Query Match 93.1%; Score 27; DB 2; Length 1676;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
DB 1656 KIIFFA 1661
RESULT 57
Q9UC33_HUMAN PRELIMINARY; PRT; 33 AA.
ID Q9UC33;
AC Q9UC33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93024877; PubMed=1406936; DOI=10.1038/359325a0;
RA Seubert P., Vigo-Pelfrey C., Esch P., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids";
RL Nature 359:325-327 (1992).
RL HSP; Q16019; 1BA4.
DR HSP; Q16019; 1BA4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.

DR PRINTS; PR00204; BETAAMYLOID.
SQ SEQUENCE 33 AA; 3674 MW; BIDEFE2F4167ABD0 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 33;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

DB 16 KLVFFA 21

RESULT 58

Q56JJ6 GRAGR

ID Q56JJ6 GRAGR PRELIMINARY; PRT; 42 AA.

AC Q56JJ6

DT 10-MAY-2005 (TREMBlrel. 30, Created)

DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)

DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)

DE Amyloid beta protein (Fragment).

OS Grampus griseus (Risso's dolphin).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;

OC Odontoceti; Delphinidae; Grampus.

OX NCBI_TaxID=83653;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Gallego C., Sarasa M.;

RT "The molecular machinery of Alzheimer's disease in the dolphin.";

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY926589; AAX81918.1; -; mRNA.

FT NON_TER 1

FT NON_TER 42

SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

DB 16 KLVFFA 21

RESULT 59

Q56JJ7 TURTR

ID Q56JJ7 TURTR PRELIMINARY; PRT; 42 AA.

AC Q56JJ7

DT 10-MAY-2005 (TREMBlrel. 30, Created)

DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)

DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)

DE Amyloid beta protein (Fragment).

OS Tursiops truncatus (Atlantic bottle-nosed dolphin).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;

OC Odontoceti; Delphinidae; Tursiops.

OX NCBI_TaxID=9739;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Gallego C., Sarasa M.;

RT "The molecular machinery of Alzheimer's disease in the dolphin.";

RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY926588; AAX81917.1; -; mRNA.

FT NON_TER 1

FT NON_TER 42

SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

DB 16 KLVFFA 21

Db 16 KLVFFA 21

RESULT 60

Q7M088 CAVPO

ID Q7M088 CAVPO PRELIMINARY; PRT; 42 AA.

AC Q7M088

DT 01-MAR-2004 (TREMBlrel. 26, Created)

DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Beta-amyloid protein (Fragment).

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

OC Hystricognathi; Caviidae; Cavia.

OX NCBI_TaxID=10141;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=93290653; PubMed=7685598;

RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,

RA Kamiya H., Ohno M.;

RT "Receptor-mediated specific biological activity of a beta-amyloid

protein fragment for NK-1 substance p receptors.";

RL Biochem. Biophys. Res. Commun. 193:624-630(1993).

DR PIR; PNO512; PNO512.

DR HSP; Q16019; 11YT.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF03494; Beta-APP; 1.

DR PRINTS; PR00204; BETAAMYLOID.

FT NON_TER 1

FT NON_TER 42

SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

DB 16 KLVFFA 21

RESULT 61

Q8WZ99 HUMAN

ID Q8WZ99 HUMAN PRELIMINARY; PRT; 52 AA.

AC Q8WZ99

DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Amyloid protein (Fragment).

GN Name=APP;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=15201367; DOI=10.1136/jnnp.2003.010611;

RA Wakutani Y., Watanabe K., Adachi Y., Wada-Isoe K., Urakami K.,

RA Ninomiya H., Saido TC., Hashimoto T., Iwatsubo T., Nakashima K.;

RT "Novel amyloid precursor protein gene missense mutation (D678N) in

probable familial Alzheimer's disease.";

RL J. Neurol. Neurosurg. Psychiatr. 75:1039-1042(2004).

DR EMBL; AB066441; BAB71958.2; -; mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF03494; Beta-APP; 1.

DR PRINTS; PR00204; BETAAMYLOID.

FT NON_TER 1

```

FT NON TER 52 52
SQ SEQUENCE 52 AA; 5597 MW; 3F08B9E3C18011AD CRC64;

Query Match 89.7%; Score 26; DB 2; Length 52;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 16 KLVFPA 21

RESULT 62
Q82VGB NITEU
ID Q82VGB NITEU PRELIMINARY; PRT; 55 AA.
AC Q82VGB;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=NE1120;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 19718 /IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773 (2003).
DR EMBL; BX321859; CAD85031.1; -; Genomic_DNA.
DR InterPro; IPR009760; DUF1328.
DR Pfam; PF07043; DUF1328; 1.
DR PIRSF; PIRSF036466; UCP036466; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 55 AA; 5845 MW; 4F68395F53BE30BC CRC64;

Query Match 89.7%; Score 26; DB 2; Length 55;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 32 KLVFPA 37

RESULT 63
A4_URSMA
ID A4_URSMA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
OC Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;

MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
"Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the APP family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X56128; CAA39593.1; -; mRNA.
CC PIR; B60045; B60045.
CC HSP; P08592; INM0.
CC InterPro; IPR008155; A4_APP.
CC InterPro; IPR001255; Beta-APP.
CC PANTHER; PTHR10083:SP6; Beta-APP; 1.
CC Pfam; PF03494; Beta-APP; 1.
CC PRINTS; PR00204; BETAAMYLOID.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Amyloid; Transmembrane.
CC KW CHAIN <1 5 Soluble APP-beta (By similarity).
CC FT CHAIN 6 >57 CTF-alpha (By similarity).
CC FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
CC FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
CC FT CHAIN 46 >57 Gamma-CTF(59) (By similarity).
CC FT CHAIN 48 >57 Gamma-CTF(57) (By similarity).
CC FT TOPO_DOM <1 33 Extracellular (Potential).
CC FT TRANSMEM 34 57 Potential.
CC FT NON_TER 1 1
CC FT NON_TER 57 57
CC SQ SEQUENCE 57 AA; 6172 MW; 84209D8EBA82DFA CRC64;

Query Match 89.7%; Score 26; DB 1; Length 57;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
Db 21 KLVFPA 26

RESULT 64
A4_CANFA
ID A4_CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

```

RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC
CC
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC
CC -!- SIMILARITY: Belongs to the APP family.
CC
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X56125; CAA39590.1; -; mRNA.
DR HSSP; P08592; INMU.
DR Ensembl; ENSCAFG00000008557; Canis familiaris.
DR InterPro; IPR008155; A4 APP.
DR PANTHER; PTHR10083:SF6; Beta-APP.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT CHAIN 7 >58 CTF-alpha (By similarity).
FT CHAIN 7 46 Beta-amyloid protein 42 (By similarity).
FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
FT CHAIN 47 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 34 Extracellular (Potential).
FT TRANSMEM 35 58 Potential.
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 89.7%; Score 26; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 22 KLVFFA 27
|:|||||
|:|||||

RESULT 65
A4_RABIT
ID A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-WAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX Medline=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).

RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC
CC -!- SIMILARITY: Belongs to the APP family.
CC
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X56129; CAA39594.1; -; mRNA.
DR HSSP; P08592; INMJ.
DR InterPro; IPR008155; A4 APP.
DR PANTHER; PTHR10083:SF6; Beta-APP.
DR PRINTS; PR03494; Beta-APP; 1.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5
FT CHAIN 6 >58 Soluble APP-beta (By similarity).
FT CHAIN 6 47 CTF-alpha (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 42 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88BA82D CRC64;

Query Match 89.7%; Score 26; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 21 KLVFFA 26
|:|||||
|:|||||

RESULT 66
A4_SHEEP
ID A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-WAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX Medline=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).

```

CC CC -1- FUNCTION: Functional neuronal receptor which couples to
CC CC intracellular signaling pathway through the GTP-binding protein
CC CC G(O) (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -1- SIMILARITY: Belongs to the APP family.
CC CC -----
CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use as long as its content is in no way modified and this statement is not
CC CC removed.
CC CC -----
CC CC EMBL; X56130; CAA39595.1; -; mRNA.
CC CC HSSP; P08592; INMJ.
CC CC InterPro; IPR008155; A4_APP.
CC CC InterPro; IPR001255; Beta-APP.
CC CC PANTHER; PTHR10083:SF6; Beta-APP; 1.
CC CC Pfam; PF03494; Beta-APP; 1.
CC CC PRINTS; PR00204; BETAAMYLOID.
CC CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC CC KW Amyloid; Transmembrane.
CC FT CHAIN <1 5 Soluble APP-beta (By similarity).
CC FT CHAIN 6 >58 CTF-alpha (By similarity).
CC FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
CC FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
CC FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
CC FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
CC FT TOPO_DOM <1 33 Extracellular (Potential).
CC FT TRANSMEM 34 57 Potential.
CC FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
CC FT NON_TER 1 1
CC FT NON_TER 58 58
CC SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 89.7%; Score 26; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 21 KLVFFA 26
|:|:|:|:|

RESULT 67
A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain.
RX MEDLINE=9201079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: Functional neuronal receptor which couples to
CC CC intracellular signaling pathway through the GTP-binding protein

```

```

CC CC G(O) (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -1- SIMILARITY: Belongs to the APP family.
CC CC -----
CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use as long as its content is in no way modified and this statement is not
CC CC removed.
CC CC -----
CC CC EMBL; X56124; CAA39589.1; -; mRNA.
CC CC EMBL; X56126; CAA39591.1; -; mRNA.
CC CC HSSP; P08592; INMJ.
CC CC InterPro; IPR008155; A4_APP.
CC CC InterPro; IPR001255; Beta-APP.
CC CC PANTHER; PTHR10083:SF6; Beta-APP; 1.
CC CC Pfam; PF03494; Beta-APP; 1.
CC CC PRINTS; PR00204; BETAAMYLOID.
CC CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC CC KW Amyloid; Transmembrane.
CC FT CHAIN <1 6 Soluble APP-beta (By similarity).
CC FT CHAIN 7 >59 CTF-alpha (By similarity).
CC FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
CC FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
CC FT CHAIN 47 >59 Gamma-CTF(59) (By similarity).
CC FT CHAIN 49 >59 Gamma-CTF(57) (By similarity).
CC FT TOPO_DOM <1 34 Extracellular (Potential).
CC FT TRANSMEM 35 58 Potential.
CC FT TOPO_DOM 59 >59 Cytoplasmic (Potential).
CC FT NON_TER 1 1
CC FT NON_TER 59 59
CC SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 89.7%; Score 26; DB 1; Length 59;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 22 KLVFFA 27
|:|:|:|:|

RESULT 68
Q5WJL8_BACSK PRELIMINARY; PRT; 79 AA.
AC Q5WJL8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Molybdopterin converting factor subunit 1 Moab.
GN Name=moab; OrderedLocNames=ABC0898;
OS Bacillus clausii (strain KSM-K16).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=66692;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KSM-K16;
RA Takaki Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,
RA Kawai S., Ito S., Horikoshi K.;
RT "The complete genome sequence of the alkaliphilic Bacillus clausii
RT KSM-K16."
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006627; BAD63437.1; -; Genomic DNA.
DR GO; GO:0006777; P-Mo-molybdopterin cofactor biosynthesis; IEA.
DR GO; GO:0006790; P-sulfur metabolism; IEA.
DR InterPro; IPR010034; Moab.
DR InterPro; IPR003749; ThisS.
DR Pfam; PF02597; ThisS; 1.
DR TIGRFAMs; TIGR01682; moab; 1.
CC Complete proteome.
CC KW Complete proteome.
CC SQ SEQUENCE 79 AA; 8341 MW; 37F0600DEC90F10A CRC64;

```

```

Query Match      89.7%; Score 26; DB 2; Length 79;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   ||:||||
Db 3 KVLFFA 8

RESULT 69
O35463 CRIGR
ID O35463_CRIGR PRELIMINARY; PRT; 79 AA.
AC O35463;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alzheimer's amyloid beta protein (Fragment).
GN Namesbeta APP;
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetinae; Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sambamurti K., Pinnix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RE EMBL; AF030413; AAB86608.1; -; mRNA.
DR HSSP; P08592; 1NMJ
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAMYL0ID.
FT NON_TER 1
FT NON_TER 79
FT NON_TER 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 79;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   ||:||||
Db 36 KLVFFA 41

RESULT 70
MOAD_ECOLI
ID MOAD_ECOLI STANDARD; PRT; 81 AA.
AC P30748; P77422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Molybdopterine converting factor subunit 1 (MPT synthase subunit 1)
DE (Molybdopterine synthase subunit 1) (Molybdenum cofactor biosynthesis
DE protein D) (Molybdopterine converting factor small subunit).
GN Namesmoad; Synonyms=chlA4, chlM; OrderedLocusNames=b0784;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K12 / MC4100;
RX MEDLINE=93368423; PubMed=8361352;
RA Rivers S.L., McNaughton E., Blasco F., Giordano G., Boxer D.H.;
RT "Molecular genetic analysis of the moa operon of Escherichia coli K-12
RT required for molybdenum cofactor biosynthesis.";
RL Mol. Microbiol. 8:1071-1081(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [4]
RP PROTEIN SEQUENCE OF 1-15, CHARACTERIZATION, AND MASS SPECTROMETRY.
RX MEDLINE=93293873; PubMed=8514782;
RA Pitterle D.M., Rajagopalan K.V.;
RT "The biosynthesis of molybdopterine in Escherichia coli. Purification
RT and characterization of the converting factor.";
RL J. Biol. Chem. 268:13499-13505(1993).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS).
RX MEDLINE=20577273; PubMed=11135669; DOI=10.1038/83034;
RA Rudolph M.J., Wuebbens M.M., Rajagopalan K.V., Schindelin H.;
RT "Crystal structure of molybdopterine synthase and its evolutionary
RT relationship to ubiquitin activation.";
RL Nat. Struct. Biol. 8:42-46(2001).
CC -|- FUNCTION: Converts molybdopterine precursor Z into molybdopterine.
CC This requires the incorporation of two sulfur atoms into precursor
CC Z to generate a dithiolene group. The sulfur atoms are provided by
CC the active form of the small subunit, whose activation involves
CC the acquisition of sulfur and the activity of moeB/chlN.
CC -|- PATHWAY: Molybdenum cofactor biosynthesis.
CC -|- SUBUNIT: Heterodimer of 2 moad subunits and 2 moeB subunits.
CC -|- INTERACTION:
CC P30749:moae; NbExp=1; IntAct=EBI-554366, EBI-554376;
CC POA7K2:rpIL; NbExp=1; IntAct=EBI-554366, EBI-543702;
CC -|- INDUCTION: By anaerobiosis, repressed by the molybdenum cofactor.
CC -|- MASS SPECTROMETRY: MW=8773.6; MW_ERR=0.2; METHOD=Electrospray;
CC RANGE=1-81; NOTE=Ref. 4.
CC -|- SIMILARITY: Belongs to the moad family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X70420; CAA49864.1; -; Genomic DNA.
CC EMBL; U00096; AAC73871.1; -; Genomic DNA.
CC EMBL; D90716; BAA35442.1; -; Genomic DNA.
CC FIR; H64814; H64814.
CC PDB; IFM0; X-ray; D=1-81.
CC PDB; IFM9; X-ray; D=1-81.
CC PDB; LJW9; X-ray; D=1-81.
CC PDB; LJWA; X-ray; D=1-81.
CC PDB; LJWB; X-ray; D=1-81.
CC PDB; LNV1; X-ray; D=3-81.
CC IntAct; P30748; -.
CC EchoBase; EBI1554; -.
CC EcoGene; EGI11597; moad.
CC InterPro; IPR010034; Moad.
CC InterPro; IPR003749; This.
CC Pfam; PF02597; This; 1.
CC TIGRFAMs; TIGR01682; moad; 1.
CC 3D-structure; Complete proteome; Direct protein sequencing;
KW

```

Molybdenum cofactor biosynthesis.
 KW CONFLICT 9 Q -> E (in Ref. 4).
 FT CONFLICT 45 A -> R (in Ref. 1).
 FT STRAND 2
 FT HELIX 8
 FT STRAND 18
 FT STRAND 27
 FT STRAND 28
 FT TURN 37
 FT HELIX 40
 FT TURN 46
 FT TURN 48
 FT TURN 52
 FT TURN 56
 FT STRAND 58
 FT TURN 62
 FT STRAND 65
 FT TURN 68
 FT STRAND 71
 SQ SEQUENCE 81 AA; 8758 MW; 1E0A440520EE82F4 CRC64;
 Query Match 89.7%; Score 26; DB 1; Length 81;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 ||:||||
 Db 3 KVLFFA 8

RESULT 71
 Q9APP7_9BACT PRELIMINARY; PRT; 81 AA.
 AC Q9APP7;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative molybdenum cofactor biosynthesis protein D.
 GN Name=moaD;
 OS uncultured bacterium pCoshE1.
 OC Bacteria; environmental samples.
 OX NCBI_TaxID=143796;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20575196; PubMed=11133432; DOI=10.1128/AEM.67.1.89-99.2001;
 RA Entcheva P., Liebl W., Johann A., Hartsch T., Streit W.R.;
 RT "Direct cloning from enrichment cultures, a reliable strategy for
 isolation of complete operons and genes from microbial consortia.";
 RL Appl. Environ. Microbiol. 67:89-99(2001).
 DR EMBL; AF250774; AAG60573.1; -; Genomic_DNA.
 DR HSSP; P30748; 1JW9.
 DR SMR; Q9APP7; 1-81.
 DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
 DR GO; GO:0006790; P:sulfur metabolism; IEA.
 DR InterPro; IPR010034; MoaD.
 DR InterPro; IPR003749; This.
 DR Pfam; PF02597; This; 1.
 DR TIGRFAMs; TIGR01682; moaD; 1.
 SQ SEQUENCE 81 AA; 8739 MW; 21361C1FCA3AA24C CRC64;

Query Match 89.7%; Score 26; DB 2; Length 81;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 ||:||||
 Db 3 KVLFFA 8

RESULT 72
 Q57RP2_SALCH PRELIMINARY; PRT; 81 AA.
 AC Q57RP2;
 ID Q57RP2_SALCH PRELIMINARY; PRT; 81 AA.

DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Molybdopterin biosynthesis protein.
 GN Name=moaD; OrderedLocusNames=SC0803;
 OS Salmonella cholerae-suis (Salmonella enterica).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=591;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SC-B67;
 RX PubMed=15781495;
 RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
 Wang H.-S., Lee Y.-S.;
 RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
 highly invasive and resistant zoonotic pathogen.";
 RL Nucleic Acids Res. 33:1690-1698(2005).
 DR EMBL; AS017220; AAX64709.1; -; Genomic_DNA.
 DR KW Complete proteome.
 SQ SEQUENCE 81 AA; 8772 MW; 5821119685621426 CRC64;
 Query Match 89.7%; Score 26; DB 2; Length 81;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 ||:||||
 Db 3 KVLFFA 8

RESULT 73
 Q65TTO_MANSN PRELIMINARY; PRT; 81 AA.
 ID Q65TTO_MANSN PRELIMINARY; PRT; 81 AA.
 AC Q65TTO;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE MoaD protein.
 GN Name=moaD; OrderedLocusNames=MS1023;
 OS Mannheimia succiniciproducens (strain MBEL55E).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Mannheimia.
 OX NCBI_TaxID=221988;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15378067; DOI=10.1038/nbt1010;
 RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
 Kim C.H., Jeong H., Hur C.G., Kim J.J.;
 RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
 succiniciproducens.";
 RL Nat. Biotechnol. 22:1275-1281(2004).
 DR EMBL; AE016827; AAC37630.1; -; Genomic DNA.
 DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
 DR GO; GO:0006790; P:sulfur metabolism; IEA.
 DR InterPro; IPR010034; MoaD.
 DR InterPro; IPR003749; This.
 DR Pfam; PF02597; This; 1.
 DR TIGRFAMs; TIGR01682; moaD; 1.
 DR KW Complete proteome.
 SQ SEQUENCE 81 AA; 8617 MW; E529ED840985D661 CRC64;
 Query Match 89.7%; Score 26; DB 2; Length 81;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 ||:||||
 Db 3 KVLFFA 8

RESULT 74
 Q7N6P4_PHOLL

ID Q7N6P4 PHOLL PRELIMINARY; PRT; 81 AA.
AC Q7N6P4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Molybdopterin.
GN Name=moaD; OrderedLocusNames=plu1501;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Ruenliok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Signier P., Vincent R., Wingate V.,
RA Zouline M., Glaeser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RL Nat. Biotechnol. 21:1307-1313 (2003).
DR EMBL; BX571864; CAE13794.1; -; Genomic_DNA.
DR HSSP; P30748; 1JW9.
DR PhotoList; plu1501; -.
DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
DR GO; GO:0006790; P:sulfur metabolism; IEA.
DR InterPro; IPR010034; Moad.
DR InterPro; IPR003749; This.
DR Pfam; PF02597; This; 1.
DR TIGRFAMS; TIGR01682; moad; 1.
KW Complete proteome.
SQ SEQUENCE 81 AA; 8886 MW; 6646B5932531F136 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 81;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
||:||||
DB 3 KVLFFA 8

RESULT 75
Q8D897 VIBVU
ID Q8D897 VIBVU PRELIMINARY; PRT; 81 AA.
AC Q8D897;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Molybdenum cofactor biosynthesis protein D.
GN OrderedLocusNames=VVI3085;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016807; AA011408.1; -; Genomic_DNA.
DR HSSP; P30748; 1JW9.
DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
DR GO; GO:0006790; P:sulfur metabolism; IEA.
DR InterPro; IPR010034; Moad.
DR InterPro; IPR003749; This.
DR Pfam; PF02597; This; 1.
DR TIGRFAMS; TIGR01682; moad; 1.
KW Complete proteome.

SQ SEQUENCE 81 AA; 8731 MW; 4BE52C0ABDE06418 CRC64;
Query Match 89.7%; Score 26; DB 2; Length 81;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
||:||||
DB 3 KVLFFA 8

Search completed: December 29, 2005, 17:47:26
Job time : 82.1936 secs

103	25	86.2	512	2	T19806	hypothetical prote	176	24	82.8	241	2	G71045	hypothetical prote
104	25	86.2	572	2	H96685	probable AMP-bindi	177	24	82.8	245	2	T49889	zinc finger transac
105	25	86.2	604	1	QXXL5M	NADH2 dehydrogenas	178	24	82.8	246	2	E90309	hypothetical prote
106	25	86.2	620	2	H69382	ABC transporter, A	179	24	82.8	248	2	F71849	amino acid ABC tra
107	25	86.2	646	2	AD3409	ABC transporter AT	180	24	82.8	248	2	C54666	glutamine transpor
108	25	86.2	657	2	G86590	exinuclease ABC su	181	24	82.8	254	2	T28170	hypothetical prote
109	25	86.2	657	2	B72034	exinuclease ABC,	182	24	82.8	256	2	AC1561	conserved hypotHet
110	25	86.2	657	2	H90523	exinuclease ABC s	183	24	82.8	256	2	AE1203	conserved hypotHet
111	25	86.2	660	1	A28153	gelatinase A (EC 3	184	24	82.8	262	2	D88930	protein R11G11.10
112	25	86.2	662	2	S70365	gelatinase A (EC 3	185	24	82.8	262	2	A81056	conserved hypotHet
113	25	86.2	662	2	A42496	gelatinase A (EC 3	186	24	82.8	263	2	C89887	hypothetical prote
114	25	86.2	662	2	S34780	gelatinase A (EC 3	187	24	82.8	269	2	A81820	conserved hypotHet
115	25	86.2	663	1	S46492	gelatinase A (EC 3	188	24	82.8	276	2	S05343	NAD ADP-ribosyltra
116	25	86.2	676	2	D81654	exinuclease ABC c	189	24	82.8	278	1	S01065	probable dehydroge
117	25	86.2	681	2	T39814	hypothetical prote	190	24	82.8	281	2	F69400	2-deoxy-D-gluconat
118	25	86.2	774	2	F96639	protein T1P9.8 [im	191	24	82.8	283	2	T20734	hypothetical prote
119	25	86.2	774	2	T34496	hypothetical prote	192	24	82.8	286	2	AI3105	hypothetical prote
120	25	86.2	804	2	G71546	probable DNA gyras	193	24	82.8	287	2	AI2038	carboxyphosphonoe
121	25	86.2	812	2	H87386	hypothetical prote	194	24	82.8	300	2	F83621	hypothetical prote
122	25	86.2	1119	2	A86340	protein F2D10.24 [195	24	82.8	301	2	C98181	sitC protein (AF12
123	25	86.2	1147	1	I53165	nitric-oxide synth	196	24	82.8	309	2	T35801	probable polyamine
124	25	86.2	1147	1	I58575	nitric-oxide synth	197	24	82.8	311	2	D64240	methionyl-tRNA for
125	25	86.2	1147	1	S38253	nitric-oxide synth	198	24	82.8	315	2	S59779	probable membrane
126	25	86.2	1147	1	S47647	nitric-oxide synth	199	24	82.8	323	2	AC2119	hypothetical prote
127	25	86.2	1147	2	JCS029	nitric-oxide synth	200	24	82.8	325	1	B40358	NADH2 dehydrogenas
128	25	86.2	1147	2	JCS028	nitric-oxide synth	201	24	82.8	330	2	T29640	mitochondrial carr
129	25	86.2	1147	2	JCS027	nitric-oxide synth	202	24	82.8	331	1	DN0BU1	NADH2 dehydrogenas
130	25	86.2	1147	2	S65440	nitric-oxide synth	203	24	82.8	335	2	A72289	oligopeptide ABC t
131	25	86.2	1324	2	T01508	mismatch repair en	204	24	82.8	337	2	AG0963	hypothetical prote
132	25	86.2	2241	2	T02857	conserved hypotHet	205	24	82.8	337	2	T48341	hypothetical prote
133	25	86.2	3623	2	T08618	intrinsic factor-B	206	24	82.8	341	2	S73685	hypothetical prote
134	25	86.2	4152	2	T31102	filamentous hemagg	207	24	82.8	342	2	AE2238	methionyl-tRNA for
135	25	86.2	4919	2	T31105	hypothetical prote	208	24	82.8	344	2	E83562	N-acetyl-gamma-glu
136	24	82.8	20	2	JU0030	hypothetical prote	209	24	82.8	345	2	A81837	hypothetical prote
137	24	82.8	20	2	A99091	hypothetical prote	210	24	82.8	352	2	E90175	NADH dehydrogenase
138	24	82.8	62	2	E64530	hypothetical prote	211	24	82.8	352	2	AB3079	transcription regu
139	24	82.8	68	2	C71970	hypothetical prote	212	24	82.8	352	2	G98207	hypothetical prote
140	24	82.8	77	2	AC1381	preprotein translo	213	24	82.8	363	2	S56273	probable membrane
141	24	82.8	91	2	H82370	conserved hypotHet	214	24	82.8	379	2	S23443	hypothetical prote
142	24	82.8	95	2	AG0277	probable phage-rel	215	24	82.8	380	2	T29248	hypothetical prote
143	24	82.8	106	2	AG2113	hypothetical prote	216	24	82.8	380	2	F86038	probable LPS biosy
144	24	82.8	108	2	C64516	hypothetical prote	217	24	82.8	380	2	E91191	probable LPS biosy
145	24	82.8	138	2	I47205	Ig heavy chain var	218	24	82.8	382	2	AI1427	efflux proteins ho
146	24	82.8	141	1	B70457	gliding motility p	219	24	82.8	383	2	AF1893	hydrogenase expres
147	24	82.8	141	2	I47177	Ig H-chain - pig {	220	24	82.8	385	2	T31493	hypothetical prote
148	24	82.8	143	1	A44397	cofilin - yeast {S	221	24	82.8	393	2	D86168	hypothetical prote
149	24	82.8	144	2	D72219	conserved hypotHet	222	24	82.8	400	2	H90009	hypothetical prote
150	24	82.8	147	2	H82313	hypothetical prote	223	24	82.8	401	2	T44831	probable emulsan r
151	24	82.8	163	2	F86878	hypothetical prote	224	24	82.8	409	2	S29124	membrane glycoprot
152	24	82.8	169	2	AF2630	hypothetical prote	225	24	82.8	415	2	C71467	probable tyrosine
153	24	82.8	171	2	C71244	hypothetical prote	226	24	82.8	416	2	I64039	hypothetical prote
154	24	82.8	174	2	G81349	periplasmic nitrat	227	24	82.8	422	2	E82904	hypothetical prote
155	24	82.8	179	2	AB0652	probable intracell	228	24	82.8	429	2	T28950	hypothetical prote
156	24	82.8	179	2	T45503	hypothetical prote	229	24	82.8	440	1	B29413	ubiquinol-cytochro
157	24	82.8	179	2	S07799	probable membrane	230	24	82.8	442	2	T39683	ubiquitin-like protei
158	24	82.8	179	2	B90848	probable membrane	231	24	82.8	448	2	A86534	integral membrane
159	24	82.8	179	2	A85706	probable membrane	232	24	82.8	448	2	A72089	integral membrane
160	24	82.8	179	2	S70898	intracellular sept	233	24	82.8	451	2	A81581	ABC transporter, p
161	24	82.8	184	2	AH3581	alkyl hydroperoxid	234	24	82.8	451	2	G71561	probable integral
162	24	82.8	193	2	A82435	conserved hypotHet	235	24	82.8	452	2	H84016	hypothetical prote
163	24	82.8	195	2	T22032	hypothetical prote	236	24	82.8	455	2	H69837	conserved hypotHet
164	24	82.8	197	2	G83597	conserved hypotHet	237	24	82.8	456	2	D95384	protein imported
165	24	82.8	210	2	C97260	probable membrane	238	24	82.8	463	2	S52754	aromatic amino aci
166	24	82.8	210	2	S67140	probable membrane	239	24	82.8	466	2	A55179	hypothetical prote
167	24	82.8	210	2	B84217	hypothetical prote	240	24	82.8	466	2	B97030	LPS glycosyltransf
168	24	82.8	216	2	B88065	protein T16A1.3 [i	241	24	82.8	467	2	H98045	hypothetical prote
169	24	82.8	219	1	A35617	HDEL receptor ERD2	242	24	82.8	471	2	T41602	hypothetical prote
170	24	82.8	219	2	A75004	hypothetical prote	243	24	82.8	485	2	B84394	argininosuccinate
171	24	82.8	221	2	G72322	glutaredoxin-relat	244	24	82.8	490	2	A35312	potassium channel
172	24	82.8	222	2	T47768	hypothetical prote	245	24	82.8	500	2	B83364	pyoverdine biosynt
173	24	82.8	225	2	A90260	conserved hypotHet	246	24	82.8	500	2	F83418	sodium/proton anti
174	24	82.8	238	2	E75169	hypothetical prote	247	24	82.8	503	2	T34694	probable cationic
175	24	82.8	240	2	G70303	cytochrome c - Aqu	248	24	82.8	507	2	F97765	hypothetical prote

A;Cross-references: UNIPROT:Q9PHV5; UNIPARC:UPI00000C217E; GB:AL139075; GB:AL1111168; NID
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: CJ0560

Query Match 100.0%; Score 29; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||||
Db 313 KVVFFA 318

RESULT 4
A43271
nitric-oxide synthase (EC 1.14.13.39), calmodulin-independent - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: A43271; A42166; JN0458; A46186
R;Xie, Q.; Cho, H.J.; Calaycay, J.; Mumford, R.A.; Swiderek, K.M.; Lee, T.D.; Ding, A.;
Science 256, 225-228, 1992
A;Title: Cloning and characterization of inducible nitric oxide synthase from mouse macrophages
A;Reference number: A43271; MUID:92229444; PMID:1373522
A;Accession: A43271
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1144 <XIE>
A;Cross-references: UNIPROT:P29477; UNIPARC:UPI000000D36; GB:M87039; NID:g198406; PIDN:
R;Byons, C.R.; Orloff, G.J.; Cunningham, J.M.
J. Biol. Chem. 267, 6370-6374, 1992
A;Title: Molecular cloning and functional expression of an inducible nitric oxide synthase
A;Reference number: A42166; MUID:92210618; PMID:1372907
A;Accession: A42166
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1144 <LYO>
A;Cross-references: UNIPARC:UPI000000D36; GB:M84373; NID:g200095; PIDN:AAA39834.1; PID:
R;Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.
Biochem. Biophys. Res. Commun. 131, 767-774, 1993
A;Title: Hepatocytes and macrophages express an identical cytokine inducible nitric oxide
A;Reference number: JN0457; MUID:93221515; PMID:7682072
A;Accession: JN0458
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-278, F', 280-682, H', 684-937, 939-1144 <WOO>
A;Cross-references: UNIPARC:UPI000017223A
R;Lowenstein, C.J.; Glatt, C.S.; Bredt, D.S.; Snyder, S.H.
Proc. Natl. Acad. Sci. U.S.A. 89, 6711-6715, 1992
A;Title: Cloned and expressed macrophage nitric oxide synthase contrasts with the brain
A;Reference number: A46186; MUID:92357701; PMID:1379716
A;Accession: A46186
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-190, V', 192-765, P', 767-843, G', 845-1144 <LOW>
A;Cross-references: UNIPARC:UPI000017223B; GB:M92649; NID:g200109
A;Experimental source: BALB/c, RAW 264.7 cells, macrophage
A;Note: sequence extracted from NCBI backbone (NCBIP:113541)
C;Genetics:
A;Gene: NOS
C;Function:
A;Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferritinoprotein reduct
C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal
F;533-1121/Domain: NADPH-ferritinoprotein reductase homology <FEH>
F;535-671/Domain: flavodoxin homology <FLX>
F;194/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 1; Length 1144;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
S23094
beta-amyloid protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C;Accession: S23094
R;Kojima, S.; Omori, M.

QY 1 KVVFFA 6
|||||
Db 514 KVVFFA 519

RESULT 5
F70399
hydrogenase expression/formaton protein HypD - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: F70399
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovi
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70399
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-380 <AOF>
A;Cross-references: UNIPROT:O67225; UNIPARC:UPI0000056543; GB:AE000726; NID:g2983612; PI
A;Experimental source: strain VF5
C;Genetics:
A;Gene: hypD
C;Superfamily: [Nipel]-hydrogenase maturation factor, HypD type

Query Match 96.6%; Score 28; DB 2; Length 380;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||||
Db 141 KVVFFA 146

RESULT 6
F71039
hypothetical protein PH1606 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Oct-2004
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: F71039
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-447 <KAW>
A;Cross-references: UNIPROT:O59243; UNIPARC:UPI00000630DE; GB:AP000006; NID:g3236133; P
A;Experimental source: strain OR3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1606
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1142

Query Match 93.1%; Score 27; DB 2; Length 447;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||||
Db 207 KIIFFA 212

FEBS Lett. 304, 57-60, 1992

A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A;Reference number: S23094; MUID:92316198; PMID:1618299
A;Accession: S23094
A;Molecule type: protein
A;Residues: 1-33 <KQ>
A;Cross-references: UNIPARC:UPI00001777EB
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 89.7%; Score 26; DB 2; Length 33;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 21 KLVFFA 26

RESULT 8

PN0512
beta-amyloid protein - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: PN0512
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment
A;Reference number: PN0512; MUID:93290653; PMID:7685598
A;Accession: PN0512
A;Molecule type: protein
A;Residues: 1-42 <SH>
A;Cross-references: UNIPROT:Q7M088; UNIPARC:UPI00000315E8
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid

Query Match 89.7%; Score 26; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 9

A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: A60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: A60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56125
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 21 KLVFFA 26

RESULT 10

F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: F60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: F60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:gl895; PIDN:CAA39592.1; PID
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 21 KLVFFA 26

RESULT 11

D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: D60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: D60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56124
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 21 KLVFFA 26

RESULT 12

E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C;Species: Ovis sp. (sheep)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: E60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: E60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56130
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 89.7%; Score 26; DB 2; Length 57;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 21 KLVFFA 26

C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 89.7%; Score 26; DB 2; Length 81;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 KVVFFA 6
||:||||
DB 3 KVLFFA 8

RESULT 16
A82251
molybdenum cofactor biosynthesis protein D VC1027 [imported] - Vibrio cholerae
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 16-Aug-2004
C:Accession: A82251
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson
R:Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; S
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholera
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: A82251
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-81 <HEI>
A:Cross-references: UNIPROT:Q9KT78; UNIPARC:UPI00000C3E5B; GB:AE004184; GB:AE00
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1027
A:Map position: 1
C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein
F:81/Modified site: 1-thioglycine (Gly) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 81;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 KVVFFA 6
||:||||
DB 3 KVLFFA 8

RESULT 17
G85586
molybdopterin biosynthesis [imported] - Escherichia coli (strain O157:H7, subs
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: G85586
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.
Nature 406, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85586
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-81 <STO>
A:Cross-references: UNIPROT:Q8X807; UNIPARC:UPI00000D09BF; GB:AE005174; NID:gi2
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: moaD
C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 89.7%; Score 26; DB 2; Length 81;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

RESULT 18

H64814
molybdopterin biosynthesis protein D chain [validated] - Escherichia coli (strain K-12)
A:Alternate names: moaD protein; molybdopterin-converting factor 10K chain; molybdopterin; C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence revision 17-Sep-1997 #text_change 05-Oct-2004
C:Accession: H64814; S35001; A46585; S31882 #text_change 05-Oct-2004
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: H64814

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-81 <BLAT>

A:Cross-references: UNIPROT:P30748; UNIPARC:UPI00001116DF; GB:AE000181; GB:U00096; NID:9

A:Experimental source: strain K-12, substrain MGL655

R:Rivers, S.L.; McNairn, E.; Biasco, F.; Giordano, G.; Boxer, D.H.

Mol. Microbiol. 8, 1071-1081, 1993

A:Title: Molecular genetic analysis of the moa operon of Escherichia coli K-12 required

A:Reference number: S34998; MUID:93368423; PMID:8361352

A:Accession: S35001

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-44, 'R', '46-81 <RIV>

A:Cross-references: UNIPARC:UPI000016F2FD; EMBL:X70420; NID:942007; PIDN:CAA49864.1; PID

A:Experimental source: strain K12

R:Pitterle, D.M.; Rajagopalan, K.V.

J. Biol. Chem. 268, 13495-13505, 1993

A:Title: The biosynthesis of molybdopterin in Escherichia coli. Purification and character

A:Reference number: A46585; MUID:93293873; PMID:8514782

A:Accession: A46585

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8, 'E', 10-15 <PIT>

A:Cross-references: UNIPARC:UPI0000178EC3

A:Note: sequence extracted from NCBI backbone (NCBIP:134491)

C:Genetics:

A:Gene: moaD

A:Map position: 17, 7 min

C:Complex: heterodimer with D chain (PIR:S31983) [validated, MUID:93293873]

C:Function:

A:Description: required for the addition of the Mo-binding dithiolene group to a molybd

C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein

C:Keywords: heterodimer; molybdopterin biosynthesis

F:81/Modified site: 1-thioglycine (Gly) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 81;

Best Local Similarity 83.3%; Pred. No. 32;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

Db 3 KVLFFA 8

RESULT 19

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Sep-1993 #sequence revision 19-Oct-1995 #text_change 19-Oct-1995

C:Accession: PQ0438; C60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 189, 905-911, 1992

A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor

A:Reference number: PQ0438; MUID:93075180; PMID:1445331

A:Accession: PQ0438

A:Molecule type: DNA

A:Residues: 1-82 <DAV>

A:Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: C60045

A:Molecule type: mRNA

A:Residues: 12-68 <JOH>

A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56129

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 89.7%; Score 26; DB 2; Length 82;

Best Local Similarity 83.3%; Pred. No. 32;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

Db 32 KLVFFA 37

RESULT 20

AC0598

molybdopterin converting factor, chain 1 [imported] - Salmonella enterica subsp. enteri

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A:Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 16-Aug-2004

C:Accession: AC0598

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar

S.; Moutle, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AC0598

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-83 <PAR>

A:Cross-references: UNIPARC:UPI000005A0EA; GB:AL513382; PIDN:CAD05253.1; PID:916502022,

C:Genetics:

A:Gene: STY0839

C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 89.7%; Score 26; DB 2; Length 83;

Best Local Similarity 83.3%; Pred. No. 33;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

Db 5 KVLFFA 10

RESULT 21

T06645

hypothetical protein T20K18.220 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T06645

R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirks, W.; Stiekema, W.; Bancroft, I.; Mc

submitted to the Protein Sequence Database, April 1999

A:Reference number: Z15790

A:Accession: T06645

A:Molecule type: DNA

A:Residues: 1-152 <BEV>

A:Cross-references: UNIPROT:Q9ST29; UNIPARC:UPI000000A0722; EMBL:AL049640; GSPDB:GN000662

A:Experimental source: cultivar Columbia; BAC clone T20K18

C:Genetics:

A:Gene: AtSP:T20K18.220

A:Map position: 4

A:Introns: 87/3; 109/3

C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match 89.7%; Score 26; DB 2; Length 152;

Best Local Similarity 83.3%; Pred. No. 58;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:|||||
Db 9 KLVFFA 14

RESULT 22
B90157
hypothetical protein SSO0168 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: B90157
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, E.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: B90157
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-193 <KUR>
A:Cross-references: UNIPROT:Q980V9; UNIPARC:UPI00000641A8; GB:AE006641; NID:gl3813299; F
C:Genetics:
A:Gene: SSO0168

Query Match 89.7%; Score 26; DB 2; Length 193;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:|||||
Db 117 KVVFFA 122

RESULT 23
B81256
phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / phosphoribosyl-ATP diphosphatase (EC 3
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81256
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: B81256
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-207 <PAR>
A:Cross-references: UNIPROT:Q9PM71; UNIPARC:UPI000012C76D; GB:AL1139079; GB:AL1111168; NID
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: hisI; Cj1604
C:Superfamily: hisI bifunctional enzyme; hisI bifunctional enzyme homology; hisI protein
C:Keywords: hydrolase

Query Match 89.7%; Score 26; DB 2; Length 207;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:|||||
Db 51 KVVFFS 56

RESULT 24
H85138
hypothetical protein AT4g12900 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85138

R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: H85138
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-231 <STO>
A:Cross-references: UNIPROT:Q9SV79; UNIPARC:UPI00000A7E0E; GB:NC_001368; NID:g7267992; I
C:Genetics:
A:Gene: AT4g12900
A:Map position: 4
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match 89.7%; Score 26; DB 2; Length 231;
Best Local Similarity 83.3%; Pred. No. 85;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:|||||
Db 12 KLVFFA 17

RESULT 25
D69355
hypothetical protein AF0844 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: D69355
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: D69355
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-293 <KLS>
A:Cross-references: UNIPROT:O29414; UNIPARC:UPI0000056F64; GB:AE001046; GB:AE000782; NI

Query Match 89.7%; Score 26; DB 2; Length 293;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:|||||
Db 140 KVLFFA 145

RESULT 26
H90318
glycerol kinase (glpK-1) [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: H90318
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, E.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: H90318
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-294 <KUR>
A:Cross-references: UNIPROT:Q97XW2; UNIPARC:UPI0000064B6; GB:AE006641; NID:gl3814829; I
C:Genetics:
A:Gene: glpK-1

Query Match 89.7%; Score 26; DB 2; Length 294;

Best Local Similarity 83.3%; Pred. No. 1.1e+02; DB 2; Length 300;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:|:|
Db 184 KVVFFA 189

RESULT 27

T26245

hypothetical protein W06G6.6 - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T26245

R;McMurray, A.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z20180

A;Accession: T26245

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-300 <WIL>

A;Cross-references: UNIPROT:Q9XU61; UNIPARC:UPI0000061208; EMBL:Z83129; PIDN: CAB05641.1;

A;Experimental source: clone W06G6

C;Genetics:

A;Gene: CESP:W06G6.6

A;Map position: 5

A;Introns: 171/2; 204/2

Query Match

89.7%; Score 26; DB 2; Length 300;

Best Local Similarity 83.3%; Pred. No. 1.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

|:|:|

Db 281 KVVFFA 286

RESULT 28

B82822

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 [similarity] - *Xylella fastidiosa*C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: B82822

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: B82822

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-330 <SIM>

A;Cross-references: UNIPROT:Q9PGI8; UNIPARC:UPI00000C2381; GB:AE003884; GB:AE003849; NID

A;Experimental source: strain 985c

R;Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrez, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak

A;Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsuchino, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF0312

C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-b

C;Keywords: membrane-associated complex; NAD; oxidoreductase

Query Match 89.7%; Score 26; DB 2; Length 330;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:|:|
Db 275 KVVFFA 280

RESULT 29

B72402

UDP-N-acetylglucosamine-N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-a

C;Species: *Thermotoga maritima*

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: B72402

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: B72402

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-339 <ARN>

A;Cross-references: UNIPROT:Q9WY74; UNIPARC:UPI0000012F9EB; GB:AE001707; GB:AE0000512; NI

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM0232

C;Superfamily: murG protein

Query Match

89.7%; Score 26; DB 2; Length 339;

Best Local Similarity 83.3%; Pred. No. 1.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

|:|:|

Db 32 KVVFFA 37

RESULT 30

T26247

hypothetical protein W06G6.8 - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T26247

R;McMurray, A.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z20180

A;Accession: T26247

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-349 <WIL>

A;Cross-references: UNIPROT:Q9XU59; UNIPARC:UPI0000061209; EMBL:Z83129; PIDN: CAB05643.1

A;Experimental source: clone W06G6

C;Genetics:

A;Gene: CESP:W06G6.8

A;Map position: 5

A;Introns: 172/2; 210/3; 247/2

Query Match

89.7%; Score 26; DB 2; Length 349;

Best Local Similarity 83.3%; Pred. No. 1.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

|:|:|

Db 324 KVVFFA 329

RESULT 31

T48903

wax synthase [imported] - *Simmondsia chinensis*C;Species: *Simmondsia chinensis*

```

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T48903
R:Lardizabal, K.D.; Metz, J.G.; Sakamoto, T.; Hutton, W.C.; Pollard, M.R.; Lassner, M.W.
Plant Physiol. 122, 645-655, 2000
A>Title: Purification of a jojoba embryo wax synthase, cloning of its cDNA and production
A:Reference number: Z25002
C:Accession: T48903
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <LAR>
A:Cross-references: UNIPROT:Q9XGV6; UNIPARC:UPI00000A1C81; EMBL:AF149919; PIDN:AAD38041.

Query Match      89.7%; Score 26; DB 2; Length 352;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFFA 6
       |:|||||
Db      135 KLVFFFA 140

RESULT 32
T48008
hypothetical protein T17J13.120 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
C:Accession: T48008
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24482
C:Accession: T48008
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-428 <RIE>
A:Cross-references: UNIPROT:Q9M1Q8; UNIPARC:UPI00000488B7; EMBL:AL1138651
A:Experimental source: cultivar Columbia; BAC clone T17J13
C:Genetics:
A:Map position: 3
A:Introns: 137/3
A>Note: T17J13.120
C:Superfamily: N-hydroxycinnamoyl/benzoyl transferase

Query Match      89.7%; Score 26; DB 2; Length 428;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFFA 6
       |:|||||
Db      271 KLVFFFA 276

RESULT 33
B28988
hypothetical protein F1696 (photosynthetic gene cluster) - Rhodobacter capsulatus
C:Species: Rhodobacter capsulatus
C>Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 09-Jul-2004
C:Accession: B28988
R:Youvan, D.C.; Bylina, E.J.; Alberti, M.; Begusch, H.; Hearst, J.E.
Cell 37, 949-957, 1984
A>Title: Nucleotide and deduced polypeptide sequences of the photosynthetic reaction-
A:Reference number: A90850; MUID:84259352; PMID:6744416
C:Accession: B28988
A:Molecule type: DNA
A:Residues: 1-477 <YOU>
A:Cross-references: UNIPROT:P26176; UNIPARC:UPI000013BE54; GB:X01183

Query Match      89.7%; Score 26; DB 2; Length 477;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFFA 6
       |:|||||
Db      349 KVLFFFA 354

```

```

RESULT 34
A81548
hypothetical protein CP0705 [imported] - Chlamydophila pneumoniae (strain AR39)
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: A81548
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
Nucleic Acids Res. 28, 1397-1406, 2000
A>Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
C:Accession: A81548
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-520 <REA>
A:Cross-references: UNIPROT:Q9K207; UNIPARC:UPI00000CCCC9E; GB:AE002229; GB:AE002161; NT1
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0705

Query Match      89.7%; Score 26; DB 2; Length 520;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFFA 6
       |:|||||
Db      381 RVVFFFA 386

RESULT 35
F86499
hypothetical protein CPJ0069 [imported] - Chlamydophila pneumoniae (strain J138)
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86499
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Res. 28, 2311-2314, 2000
A>Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
C:Accession: F86499
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-594 <STO>
A:Cross-references: UNIPROT:Q9JSK0; UNIPARC:UPI00000CCCC9F; GB:BA000008; NID:g8978443; PI
A:Experimental source: strain J138
C:Genetics:
A:Gene: CPJ0069

Query Match      89.7%; Score 26; DB 2; Length 594;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFFA 6
       |:|||||
Db      455 RVVFFFA 460

RESULT 36
F72237
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: F72237
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.,
C.M.
Nature 399, 323-329, 1999
A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A:Reference number: A72200; MUID:99287316; PMID:10360571
C:Accession: F72237
A>Status: preliminary

```

A:Molecule type: DNA
A:Residues: 1-603 <ARN>
A:Cross-references: UNIPROT:Q9X1Q9; UNIPARC:UPI00000C125F; GB:AE001802; GB:AE000512; NID:
C:Date: 31-Mar-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1573

Query Match 89.7%; Score 26; DB 2; Length 603;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||| 198

Db 193 KVVFFS 198

RESULT 37

hypothetical protein CT326 homolog - Chlamydophila pneumoniae (strain CWL029)

C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
A:Cross-references: A72123
R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A:Reference number: A72000; MUID:99206606; PMID:10192388

A:Accession: A72123

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-617 <ARN>

A:Cross-references: UNIPROT:Q9Z9B2; UNIPARC:UPI00000C11C1; GB:AE001592; GB:AE001363; NID:
A:Experimental source: strain CWL029

C:Genetics:
A:Gene: CPn069

Query Match 89.7%; Score 26; DB 2; Length 617;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||| 483

Db 478 RVVFFA 483

RESULT 38

Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A49795

R:Podlany, M.B.; Tolan, D.R.; Selkoe, D.J.

Am. J. Pathol. 138, 1423-1435, 1991

A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a

A:Reference number: A49795; MUID:91273117; PMID:1905108

A:Accession: A49795

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-695 <POD>

A:Cross-references: UNIPARC:UPI000002A2F2; GB:MS8727; NID:9342062; PIDN:AAA36829.1; PID:
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

C:Keywords: alternative splicing

Query Match 89.7%; Score 26; DB 1; Length 695;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||| 617

Db 612 KLVFFA 617

RESULT 39

A27485

Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse

N:Alternate names: proteinase nexin II

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004

A:Experimental source: strain MSB8

C:Genetics:
A:Gene: TM1573

R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.

Biochem. Biophys. Res. Commun. 149, 665-671, 1987

A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein prec

A:Reference number: A27485; MUID:88106489; PMID:3322280

A:Accession: A27485

A:Molecule type: mRNA

A:Residues: 1-695 <YAM>

A:Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:g191568; PIDN:
A:Experimental source: brain

R:de Strooper, B.; van Leuven, F.; van den Berghe, H.

Biochim. Biophys. Acta 1129, 141-143, 1991

A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer

A:Reference number: S19727; MUID:92096458; PMID:1756177

A:Accession: S19727

A:Molecule type: mRNA

A:Residues: 1-210, 'G', 212-220, 'S', 222-386, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>

A:Cross-references: UNIPARC:UPI000002A2F9; EMBL:X59379

R:Zumli, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.

Gene 112, 189-195, 1992

A:Title: Positive and negative regulatory elements for the expression of the Alzheimer'

A:Reference number: I49485; MUID:92209998; PMID:1555768

A:Accession: I49485

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-19 <RES>

A:Cross-references: UNIPARC:UPI0000000387; GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:
A:Map position: 16C3

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 89.7%; Score 26; DB 2; Length 695;

Best Local Similarity 83.3%; Pred. No. 2.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

|:||||| 617

Db 612 KLVFFA 617

RESULT 40

S00550

Alzheimer's disease amyloid beta protein precursor - rat

N:Alternate names: beta-A4 amyloid protein

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C:Accession: S00550; A41245; A39820; S46251

R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.

EMBO J. 7, 1365-1370, 1988

A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brai

A:Reference number: S00550; MUID:88312583; PMID:2900758

A:Accession: S00550

A:Molecule type: mRNA

A:Residues: 1-695 <SHI>

A:Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2F8; EMBL:X07648; NID:g555616; PID:
R:Schubert, D.; Schroeder, R.; Lacorbriere, M.; Saitoh, T.; Cole, G.

Science 241, 223-226, 1988

A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core

A:Reference number: A41245; MUID:88264430; PMID:2968652

A:Accession: A41245

A:Molecule type: protein

A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>

A:Cross-references: UNIPARC:UPI0000177FD

A:Note: evidence for heparan sulfate attachment

R:Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.

FEBS Lett. 349, 109-116, 1994

A:Title: The beta-A4 amyloid precursor protein binding to copper.

A:Reference number: S46251; MUID:94320627; PMID:7913895

A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POR>
A;Cross-references: UNIPARC:UPI00001777FE
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitors; alternative splicing; amyloid; glycoprotein; transmembrane protein
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 89.7%; Score 26; DB 2; Length 695;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:|||||
Db 612 KLVFFA 617

RESULT 41

JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
R;Okada, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: UNIPARC:UPI00000FC980; GB:S52417; NID:Q263150; PIDN:AAB24853.1; PID:
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitors
C;Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 89.7%; Score 26; DB 2; Length 747;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:|||||
Db 664 KLVFFA 669

RESULT 42

ORHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibitor
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
468; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252; S3
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PrA4 (695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288, 'V', 365-770 <LEW1>
A;Cross-references: UNIPARC:UPI000002A2F2; EMBL:X13466
A;Note: alternative splice form APP(695)

R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEW2>
A;Cross-references: UNIPARC:UPI000016AEFC; EMBL:X13466; NID:G35598; PIDN:CAA31830.1; PII
A;Note: alternative splice form APP(695)
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAF>
A;Cross-references: UNIPARC:UPI000016A57D; GB:M24546; GB:M24547; NID:G341202; PIDN:AAAC13
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A;Reference number: A33260; MUID:89392030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:G178863; PIDN:AAAS1768.1; PID
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Cross-references: UNIPARC:UPI0000148176
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: UNIPARC:UPI000002DB1C; GB:M33112; NID:G178613; PIDN:AAB59502.1; PID
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A;Molecule type: DNA
A;Residues: 1-530, 'QWLMPVIPAFWEAKVGR' <YOS2>
A;Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:G178608; PIDN:AAB59501.1; PID
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:G178618; PIDN:AAAS1727.1; PID
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A;Reference number: I59562; MUID:9022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 689-716, 'F', 718-737 <MUR>
A;Cross-references: UNIPARC:UPI000011F7EA; GB:S57665; NID:G236720; PIDN:AAB19991.1; PID
R;Kamino, K.; Orr, H.T.; Payami, H.; Wajsbman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,

Am. J. Hum. Genet. 51, 998-1014, 1992
 A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
 A;Reference number: A44017; MUID:93035397; PMID:1415269
 A;Accession: A44017
 A;Molecule type: DNA
 A;Residues: 687-692, 'G', 694-718 <KAM1>
 A;Cross-references: UNIPARC:UPI0000117EB; GB:S45135; NID:G257377; PIDN:AAB23645.1; PID:
 A;Experimental source: familial Alzheimer disease family SB
 A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
 A;Accession: B44017
 A;Molecule type: DNA
 A;Residues: 687-718 <KAM2>
 A;Cross-references: UNIPARC:UPI000016B394; GB:S45136; NID:G257379; PIDN:AAB23646.1; PID:
 A;Experimental source: familial Alzheimer disease family Lit
 A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
 A;Note: this sequence has a silent mutation
 R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
 Nature 325, 733-736, 1987
 A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
 A;Reference number: A03134; MUID:87144572; PMID:2881207
 A;Accession: A03134
 A;Molecule type: mRNA
 A;Residues: 1-288, 'V', 365-770 <KAN>
 A;Cross-references: UNIPARC:UPI00002A2F2; GB:Y00264; NID:G28525; PIDN:CAA68374.1; PID:
 A;Note: alternative splice form APP(695)
 R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular
 A;Reference number: A29030; MUID:87231971; PMID:3035574
 A;Accession: A29030
 A;Molecule type: mRNA
 A;Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A;Cross-references: UNIPARC:UPI000016A545; GB:M16765; NID:G178539; PIDN:AAA51722.1; PID:
 A;Note: the authors translated the codon GAG for residue 647 as Asp
 R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
 A;Reference number: A47584; MUID:87120328; PMID:3810169
 A;Accession: A47584
 A;Molecule type: mRNA
 A;Residues: 674-756, 'S', 758-770 <GOL>
 A;Cross-references: UNIPARC:UPI00001420B5; GB:M15533; NID:G178706; PIDN:AAA35540.1; PID:
 A;Experimental source: brain
 R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
 Science 235, 880-884, 1987
 A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
 A;Reference number: A47585; MUID:87120329; PMID:2949367
 A;Accession: A47585
 A;Molecule type: mRNA
 A;Residues: 674-703 <TAN1>
 A;Cross-references: UNIPARC:UPI000016A46F; GB:M15532; NID:G177957; PIDN:AAA51564.1; PID:
 R;Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
 EMBO J. 7, 949-957, 1988
 A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
 A;Reference number: S02638; MUID:88296437; PMID:2900137
 A;Accession: S02638
 A;Molecule type: mRNA
 A;Residues: 672-678 <DYR>
 A;Cross-references: UNIPARC:UPI0000035AB0
 R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
 Nature 331, 528-530, 1988
 A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
 A;Reference number: S00707; MUID:88122640; PMID:2893290
 A;Accession: S00707
 A;Molecule type: mRNA
 A;Residues: 286-344, 'I', 365-366 <TAN2>
 A;Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:G28817; PIDN:CAA30042.1; PID:
 A;Experimental source: promyelocytic leukemia cell line HL60
 A;Note: alternative splice form APP(751)
 R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
 Nature 331, 525-527, 1988
 A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
 A;Reference number: S00925; MUID:88122639; PMID:2893289

A;Accession: S00925
 A;Molecule type: mRNA
 A;Residues: 1-344, 'I', 365-770 <PO2>
 A;Cross-references: UNIPARC:UPI000002A2F6; GB:X06989; EMBL:X00287; NID:G28720; PIDN:CAA
 R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibito
 A;Reference number: A38949; MUID:88122641; PMID:2893291
 A;Accession: A38949
 A;Molecule type: mRNA
 A;Residues: 287-367 <KIT>
 A;Cross-references: UNIPARC:UPI000014553B; GB:X06981; NID:G28816; PIDN:CAA30041.1; PID:
 A;Experimental source: glioblastoma cell line
 A;Note: alternative splice form APP(770)
 R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Asht
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three
 A;Reference number: A30320
 A;Accession: A30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 284-288, 'V', 365-770 <VIT1>
 A;Cross-references: UNIPARC:UPI0000174094
 A;Accession: B30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 122-288, 'V', 365-770 <VIT2>
 A;Cross-references: UNIPARC:UPI0000174094
 A;Accession: C30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 606-770 <VIT3>
 A;Cross-references: UNIPARC:UPI0000174094
 R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b
 A;Reference number: A31087; MUID:88124954; PMID:2893379
 A;Accession: A31087
 A;Molecule type: mRNA
 Query Match 89.7%; Score 26; DB 1; Length 770;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KWVFFA 6
 |:|||
 Db 687 KLVFFA 692
 RESULT 43
 A82511
 C;Species: Vibrio cholerae
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 18-Aug-2003
 C;Accession: A82511
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.B.; Dodson, R.J
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Basse, S.; Qin, H.; Dragoi, I.; Sellers,
 L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A;Reference number: A82035; MUID:20408833; PMID:10952301
 A;Accession: A82511
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-817 <HRI>
 A;Cross-references: UNIPARC:UPI00000C33C4; GB:AE004345; GB:AE003853; NID:G9657390; PID
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VCA0013
 A;Map position: 2
 C;Superfamily: glucan phosphorylase
 C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phospho

F:664/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 817;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
:|||||
Db 585 RVVFFA 590

RESULT 44

S30236
genome polyprotein - zucchini yellow mosaic virus (strain Singapore) (fragment)
N:Contains: coat protein; nuclear inclusion protein a; RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: zucchini yellow mosaic virus, ZYMV
A:Variety: strain Singapore
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
A:Accession: S30236
R:Wu, M.; Yeong, C.Y.; Lee, S.C.; Wong, S.M.
Nucleic Acids Res. 21, 1317, 1993
A:Title: Nucleotide sequence of the 3' half of zucchini yellow mosaic virus (Singapore)
A:Reference number: S30236; MUID:93219099; PMID:8464715
A:Accession: S30236
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-1016 <WUM>
A:Cross-references: UNIPROT:Q05912; UNIPARC:UPI000008CC69; EMBL:X68509; NID:g288233; PID:1000000000
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1992
C:Superfamily: tobacco etch virus genome polyprotein
C:Keywords: coat protein; genome-linked protein; nucleotidyltransferase; phosphoprotein;
F:9-61/Product: VPg protein #status predicted <VPG>
F:62-494/Product: nuclear inclusion protein a #status predicted <NIA>
F:495-1010/Product: RNA-directed RNA polymerase #status predicted <POL>
F:1011-1016/Product: coat protein (fragment) #status predicted <CP>
F:125/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 1016;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
:|||||
Db 837 KLVFFA 842

RESULT 45

E64214
hypothetical protein homolog MG131 - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
A:Accession: E64214
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; M.; Fuhmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.; C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: E64214
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-74 <TIGR>
A:Cross-references: UNIPROT:P47377; UNIPARC:UPI000013931D; GB:U39691; GB:L43967; NID:g1000000000
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3

Query Match 86.2%; Score 25; DB 2; Length 74;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
:|:|:|

Db 34 KILFFA 39

RESULT 46

B72213
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
A:Accession: B72213
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D., C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome ser
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: B72213
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <ARN>
A:Cross-references: UNIPROT:Q9X292; UNIPARC:UPI000000C120B; GB:AE001815; GB:AE000512; NID:1000000000
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1771
C:Superfamily: Bacillus subtilis conserved hypothetical protein yghY

Query Match 86.2%; Score 25; DB 2; Length 109;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
:|:|:|
Db 19 KIVVFA 24

RESULT 47

T19479
hypothetical protein C26C6.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A:Accession: T19479
R:McMurray, A.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19128
A:Accession: T19479
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-136 <WIL>
A:Cross-references: UNIPROT:Q18208; UNIPARC:UPI000007BE59; EMBL:Z72503; PIDN:CAA96598.1
A:Experimental source: clone C26C6
C:Genetics:
A:Gene: CESP:C26C6.6
A:Map position: 1
A:Introns: 22/3; 44/3; 78/1

Query Match 86.2%; Score 25; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
:|:|:|
Db 24 KVVFF 28

RESULT 48

E75134
hypothetical protein PAB1779 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Dec-2002
A:Accession: E75134
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A:Reference number: A75001

A;Accession: E75134
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 <KAW>
A;Cross-references: UNIPARC:UPI000063351; GB:AJ248285; GB:AL096836; NID:95458067; PIDN:
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1779
C;Superfamily: uncharacterized conserved protein

Query Match 86.2%; Score 25; DB 2; Length 146;
Best Local Similarity 66.7%; Pred. No. 96;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:|:|:
Db 39 KVIFFA 44

RESULT 49

T32362
hypothetical protein C08E3.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32362
R;Miller, N.; Kramer, J.; Keppler, D.
A;Description: The EMBL Data Library, September 1997
submitted to the EMBL Data Library, September 1997
A;Reference number: 221155
A;Accession: T32362
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-148 <MIL>
A;Cross-references: UNIPROT:O17202; UNIPARC:UPI0000076D24; EMBL:AF025457; PIDN:AAB70972.
A;Experimental source: strain Bristol N2; clone C08E3
C;Genetics:
A;Gene: CESP:C08E3.11
A;Map position: 2
A;Introns: 66/2

Query Match 86.2%; Score 25; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5
|:|:|:
Db 126 KVVFF 130

RESULT 50

H95252
PTS system, IIB component [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: H95252
R;Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: H95252
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <KUR>
A;Cross-references: UNIPROT:Q97N92; UNIPARC:UPI0000051B4E; GB:AE005672; PIDN:AAK76217.1;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP2163
C;Superfamily: phosphotransferase system mannose-specific enzyme II, factor III

Query Match 86.2%; Score 25; DB 2; Length 156;

Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:|:|:
Db 56 KIVFFS 61

RESULT 51

F98117
hypothetical protein PTS-EII [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: F98117
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: F98117
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <KUR>
A;Cross-references: UNIPROT:Q8DN20; UNIPARC:UPI00000E3754; GB:AE007317; PIDN:AAL00771.1;
C;Genetics:
A;Gene: PTS-EII
C;Superfamily: phosphotransferase system mannose-specific enzyme II, factor III

Query Match 86.2%; Score 25; DB 2; Length 156;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:|:|:
Db 56 KIVFFS 61

RESULT 52

C71080
hypothetical protein PH0907 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Aug-2004
C;Accession: C71080
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: C71080
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-159 <KAW>
A;Cross-references: UNIPARC:UPI0000062F34; GB:AP000004; NID:g3236131; PIDN:BA330001.1;
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBan
C;Genetics:
A;Gene: PH0907
C;Superfamily: uncharacterized conserved protein

Query Match 86.2%; Score 25; DB 2; Length 159;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:|:|:
Db 54 KVIFFA 59

RESULT 53

T13659
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia sagittata chloroplast

C:Species: chloroplast Pontederia sagittata
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13659
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.
Syst. Biol. 47, 545-567, 1998
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets
A:Reference number: Z17600
A:Accession: T13659
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-162 <GRA>
A:Cross-references: UNIPROT:Q32915; UNIPARC:UPI0000096540; EMBL:U41621; NID:g1174015; P13659
C:Genetics:
A:Genome: chloroplast
A>Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||:
Db 13 KVIFFS 18

RESULT 54
T13656
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia rotundifolia chloroplast
C:Species: chloroplast Pontederia rotundifolia
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13656
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.
Syst. Biol. 47, 545-567, 1998
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets
A:Reference number: Z17600
A:Accession: T13656
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-162 <GRA>
A:Cross-references: UNIPROT:Q32892; UNIPARC:UPI000008CB4C; EMBL:U41620; NID:g1174011; P13656
C:Genetics:
A:Genome: chloroplast
A>Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||:
Db 13 KVIFFS 18

RESULT 55
T13563
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia cordata chloroplast
C:Species: chloroplast Pontederia cordata
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13563
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.
Syst. Biol. 47, 545-567, 1998
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets
A:Reference number: Z17600
A:Accession: T13563
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-162 <GRA>
A:Cross-references: UNIPROT:Q32802; UNIPARC:UPI000008F006; EMBL:U41619; NID:g1174003; P13563
A:Experimental source: var. ovalis

C:Genetics:
A:Genome: chloroplast
A>Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||:
Db 13 KVIFFS 18

RESULT 56
T13487
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Monochoria vaginalis chloroplast
C:Species: chloroplast Monochoria vaginalis
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13487
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.
Syst. Biol. 47, 545-567, 1998
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets
A:Reference number: Z17600
A:Accession: T13487
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-162 <GRA>
A:Cross-references: UNIPROT:Q32648; UNIPARC:UPI00000976P4; EMBL:U41616; NID:g1173991; P13487
C:Genetics:
A:Genome: chloroplast
A>Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 162;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||:
Db 13 KVIFFS 18

RESULT 57
T13562
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pontederia cordata chloroplast
C:Species: chloroplast Pontederia cordata
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13562
R:Graham, S.W.; Kohn, J.R.; Morton, B.R.; Eckenwalder, J.E.; Barrett, S.C.
Syst. Biol. 47, 545-567, 1998
A:Title: Phylogenetic congruence and discordance among one morphological and three molecular datasets
A:Reference number: Z17600
A:Accession: T13562
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-164 <GRA>
A:Cross-references: UNIPROT:Q37011; UNIPARC:UPI000016D3B6; EMBL:U41617; NID:g1173999; P13562
A:Experimental source: var. cordata
C:Genetics:
A:Genome: chloroplast
A>Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 86.2%; Score 25; DB 2; Length 164;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||:
Db 13 KVIFFS 18

Db 13 KVIPP 18

RESULT 58
G70475
conserved hypothetical protein aq_2049 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: G70475
V: Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: G70475
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-188 <AOF>
A:Cross-references: UNIPROT:Q67835; UNIPARC:UPI000005679F; GB:AE000770; NID:G2984274; PI
A:Experimental source: strain VFS
C:Genetics:
A:Gene: aq_2049

Query Match 86.2%; Score 25; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVPF 5
|||||
79 KVVPF 83

Db 79 KVVPF 83

RESULT 59
A95895
probable permease protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: A95895
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: A95895
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-190 <KUR>
A:Cross-references: UNIPROT:Q92WB8; UNIPARC:UPI00000CB514; GB:AL591985; PIDN:CAC48825.1;
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Fuhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Smb20443
A:Genome: plasmid

Query Match 86.2%; Score 25; DB 2; Length 190;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVPFA 6
|||||
116 KVVPFA 121

Db 116 KVVPFA 121

RESULT 60
B97211
uncharacterized conserved membrane protein CAC2524 [imported] - Clostridium acetobutylic

C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97211
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl.
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: B97211
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-194 <KUR>
A:Cross-references: UNIPROT:Q97G46; UNIPARC:UPI00000CA55C; GB:AE001437; PIDN:AAK80477.1
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2524

Query Match 86.2%; Score 25; DB 2; Length 194;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVPFA 6
|||||
165 KILFFA 170

Db 165 KILFFA 170

RESULT 61
AE1632
hypothetical protein homolog lin1598 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE1632
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kohn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlan
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1632
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-200 <GLA>
A:Cross-references: UNIPROT:Q92BF2; UNIPARC:UPI0000127CE2; GB:AL592022; PIDN:CAC96829.1
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin1598
C:Superfamily: conserved hypothetical protein YDR196c

Query Match 86.2%; Score 25; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVPF 5
|||||
109 KVVPF 113

Db 109 KVVPF 113

RESULT 62
A71495
probable polysaccharide transporter - Chlamydia trachomatis (serotype D, strain UM3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C:Accession: A71495
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tr
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: A71495
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <ARN>

A;Cross-references: UNIPROT:O84601; UNIPARC:UPI00000D336C; GB:AE001330; GB:AE001273; NID
 A;Experimental source: serotype D, strain UW-3/Cx

C;Genetics:
 A;Gene: exbB
 C;Superfamily: biopolymer transport protein

Query Match 86.2%; Score 25; DB 2; Length 232;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6
 ||:||:
 Db 21 KVIFFS 26

RESULT 63

T23466
 hypothetical protein K08E4.6 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T23466

R;Percy, C.

submitted to the EMBL Data Library, December 1995

A;Reference number: Z19744

A;Accession: T23466

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-234 <WIL>

A;Cross-references: UNIPROT:Q21336; UNIPARC:UPI00000765B4; EMBL:Z68316; PIDN:CAA92683.1;

A;Experimental source: clone K08E4

C;Genetics:

A;Gene: CESP:K08E4.6

A;Map position: 4

A;Introns: 54/3; 154/3

Query Match 86.2%; Score 25; DB 2; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVF 5
 |||||
 Db 109 KVVF 113

RESULT 64

T32514
 hypothetical protein C44B12.1 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
 C;Accession: T32514

R;Tin-Wollam, A.

submitted to the EMBL Data Library, December 1997

A;Description: The sequence of C. elegans cosmid C44B12.

A;Reference number: Z21183

A;Accession: T32514

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-247 <TIN>

A;Cross-references: UNIPROT:O44145; UNIPARC:UPI00001793B3; EMBL:AF036692; PIDN:AA888324.

A;Experimental source: strain Bristol N2; clone C44B12

C;Genetics:

A;Gene: CESP:C44B12.1

A;Map position: 4

A;Introns: 28/3; 82/1; 164/1; 192/1

Query Match 86.2%; Score 25; DB 2; Length 247;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6
 ||:||:
 Db 224 KIVFFS 229

RESULT 65

DB2405
 transcription regulator LuxR family VCA0888 [imported] - Vibrio cholerae (strain N16961
 C;Species: Vibrio cholerae
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: DB2405
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I.;
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: DB2405

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-253 <HEI>

A;Cross-references: UNIPROT:Q9KL60; UNIPARC:UPI00000C36AA; GB:AE004416; GB:AE003853; NID

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VCA0888

A;Map position: 2

Query Match 86.2%; Score 25; DB 2; Length 253;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFPA 6
 ||:||:
 Db 51 KIVFFS 56

RESULT 66

CB7434
 2-deoxy-D-glucuronate 3-dehydrogenase [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
 C;Accession: CB7434

R;Nieman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: CB7434

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-255 <STO>

A;Cross-references: UNIPROT:Q9A872; UNIPARC:UPI00000C73DC; GB:AE005673; NID:gl3422867; F

C;Genetics:

A;Gene: CC1492

C;Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 86.2%; Score 25; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVF 5
 |||||
 Db 117 KVVF 121

RESULT 67

CB3982
 hypothetical protein BH2659 [imported] - Bacillus halodurans (strain C-125)
 C;Species: Bacillus halodurans
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C;Accession: CB3982

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A;Reference number: AB3650; MUID:20512582; PMID:11056132

A;Accession: CB3982

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <STO>
A;Cross-references: UNIPROT:Q9K9I8; UNIPARC:UPI00000C3F80; GB:AP001516; GB:BA000004; NID:
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2659

Query Match 86.2%; Score 25; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5
| | | | |
Db 4 KVVFF 8

RESULT 68
D64166
hypothetical protein H11086 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: D64166
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: D64166
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-261 <TIGR>
A;Cross-references: UNIPROT:P45030; UNIPARC:UPI000013BFA0; GB:U32788; GB:L42023; NID:915
A;Note: best homolog was a hypothetical protein from Escherichia coli
C;Superfamily: conserved hypothetical protein H11086

Query Match 86.2%; Score 25; DB 2; Length 261;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFF 6
| | | | |
Db 205 KAVFFA 210

RESULT 69
T31855
hypothetical protein C02E7.12 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31855
R;Fulton, B.; Wohldmann, P.
submitted to the EMBL Data Library, June 1998
A;Description: The sequence of C. elegans cosmid C02E7.
A;Reference number: Z21093
A;Accession: T31855
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-277 <FUL>
A;Cross-references: UNIPARC:UPI000017B71A; EMBL:AF016446; PIDN:AAC24170.1; GSPDB:GN00023
A;Experimental source: strain Bristol N2; clone C02E7
C;Genetics:
A;Gene: CESP:C02E7.12
A;Map position: 5
A;Introns: 45/2; 146/3

Query Match 86.2%; Score 25; DB 2; Length 277;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 6

Db 112 KVVFFA 117
| | | | |

RESULT 70
C84857
hypothetical protein At2g42710 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: C84857
R;Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Status: preliminary
A;Accession: C84857
A;Molecule type: DNA
A;Residues: 1-286 <STO>
A;Cross-references: UNIPROT:Q9SJ15; UNIPARC:UPI00000A82D6; GB:AE002093; NID:94512681; P:
C;Genetics:
A;Gene: At2g42710
A;Map position: 2
C;Superfamily: ribosomal protein L1p/L10e

Query Match 86.2%; Score 25; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFF 6
| | | | |
Db 241 KVAFFA 246

RESULT 71
JC4744
NAD-dinitrogen-reductase ADP-D-ribosyltransferase (EC 2.4.2.37) - rice
C;Species: Oryza sativa (rice)
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 02-Aug-2002
C;Accession: JC4744
R;Inoue, A.; Shigematsu, T.; Hidaka, M.; Masaki, H.; Uozumi, T.
Gene 170, 101-106, 1996
A;Title: Cloning, sequencing and transcriptional regulation of the draT and draG genes
A;Reference number: JC4744; MUID:96200864; PMID:8621068
A;Accession: JC4744
A;Molecule type: DNA
A;Residues: 1-295 <INO>
A;Cross-references: UNIPARC:UPI00000BDA45; DBJ:D55631; NID:9862322; PID:9862323
C;Comment: This enzyme is responsible for the post-translation regulation of nitrogenase
C;Genetics:
A;Gene: draT
C;Superfamily: Azospirillum NAD+-nitrogenase ADP-D-ribosyltransferase
C;Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 86.2%; Score 25; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5
| | | | |
Db 262 KVVFF 266

RESULT 72
I39751
NAD-dinitrogen-reductase ADP-D-ribosyltransferase (EC 2.4.2.37) - Azospirillum brasilense
C;Species: Azospirillum brasilense
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: I39751
R;Zhang, Y.; Burris, R.H.; Roberts, G.P.
J. Bacteriol. 174, 3364-3369, 1992
A;Title: Cloning, sequencing, mutagenesis, and functional characterization of draT and

A:Reference number: I39751; MUID:92250433; PMID:1577701
 A:Accession: I39751
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-295 <RES>
 A:Cross-references: UNIPROT:Q43903; UNIPARC:UPI00000B0CDE; GB:M87319; NID:g142411; PIDN:
 C:Genetics:
 A:Gene: drat
 C:Superfamily: Azospirillum NAD+-nitrogenase ADP-D-ribosyltransferase
 C:Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 86.2%; Score 25; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
 |||||
 Db 262 KVVFF 266

RESULT 73

C70736
 Hypothetical protein RV3406 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: C70736
 R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Reltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998
 A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: C70736
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-295 <COL>
 A:Cross-references: UNIPROT:Q50719; UNIPARC:UPI000013C263; GB:Z77165; GB:AL123456; NID:9
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: RV3406

Query Match 86.2%; Score 25; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
 |||||
 Db 43 KVVFF 47

RESULT 74

A39074

Hypothetical protein ABC-MSP [imported] - Streptococcus pneumoniae (strain R6)

C:Species: Streptococcus pneumoniae
 C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: A39074
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: A39074
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-302 <KUR>
 A:Cross-references: UNIPROT:Q8DNN8; UNIPARC:UPI00000E36B3; GB:AE007317; PIDN:AAL00422.1;
 C:Genetics:
 A:Gene: ABC-MSP
 C:Superfamily: inner membrane protein ugpa

Query Match 86.2%; Score 25; DB 2; Length 302;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 Db 118 KVVFFA 123

RESULT 75

B35961

Hypothetical 21K protein - Pseudomonas syringae pv. savastanoi

C:Species: Pseudomonas syringae pv. savastanoi
 C>Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
 C:Accession: B35961

R:Robertson, F.F.; Klee, H.; White, F.; Nordeen, R.; Kosuge, T.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5797-5801, 1990
 A:Title: Expression and fine structure of the gene encoding N(epsilon)-(indole-3-acetyl)

A:Reference number: A35961; MUID:90332669; PMID:2377619
 A:Accession: B35961
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-302 <ROB>
 A:Cross-references: UNIPROT:P18205; UNIPARC:UPI000013B36E; GB:M35373; NID:g151286; PIDN:

Query Match 86.2%; Score 25; DB 2; Length 302;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 :|||||
 Db 197 QVVFFA 202

Search completed: December 29, 2005, 17:49:17
 Job time : 14.9677 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.29032 Seconds
(without alignments)
13.656 Million cell updates/sec

Title: US-10-009-122-9

Perfect score: 29

Sequence: 1 KVFPPA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA New:*

1: /cgn2_6/ptodata/2/pubaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB pep.*
5: /cgn2_6/ptodata/2/pubaa/US09_NEW_PUB pep.*
6: /cgn2_6/ptodata/2/pubaa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/2/pubaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	26	89.7	19	6	US-10-923-605-5
2	26	89.7	19	6	US-10-934-818-5
3	26	89.7	40	7	US-11-016-706-36
4	26	89.7	40	7	US-11-098-674-12
5	26	89.7	42	6	US-10-923-605-1
6	26	89.7	42	6	US-10-934-818-1
7	26	89.7	42	7	US-11-016-706-37
8	26	89.7	43	6	US-10-934-818-6
9	26	89.7	43	6	US-10-250-581-1
10	26	89.7	43	6	US-10-250-581-1
11	26	89.7	770	6	US-10-982-545-15
12	26	89.7	770	6	US-10-789-273-38
13	25	86.2	660	7	US-11-186-284-125
14	25	86.2	708	6	US-10-821-234-917
15	24	82.8	229	6	US-10-131-826A-410
16	24	82.8	269	6	US-10-467-657-330
17	24	82.8	311	6	US-10-793-626-2450
18	24	82.8	400	6	US-10-793-626-1056
19	24	82.8	3623	6	US-10-995-561-593
20	23	79.3	50	6	US-10-467-657-7892
21	23	79.3	167	7	US-11-210-316-18
22	23	79.3	239	6	US-10-467-657-432
23	23	79.3	265	6	US-10-793-626-2500
24	23	79.3	347	6	US-10-467-657-2014
25	23	79.3	402	6	US-10-467-657-9070

26	79.3	426	6	US-10-467-657-2120	Sequence 2120, Ap
27	79.3	481	6	US-10-995-561-959	Sequence 959, App
28	79.3	510	7	US-11-210-316-22	Sequence 22, Appl
29	79.3	524	6	US-10-689-742-13	Sequence 13, Appl
30	79.3	539	7	US-11-210-316-26	Sequence 26, Appl
31	79.3	677	6	US-10-131-826A-230	Sequence 230, App
32	79.3	2233	7	US-10-873-528-2	Sequence 2, Appli
33	79.3	5	7	US-11-098-674-1	Sequence 1, Appli
34	75.9	43	6	US-10-467-657-7886	Sequence 7886, Ap
35	75.9	47	6	US-10-467-657-5436	Sequence 5436, Ap
36	75.9	182	6	US-10-793-626-2836	Sequence 2836, Ap
37	75.9	190	6	US-10-467-657-3436	Sequence 3436, Ap
38	75.9	211	6	US-10-821-234-1372	Sequence 1372, Ap
39	75.9	278	6	US-10-957-569-45	Sequence 45, Appl
40	75.9	440	7	US-11-082-389-106	Sequence 106, App
41	75.9	482	6	US-10-793-626-24	Sequence 24, Appl
42	75.9	522	7	US-11-080-991-104	Sequence 104, App
43	75.9	528	6	US-10-793-626-1930	Sequence 1930, Ap
44	75.9	533	6	US-10-467-657-2868	Sequence 2868, Ap
45	75.9	569	7	US-11-082-389-104	Sequence 104, App
46	75.9	1061	7	US-11-000-463-347	Sequence 347, App
47	75.9	1091	7	US-11-000-463-348	Sequence 348, App
48	75.9	3507	7	US-11-075-185-7	Sequence 7, Appli
49	72.4	83	6	US-10-510-386-114	Sequence 114, App
50	72.4	98	6	US-10-467-657-4746	Sequence 4746, Ap
51	72.4	105	6	US-10-467-657-9209	Sequence 9209, Ap
52	72.4	137	6	US-10-821-234-1701	Sequence 1701, Ap
53	72.4	140	6	US-10-467-657-2486	Sequence 2486, Ap
54	72.4	155	6	US-10-467-657-2420	Sequence 2420, Ap
55	72.4	179	6	US-10-467-657-2232	Sequence 2232, Ap
56	72.4	210	6	US-10-467-657-6318	Sequence 6318, Ap
57	72.4	211	6	US-10-467-657-6932	Sequence 6932, Ap
58	72.4	215	6	US-10-131-826A-4	Sequence 4, Appli
59	72.4	228	6	US-10-467-657-568	Sequence 568, App
60	72.4	228	6	US-10-467-657-4838	Sequence 4838, Ap
61	72.4	233	6	US-10-821-234-1322	Sequence 1322, Ap
62	72.4	266	6	US-10-995-561-544	Sequence 544, App
63	72.4	267	6	US-10-995-561-543	Sequence 543, App
64	72.4	312	7	US-11-055-822-16	Sequence 16, Appl
65	72.4	330	6	US-10-793-626-2476	Sequence 2476, Ap
66	72.4	330	6	US-10-793-626-2734	Sequence 2734, Ap
67	72.4	337	6	US-10-485-517-234	Sequence 234, App
68	72.4	338	6	US-10-878-556A-19	Sequence 19, Appl
69	72.4	344	6	US-10-131-826A-376	Sequence 376, App
70	72.4	355	6	US-10-467-657-7996	Sequence 7996, Ap
71	72.4	358	7	US-11-055-822-572	Sequence 572, App
72	72.4	358	7	US-11-055-822-836	Sequence 836, App
73	72.4	406	6	US-10-467-657-7420	Sequence 7420, Ap
74	72.4	414	6	US-10-878-556A-1	Sequence 1, Appli
75	72.4	432	7	US-11-194-246-308	Sequence 308, App
76	72.4	448	6	US-10-763-712A-69	Sequence 69, Appl
77	72.4	448	6	US-10-763-712A-112	Sequence 112, App
78	72.4	449	6	US-10-821-234-1075	Sequence 1075, Ap
79	72.4	449	6	US-10-467-657-678	Sequence 678, App
80	72.4	450	6	US-10-467-657-7094	Sequence 7094, Ap
81	72.4	450	6	US-10-467-657-8028	Sequence 8028, Ap
82	72.4	450	6	US-10-763-712A-76	Sequence 76, Appl
83	72.4	451	6	US-10-467-657-7104	Sequence 7104, Ap
84	72.4	453	7	US-11-082-389-198	Sequence 198, App
85	72.4	508	7	US-11-082-389-178	Sequence 178, App
86	72.4	525	7	US-11-082-389-350	Sequence 350, App
87	72.4	560	6	US-10-623-155-225	Sequence 225, App
88	72.4	563	6	US-10-821-234-1067	Sequence 1067, Ap
89	72.4	601	6	US-10-467-657-7120	Sequence 7120, Ap
90	72.4	635	6	US-10-821-234-1673	Sequence 1673, Ap
91	72.4	739	7	US-11-082-389-94	Sequence 94, Appl
92	72.4	817	6	US-10-793-626-2948	Sequence 2948, Ap
93	72.4	858	6	US-10-613-744-6	Sequence 6, Appli
94	72.4	896	7	US-11-192-219-3	Sequence 3, Appli
95	72.4	898	7	US-11-166-730-3	Sequence 3, Appli
96	72.4	902	7	US-11-057-058-64	Sequence 64, Appl
97	72.4	923	7	US-11-192-219-4	Sequence 4, Appli
98	72.4	1013	7	US-11-103-957-9	Sequence 9, Appli

99	21	72.4	1165	7	US-11-192-219-2	Sequence 2, Appli	172	20	69.0	329	6	US-10-524-647-80	Sequence 80, Appl
100	21	72.4	1217	7	US-11-074-176-252	Sequence 252, App	173	20	69.0	335	6	US-10-467-657-3818	Sequence 3818, Ap
101	21	72.4	7968	7	US-11-186-731-5	Sequence 5, Appli	174	20	69.0	341	6	US-10-524-647-27	Sequence 27, Appl
102	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	175	20	69.0	348	6	US-10-821-234-1402	Sequence 1402, Ap
103	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	176	20	69.0	355	6	US-10-454-437-102	Sequence 102, App
104	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	177	20	69.0	356	7	US-11-012-762-46	Sequence 46, Appl
105	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	178	20	69.0	362	7	US-11-012-762-62	Sequence 62, Appl
106	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	179	20	69.0	364	6	US-10-131-826A-186	Sequence 186, App
107	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	180	20	69.0	370	6	US-10-821-234-1105	Sequence 1105, Ap
108	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	181	20	69.0	370	7	US-11-073-605-2	Sequence 2, Appli
109	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	182	20	69.0	370	7	US-11-075-600-14	Sequence 14, Appl
110	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	183	20	69.0	386	7	US-11-012-762-44	Sequence 44, Appl
111	20	69.0	42	6	US-10-250-581-19	Sequence 19, Appl	184	20	69.0	389	7	US-11-069-642-18	Sequence 18, Appl
112	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	185	20	69.0	395	6	US-10-467-657-1950	Sequence 1950, Ap
113	20	69.0	42	6	US-10-250-581-19	Sequence 19, Appl	186	20	69.0	396	6	US-10-510-386-238	Sequence 238, App
114	20	69.0	43	7	US-11-075-400-28	Sequence 28, Appl	187	20	69.0	399	6	US-10-510-386-30	Sequence 30, Appl
115	20	69.0	52	6	US-10-467-657-2216	Sequence 2216, Ap	188	20	69.0	413	6	US-10-467-657-1858	Sequence 1858, Ap
116	20	69.0	54	6	US-10-467-657-4978	Sequence 4978, Ap	189	20	69.0	418	6	US-10-467-657-5788	Sequence 5788, Ap
117	20	69.0	56	6	US-10-467-657-1050	Sequence 1050, Ap	190	20	69.0	423	6	US-10-525-710-44	Sequence 44, Appl
118	20	69.0	76	6	US-10-467-657-5690	Sequence 5690, Ap	191	20	69.0	436	6	US-10-467-657-7694	Sequence 7694, Ap
119	20	69.0	80	6	US-10-986-501-200	Sequence 200, App	192	20	69.0	443	6	US-10-793-626-1860	Sequence 1860, Ap
120	20	69.0	86	6	US-10-467-657-3962	Sequence 3962, Ap	193	20	69.0	444	6	US-10-467-657-362	Sequence 362, App
121	20	69.0	91	6	US-10-821-234-1703	Sequence 1703, Ap	194	20	69.0	445	6	US-10-454-437-312	Sequence 312, App
122	20	69.0	98	6	US-10-467-657-3376	Sequence 3376, Ap	195	20	69.0	445	7	US-11-082-389-376	Sequence 376, App
123	20	69.0	107	6	US-10-467-657-2102	Sequence 2102, Ap	196	20	69.0	445	7	US-11-103-240-32	Sequence 32, Appl
124	20	69.0	115	6	US-10-793-626-1554	Sequence 1554, Ap	197	20	69.0	456	6	US-10-467-657-4150	Sequence 4150, Ap
125	20	69.0	115	6	US-10-432-483-10	Sequence 10, Appl	198	20	69.0	463	6	US-10-467-657-6352	Sequence 6352, Ap
126	20	69.0	123	6	US-10-793-626-430	Sequence 430, App	199	20	69.0	463	6	US-10-467-657-7604	Sequence 7604, Ap
127	20	69.0	123	6	US-10-467-657-5166	Sequence 5166, Ap	200	20	69.0	465	6	US-10-793-626-2928	Sequence 2928, Ap
128	20	69.0	126	6	US-10-793-626-2766	Sequence 2766, Ap	201	20	69.0	475	7	US-11-180-997-4	Sequence 4, Appli
129	20	69.0	127	7	US-11-106-796-10	Sequence 10, Appl	202	20	69.0	485	6	US-10-204-029-7	Sequence 7, Appli
130	20	69.0	134	6	US-10-501-039-8	Sequence 8, Appli	203	20	69.0	489	6	US-10-467-657-7846	Sequence 7846, Ap
131	20	69.0	139	6	US-10-793-626-2374	Sequence 2374, Ap	204	20	69.0	490	7	US-11-074-176-316	Sequence 316, App
132	20	69.0	137	6	US-10-793-626-530	Sequence 530, App	205	20	69.0	492	6	US-10-793-626-770	Sequence 770, App
133	20	69.0	139	6	US-10-467-657-5728	Sequence 5728, Ap	206	20	69.0	495	7	US-11-074-176-60	Sequence 60, Appl
134	20	69.0	164	6	US-10-793-626-2478	Sequence 2478, Ap	207	20	69.0	496	7	US-11-067-121-12	Sequence 12, Appl
135	20	69.0	165	6	US-10-467-657-4990	Sequence 4990, Ap	208	20	69.0	508	7	US-11-075-185-26	Sequence 26, Appl
136	20	69.0	175	6	US-10-965-694-23	Sequence 23, Appl	209	20	69.0	522	6	US-10-995-561-1030	Sequence 1030, Ap
137	20	69.0	182	6	US-10-467-657-3510	Sequence 3510, Ap	210	20	69.0	555	6	US-10-454-437-100	Sequence 100, App
138	20	69.0	183	6	US-10-467-657-6906	Sequence 6906, Ap	211	20	69.0	558	6	US-10-467-657-4258	Sequence 4258, Ap
139	20	69.0	183	6	US-10-467-657-8138	Sequence 8138, Ap	212	20	69.0	578	6	US-10-858-730-103	Sequence 103, App
140	20	69.0	196	6	US-10-793-626-630	Sequence 630, App	213	20	69.0	582	7	US-11-090-439-58	Sequence 58, Appl
141	20	69.0	200	6	US-10-524-198-2	Sequence 2, Appli	214	20	69.0	585	7	US-11-012-762-6	Sequence 6, Appli
142	20	69.0	200	7	US-11-073-605-3	Sequence 3, Appli	215	20	69.0	592	6	US-10-467-657-4888	Sequence 4888, Ap
143	20	69.0	204	6	US-10-467-657-5874	Sequence 5874, Ap	216	20	69.0	601	7	US-11-103-957-3	Sequence 3, Appli
144	20	69.0	210	6	US-10-986-501-126	Sequence 126, App	217	20	69.0	615	6	US-10-995-561-940	Sequence 940, App
145	20	69.0	216	6	US-10-467-657-8102	Sequence 8102, Ap	218	20	69.0	626	6	US-10-467-657-1196	Sequence 1196, Ap
146	20	69.0	220	6	US-10-467-657-3154	Sequence 3154, Ap	219	20	69.0	657	7	US-11-080-991-48	Sequence 48, Appl
147	20	69.0	221	6	US-10-467-657-290	Sequence 290, App	220	20	69.0	662	6	US-10-995-561-943	Sequence 943, App
148	20	69.0	221	6	US-10-467-657-5750	Sequence 5750, App	221	20	69.0	690	6	US-10-131-826A-306	Sequence 306, App
149	20	69.0	231	6	US-10-689-742-132	Sequence 132, App	222	20	69.0	702	6	US-10-995-561-942	Sequence 942, App
150	20	69.0	254	6	US-10-467-657-6144	Sequence 6144, Ap	223	20	69.0	721	6	US-10-467-962B-49	Sequence 49, Appl
151	20	69.0	272	6	US-10-632-150-46	Sequence 46, Appl	224	20	69.0	738	7	US-11-147-047-48	Sequence 48, Appl
152	20	69.0	272	7	US-11-073-457-46	Sequence 46, Appl	225	20	69.0	741	6	US-10-467-657-6266	Sequence 6266, Ap
153	20	69.0	272	7	US-11-073-460-46	Sequence 46, Appl	226	20	69.0	747	7	US-11-018-018-1	Sequence 1, Appli
154	20	69.0	288	6	US-10-467-657-1272	Sequence 1272, Ap	227	20	69.0	747	7	US-11-047-757-1	Sequence 1, Appli
155	20	69.0	291	7	US-11-102-883-22	Sequence 22, Appl	228	20	69.0	754	6	US-10-995-561-941	Sequence 941, App
156	20	69.0	292	7	US-11-102-883-24	Sequence 24, Appl	229	20	69.0	797	6	US-10-995-561-802	Sequence 802, App
157	20	69.0	294	6	US-10-467-657-7686	Sequence 7686, Ap	230	20	69.0	852	6	US-10-467-657-5004	Sequence 5004, Ap
158	20	69.0	296	6	US-10-965-972-8	Sequence 8, Appli	231	20	69.0	916	6	US-10-467-657-4342	Sequence 4342, Ap
159	20	69.0	296	7	US-11-102-978-7	Sequence 7, Appli	232	20	69.0	926	6	US-10-841-129-2	Sequence 2, Appli
160	20	69.0	314	7	US-11-018-018-4	Sequence 4, Appli	233	20	69.0	928	6	US-10-841-129-4	Sequence 4, Appli
161	20	69.0	314	7	US-11-047-757-4	Sequence 4, Appli	234	20	69.0	984	7	US-11-055-822-508	Sequence 508, App
162	20	69.0	315	6	US-10-524-647-25	Sequence 25, Appl	235	20	69.0	984	7	US-11-055-822-594	Sequence 594, App
163	20	69.0	317	6	US-10-995-561-798	Sequence 798, App	236	20	69.0	989	6	US-10-821-234-975	Sequence 975, App
164	20	69.0	319	6	US-10-467-657-640	Sequence 640, App	237	20	69.0	1070	7	US-11-147-047-49	Sequence 49, Appl
165	20	69.0	321	6	US-10-467-657-2504	Sequence 2504, Ap	238	20	69.0	1278	6	US-10-995-561-952	Sequence 952, App
166	20	69.0	322	6	US-11-073-605-4	Sequence 4, Appli	239	20	69.0	1451	7	US-11-046-346-1	Sequence 1, Appli
167	20	69.0	334	6	US-10-467-657-7692	Sequence 7692, Ap	240	20	69.0	1857	7	US-11-102-217-2	Sequence 2, Appli
168	20	69.0	334	6	US-10-467-657-8440	Sequence 8440, Ap	241	20	69.0	2261	6	US-10-995-561-600	Sequence 600, App
169	20	69.0	325	6	US-10-454-437-142	Sequence 142, App	242	20	69.0	2261	7	US-11-055-309A-9	Sequence 9, Appli
170	20	69.0	329	6	US-10-524-647-2	Sequence 2, Appli	243	20	69.0	2261	7	US-11-055-309A-10	Sequence 10, Appl
171	20	69.0	329	6	US-10-524-647-23	Sequence 23, Appl	244	20	69.0	2504	6	US-10-647-956A-8	Sequence 8, Appli

245 19 65.5 9 6 US-10-982-891-44
246 19 65.5 13 6 US-10-511-559-836
247 19 65.5 13 6 US-10-511-559-837
248 19 65.5 13 6 US-10-511-559-838
249 19 65.5 13 6 US-10-511-559-839
250 19 65.5 13 6 US-10-511-559-840
251 19 65.5 13 6 US-10-511-559-841
252 19 65.5 13 6 US-10-511-559-842
253 19 65.5 19 6 US-10-467-657-8712
254 19 65.5 27 6 US-10-986-501-347
255 19 65.5 28 6 US-10-250-581-2
256 19 65.5 28 6 US-10-250-581-2
257 19 65.5 30 6 US-10-467-657-6336
258 19 65.5 38 6 US-10-467-657-6336
259 19 65.5 40 6 US-10-467-657-1296
260 19 65.5 40 6 US-10-250-581-3
261 19 65.5 42 6 US-10-250-581-3
262 19 65.5 42 6 US-10-467-657-8811
263 19 65.5 42 6 US-10-250-581-4
264 19 65.5 42 6 US-10-250-581-4
265 19 65.5 76 7 US-11-000-463-318
266 19 65.5 76 7 US-11-000-463-790
267 19 65.5 83 6 US-10-467-657-5366
268 19 65.5 95 6 US-10-467-657-2518
269 19 65.5 98 6 US-10-467-657-6988
270 19 65.5 100 7 US-11-123-896-137
271 19 65.5 102 6 US-10-793-626-2592
272 19 65.5 102 6 US-10-485-788A-650
273 19 65.5 102 7 US-11-053-076-122
274 19 65.5 105 6 US-10-131-826A-470
275 19 65.5 107 6 US-10-793-626-1586
276 19 65.5 107 6 US-10-467-657-1018
277 19 65.5 108 6 US-10-467-657-4266
278 19 65.5 114 6 US-10-821-234-1140
279 19 65.5 114 6 US-10-467-657-124
280 19 65.5 114 6 US-10-467-657-1414
281 19 65.5 114 6 US-10-467-657-3162
282 19 65.5 114 6 US-10-467-657-3754
283 19 65.5 114 6 US-10-467-657-5012
284 19 65.5 116 6 US-10-467-657-8674
285 19 65.5 131 6 US-10-467-657-5308
286 19 65.5 137 7 US-11-193-512-31
287 19 65.5 138 6 US-10-793-626-1254
288 19 65.5 138 7 US-11-137-465-37
289 19 65.5 139 6 US-10-467-657-28
290 19 65.5 139 6 US-10-467-657-8188
291 19 65.5 140 7 US-11-083-800-7
292 19 65.5 144 6 US-10-793-626-1640
293 19 65.5 144 6 US-10-793-626-1958
294 19 65.5 156 6 US-10-467-657-1280
295 19 65.5 157 7 US-11-116-144-167
296 19 65.5 160 6 US-10-793-626-750
297 19 65.5 182 6 US-10-980-388-89
298 19 65.5 186 6 US-10-467-657-3918
299 19 65.5 192 6 US-10-467-657-5588
300 19 65.5 193 7 US-11-102-240-142

ALIGNMENTS

RESULT 1
US-10-923-605-5
; Sequence 5, Application US/10923605
; Publication No. US2005024972A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289

; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-923-605-5

Query Match 89.7%; Score 26; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 2
US-10-934-818-5
; Sequence 5, Application US/10934818
; Publication No. US2005025512A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5

Query Match 89.7%; Score 26; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 3
US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US2005024433A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.

; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-36

Query Match 89.7%; Score 26; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 4

US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

Query Match 89.7%; Score 26; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 5

US-10-923-605-1
; Sequence 1, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605

; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-923-605-1

Query Match 89.7%; Score 26; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 6

US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1

Query Match 89.7%; Score 26; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 7

US-11-016-706-37
; Sequence 37, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24

; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-37

Query Match 89.7%; Score 26; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 8

US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match 89.7%; Score 26; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.9;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 9

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 89.7%; Score 26; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.9;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 10

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 89.7%; Score 26; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.9;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 11

US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hvild
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease
US-10-982-545-15

OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
OTHER INFORMATION: Alzheimer's disease amyloid protein

NAME/KEY: SIGNAL
LOCATION: (1)..(17)
OTHER INFORMATION: signal peptide
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(40)
OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40
OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor

NAME/KEY: PEPTIDE
LOCATION: (18)..(687)
OTHER INFORMATION: soluble APP-alpha
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (18)..(671)
OTHER INFORMATION: soluble APP-beta

NAME/KEY: PEPTIDE
LOCATION: (672)..(770)
OTHER INFORMATION: C99
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (672)..(713)
OTHER INFORMATION: beta-amyloid protein 42

NAME/KEY: PEPTIDE
LOCATION: (672)..(711)
OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (688)..(770)
OTHER INFORMATION: C83

NAME/KEY: PEPTIDE
LOCATION: (688)..(713)
OTHER INFORMATION: P3(42)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (688)..(711)
OTHER INFORMATION: P3(40)

NAME/KEY: PEPTIDE
LOCATION: (712)..(770)
OTHER INFORMATION: gamma-CTF (59)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (714)..(770)
OTHER INFORMATION: gamma-CTF (57)

NAME/KEY: PEPTIDE
LOCATION: (721)..(770)
OTHER INFORMATION: gamma-CTF (50)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (740)..(770)
OTHER INFORMATION: C31

US-10-982-545-15

Query Match 89.7%; Score 26; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:|||||
Db 687 KLVFFA 692

RESULT 12

US-10-789-273-38
Sequence 38, Application US/10789273
Publication No. US20050249725A1
GENERAL INFORMATION:
APPLICANT: Basi, Guriq
APPLICANT: Saidanna, Jose
APPLICANT: Yednock, Ted
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
FILE REFERENCE: ELN-002CP
CURRENT APPLICATION NUMBER: US/10/789,273
CURRENT FILING DATE: 2004-02-27
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/388,389
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US 60/251,892
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 770
TYPE: PRT
ORGANISM: Homo sapiens
US-10-789-273-38

Query Match 89.7%; Score 26; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:|||||
Db 687 KLVFFA 692

RESULT 13

US-11-186-284-125
Sequence 125, Application US/11186284
Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF COLON CANCER
FILE REFERENCE: MPM01-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 125
LENGTH: 660
TYPE: PRT
ORGANISM: Homo Sapiens
US-11-186-284-125

Query Match 86.2%; Score 25; DB 7; Length 660;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 Db 531 KAVFFA 536

RESULT 14
 US-10-821-234-917
 ; Sequence 917, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pt_seq_genes Version 1.0
 ; SEQ ID NO 917
 ; LENGTH: 708
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-821-234-917

Query Match 86.2%; Score 25; DB 6; Length 708;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 Db 579 KAVFFA 584

RESULT 15
 US-10-131-826A-410
 ; Sequence 410, Application US/10131826A
 ; Publication No. US20050245730A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330R1C128
 ; CURRENT APPLICATION NUMBER: US/10/131,826A
 ; CURRENT FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: 60/049911
 ; PRIOR FILING DATE: 1997-06-18
 ; PRIOR APPLICATION NUMBER: 60/056974
 ; PRIOR FILING DATE: 1997-08-26
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059115
 ; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059122
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059184
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059352
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: 60/059588
 ; PRIOR FILING DATE: 1997-09-19
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 410
 ; LENGTH: 229
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-131-826A-410

Query Match 82.8%; Score 24; DB 6; Length 229;
 Best Local Similarity 80.0%; Pred. No. 79;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
 Db 118 KVIFF 122

RESULT 16
 US-10-467-657-330
 ; Sequence 330, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 330
 ; LENGTH: 269
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-330

Query Match 82.8%; Score 24; DB 6; Length 269;
 Best Local Similarity 80.0%; Pred. No. 92;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
 Db 11 KVIFF 15

RESULT 17
 US-10-793-626-2450
 ; Sequence 2450, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3480US
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; CURRENT FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258

; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2450
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2450

Query Match 82.8%; Score 24; DB 6; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
DB 296 VVFFA 300
|||

RESULT 18

US-10-793-626-1056
; Sequence 1056, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1056
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1056

Query Match 82.8%; Score 24; DB 6; Length 400;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVPF 5
DB 7 KIVFF 11
|||

RESULT 19

US-10-995-561-593
; Sequence 593, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 593
; LENGTH: 3623
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-593

Query Match 82.8%; Score 24; DB 6; Length 3623;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVPF 5
DB 2544 KVVPF 2548
|||

RESULT 20
US-10-467-657-7892
; Sequence 7892, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7892
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7892

Query Match 79.3%; Score 23; DB 6; Length 50;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVPF 5
DB 33 KIIFP 37
|||

RESULT 21

US-11-210-316-18
; Sequence 18, Application US/11210316
; Publication No. US20050282278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (34)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (85)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:

; NAME/KEY: UNSURE
; LOCATION: (98)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (112)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (151)
; OTHER INFORMATION: Xaa = any amino acid
US-11-210-316-18

Query Match 79.3%; Score 23; DB 7; Length 167;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KVFFFA 6
|:|:|
Db 105 KVIFA 109

RESULT 22
US-10-467-657-432
; Sequence 432, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 432
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-432

Query Match 79.3%; Score 23; DB 6; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFFFA 6
|:|:|
Db 128 KVIFA 133

RESULT 23
US-10-793-626-2500
; Sequence 2500, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2500
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2500

Query Match 79.3%; Score 23; DB 6; Length 265;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFFFA 6
|:|:|
Db 230 KVFFFA 235

RESULT 24
US-10-467-657-2014
; Sequence 2014, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2014
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2014

Query Match 79.3%; Score 23; DB 6; Length 347;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFFA 6
|:|:|
Db 73 IVFFFA 77

RESULT 25
US-10-467-657-9070
; Sequence 9070, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9070
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9070

Query Match 79.3%; Score 23; DB 6; Length 402;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
:||||
Db 264 IVFFA 268

RESULT 26

US-10-467-657-2120
; Sequence 2120, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2120
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2120

Query Match 79.3%; Score 23; DB 6; Length 426;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
:||||
Db 414 IVFFA 418

RESULT 27

US-10-995-561-959
; Sequence 959, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 959
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-959

Query Match 79.3%; Score 23; DB 6; Length 481;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
:||||
Db 275 KVVFFA 280

RESULT 28

US-11-210-316-22
; Sequence 22, Application US/11210316
; Publication No. US20050282278A1

; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 22
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (102)
; OTHER INFORMATION: Xaa = any amino acid
US-11-210-316-22

Query Match 79.3%; Score 23; DB 7; Length 510;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
:||||
Db 96 IVFFA 100

RESULT 29

US-10-689-742-13
; Sequence 13, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: Lavallie, Edward R
; APPLICANT: Racine, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-13

Query Match 79.3%; Score 23; DB 6; Length 524;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
:||||
Db 404 IVFFA 408

RESULT 30

US-11-210-316-26
; Sequence 26, Application US/11210316
; Publication No. US20050282278A1

; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-210-316-26

Query Match 79.3%; Score 23; DB 7; Length 539;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6
|:|
Db 121 VIFFA 125

RESULT 31
US-10-131-826A-230
; Sequence 230, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 230
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-230
Query Match 79.3%; Score 23; DB 6; Length 677;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6
|:|
Db 557 VVFFA 561

RESULT 32
US-10-873-528-2
; Sequence 2, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2233
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-2

Query Match 79.3%; Score 23; DB 6; Length 2233;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFFFA 6
|:|
Db 1895 KVQFFA 1900

RESULT 33
US-11-098-674-1
; Sequence 1, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elmova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-098-674-1

Query Match 75.9%; Score 22; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.3e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
|:|
Db 1 KLVFF 5

RESULT 34
US-10-467-657-7886
; Sequence 7886, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7886
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7886

Query Match 75.9%; Score 22; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFF 6
|:|
Db 14 KVRFF 19

RESULT 35
US-10-467-657-5436
; Sequence 5436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5436
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5436

Query Match 75.9%; Score 22; DB 6; Length 47;
Best Local Similarity 80.0%; Pred. No. 47;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
|:|
Db 36 KVVFF 40

RESULT 36
US-10-793-626-2836
; Sequence 2836, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatencIn Ver. 2.1
; SEQ ID NO 2836
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2836

Query Match 75.9%; Score 22; DB 6; Length 182;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFF 6
|:|
Db 14 KVTFF 19

RESULT 37
US-10-467-657-3436
; Sequence 3436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3436
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3436

Query Match 75.9%; Score 22; DB 6; Length 190;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFF 6
|:|
Db 46 KTVFY 51


```
RESULT 38
US-10-821-234-1372
; Sequence 1372, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_Genes Version 1.0
; SEQ ID NO 1372
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1372

Query Match          75.9%; Score 22; DB 6; Length 211;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
Db      33 KTVYFA 38

RESULT 39
US-10-957-569-45
; Sequence 45, Application US/10957569
; Publication No. US20050246785A1
; GENERAL INFORMATION:
; APPLICANT: COOK, Zhihong et al.
; TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 2750-1577PUS3
; CURRENT APPLICATION NUMBER: US/10/957,569
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/950,321
; PRIOR FILING DATE: 2004-09-23
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-957-569-45

Query Match          75.9%; Score 22; DB 6; Length 278;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFF 5
Db      55 KVLFF 59

RESULT 40
US-11-082-389-106
; Sequence 106, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
```

```
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: EGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 106
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-106

Query Match          75.9%; Score 22; DB 7; Length 440;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFF 5
Db      333 RVVFF 337

RESULT 41
US-10-793-626-24
; Sequence 24, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-24

Query Match          75.9%; Score 22; DB 6; Length 482;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
Db      388 KVLFFA 393
```

RESULT 42
US-11-080-991-104
; Sequence 104, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-104

Query Match 75.9%; Score 22; DB 7; Length 522;
Best Local Similarity 60.0%; Pred. No. 4.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
: : : :
DB 260 IIFFA 264

RESULT 43
US-10-793-626-1930
; Sequence 1930, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1930
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1930

Query Match 75.9%; Score 22; DB 6; Length 528;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
: : : :
DB 477 KLVFF 481

RESULT 44
US-10-467-657-2868
; Sequence 2868, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2868
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2868

Query Match 75.9%; Score 22; DB 6; Length 533;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
: : : :
DB 371 IIFFA 375

RESULT 45
US-11-082-389-104
; Sequence 104, Application US/11082389
; Publication No. US2005024935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGI-131CPGN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 104
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-104

Query Match 75.9%; Score 22; DB 7; Length 569;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5
Db 462 RVVFF 466

RESULT 46

US-11-000-463-347
; Sequence 347, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong B.
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 347
; LENGTH: 1061
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-347

Query Match 75.9%; Score 22; DB 7; Length 1061;
Best Local Similarity 83.3%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFF 6
Db 131 KVDFFA 136

RESULT 47

US-11-000-463-348
; Sequence 348, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong B.
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-348

Query Match 75.9%; Score 22; DB 7; Length 1091;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFF 6
Db 131 KVDFFA 136

RESULT 48

US-11-075-185-7
; Sequence 7, Application US/11075185
; Publication No. US20050266434A1
; GENERAL INFORMATION:
; APPLICANT: REEVES, CHRISTOPHER D
; APPLICANT: JULIEN, BRYAN
; APPLICANT: REID, RALPH
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
; FILE REFERENCE: 010099.03
; CURRENT APPLICATION NUMBER: US/11/075,185
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/568,290
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 3507
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-11-075-185-7

Query Match 75.9%; Score 22; DB 7; Length 3507;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFF 6
Db 565 KVVFFA 570

RESULT 49

US-10-510-386-114
; Sequence 114, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne

```

; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 114
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-114

```

```

Query Match          72.4%; Score 21; DB 6; Length 83;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 VVFFA 6
        |:|
Db      17 VLFFA 21

```

```

RESULT 50
US-10-467-657-4746
; Sequence 4746, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4746
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4746

```

```

Query Match          72.4%; Score 21; DB 6; Length 98;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KVFFF 5
        |:|
Db      62 KIVFY 66

```

```

RESULT 51
US-10-467-657-9209
; Sequence 9209, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8

```

```

; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9209
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9209

```

```

Query Match          72.4%; Score 21; DB 6; Length 105;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 KVVFPA 6
        |:|
Db      3 QTVFPA 8

```

```

RESULT 52
US-10-821-234-1701
; Sequence 1701, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1701
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1701

```

```

Query Match          72.4%; Score 21; DB 6; Length 137;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 KVFFF 5
        |:|
Db      28 KVTFP 32

```

```

RESULT 53
US-10-467-657-2486
; Sequence 2486, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2486
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2486

```

```
Query Match      72.4%; Score 21; DB 6; Length 140;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVPF 5
Db 89 KVIFY 93

RESULT 54
US-10-467-657-2420
; Sequence 2420, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2420
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2420

Query Match      72.4%; Score 21; DB 6; Length 155;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6
Db 18 MVFFA 22

RESULT 55
US-10-467-657-2232
; Sequence 2232, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2232
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2232

Query Match      72.4%; Score 21; DB 6; Length 179;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVPFA 6
Db 19 LVFFA 23

RESULT 58
US-10-131-826A-4
; Sequence 4, Application US/10131826A
; Publication No. US20050245730A1
```

```
Db 107 KVVSPA 112

RESULT 56
US-10-467-657-6318
; Sequence 6318, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6318
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6318

Query Match      72.4%; Score 21; DB 6; Length 210;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVPF 5
Db 116 KAVFF 120

RESULT 57
US-10-467-657-6932
; Sequence 6932, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6932
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6932

Query Match      72.4%; Score 21; DB 6; Length 211;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVFFA 6
Db 19 LVFFA 23

RESULT 58
US-10-131-826A-4
; Sequence 4, Application US/10131826A
; Publication No. US20050245730A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 4
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-4

Query Match          72.4%; Score 21; DB 6; Length 215;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VVFFA 6
Db      166 LVFFA 170

RESULT 59
US-10-467-657-568
; Sequence 568, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838
; Sequence 4838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838

Query Match          72.4%; Score 21; DB 6; Length 228;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VVFFA 6
Db      156 LVFFA 160

RESULT 60
US-10-467-657-4838
; Sequence 4838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838

Query Match          72.4%; Score 21; DB 6; Length 228;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VVFFA 6
Db      156 LVFFA 160

RESULT 61
US-10-821-234-1322
; Sequence 1322, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1322
; LENGTH: 233
; TYPE: PRT
US-10-821-234-1322
```

; ORGANISM: Homo sapiens
US-10-821-234-1322

Query Match 72.4%; Score 21; DB 6; Length 233;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KVFFA 6
Db 166 LVFFA 170

RESULT 62

US-10-995-561-544
; Sequence 544, Application US/10995561
; Publication No. US2005027054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 544

; LENGTH: 266

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (1)...(266)

; OTHER INFORMATION: Xaa = Any Amino Acid

US-10-995-561-544

Query Match 72.4%; Score 21; DB 6; Length 266;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVPF 5
Db 152 KVTFP 156

RESULT 63

US-10-995-561-543

; Sequence 543, Application US/10995561

; Publication No. US2005027054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 543

; LENGTH: 267

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (1)...(267)

; OTHER INFORMATION: Xaa = Any Amino Acid

US-10-995-561-543

Query Match 72.4%; Score 21; DB 6; Length 267;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVPF 5
Db 153 KVTFP 157

RESULT 64

US-11-055-822-16

; Sequence 16, Application US/11055822

; Publication No. US20050260707A1

; GENERAL INFORMATION:

; APPLICANT: Pompeius, Markus

; APPLICANT: Kroger, Burkhard

; APPLICANT: Schroder, Hartwig

; APPLICANT: Zelder, Oskar

; APPLICANT: Habernauer, Gregor

; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING

; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS

; FILE REFERENCE: BGI-121CPCN

; CURRENT APPLICATION NUMBER: US/11/055,822

; CURRENT FILING DATE: 2005-02-11

; PRIOR APPLICATION NUMBER: 09/606,740

; PRIOR FILING DATE: 2000-06-23

; PRIOR APPLICATION NUMBER: 60/141,031

; PRIOR FILING DATE: 1999-06-25

; PRIOR APPLICATION NUMBER: 60/142,101

; PRIOR FILING DATE: 1999-07-02

; PRIOR APPLICATION NUMBER: 60/148,613

; PRIOR FILING DATE: 1999-08-12

; PRIOR APPLICATION NUMBER: 60/187,970

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: DE 19930476.9

; PRIOR FILING DATE: 1999-07-01

; PRIOR APPLICATION NUMBER: DE 19931415.2

; PRIOR FILING DATE: 1999-07-08

; PRIOR APPLICATION NUMBER: DE 19931418.7

; PRIOR FILING DATE: 1999-07-08

; PRIOR APPLICATION NUMBER: DE 19931419.5

; PRIOR FILING DATE: 1999-07-08

; PRIOR APPLICATION NUMBER: DE 19931420.9

; PRIOR FILING DATE: 1999-07-08

; Remaining prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1158

; SEQ ID NO 16

; LENGTH: 312

; TYPE: PRT

; ORGANISM: Corynebacterium glutamicum

US-11-055-822-16

Query Match 72.4%; Score 21; DB 7; Length 312;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVPF 5
Db 133 EVVPF 137

RESULT 65

US-10-793-626-2476

; Sequence 2476, Application US/10793626

; Publication No. US20050255478A1

; GENERAL INFORMATION:

; APPLICANT: KIMMERLY, WILLIAM JOHN

; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

; FILE REFERENCE: PU3480US

; CURRENT APPLICATION NUMBER: US/10/793,626

; CURRENT FILING DATE: 2004-03-04

; PRIOR APPLICATION NUMBER: 60/164,258

; PRIOR FILING DATE: 1999-11-09

; NUMBER OF SEQ ID NOS: 4472

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2476

; LENGTH: 330

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2476

Query Match 72.4%; Score 21; DB 6; Length 330;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVPF 5
|::||
DB 3 KIMFF 7

RESULT 66
US-10-793-626-2734
; Sequence 2734, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2734
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2734

Query Match 72.4%; Score 21; DB 6; Length 330;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVPF 5
|::||
DB 3 KIMFF 7

RESULT 67
US-10-485-517-234
; Sequence 234, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynex Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 234
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-234

Query Match 72.4%; Score 21; DB 6; Length 337;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVPF 5
|::||
DB 175 KVAFP 179

RESULT 68
US-10-878-556A-19
; Sequence 19, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/cn03_human
; DATABASE ENTRY DATE: 2001-10-16
US-10-878-556A-19

Query Match 72.4%; Score 21; DB 6; Length 338;
Best Local Similarity 60.0%; Pred. No. 5.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVPF 5
|::||
DB 76 KLIFF 80

RESULT 69
US-10-131-826A-376
; Sequence 376, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115


```

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 376
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-376

Query Match          72.4%; Score 21; DB 6; Length 344;
Best Local Similarity 60.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5
Db 279 KLIPF 283

RESULT 70
US-10-467-657-7996
; Sequence 7996, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7996
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7996

Query Match          72.4%; Score 21; DB 6; Length 355;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KVVFF 6
Db 5 KTTFF 10

RESULT 71
US-11-055-822-572
; Sequence 572, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor

```

```

; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 572
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-572

Query Match          72.4%; Score 21; DB 7; Length 358;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVVFF 6
Db 61 KIVFF 66

RESULT 72
US-11-055-822-836
; Sequence 836, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08

```

```
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 836
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-055-822-836

Query Match          72.4%; Score 21; DB 7; Length 358;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 61 KIWFFA 66

RESULT 73
US-10-467-657-7420
; Sequence 7420, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7420
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7420

Query Match          72.4%; Score 21; DB 6; Length 406;
Best Local Similarity 66.7%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 310 KTAFFA 315

RESULT 74
US-10-878-556A-1
; Sequence 1, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (307)..(307)
```

```
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: haugp:006101-3-0
; DATABASE ENTRY DATE: 2003-02-16
US-10-878-556A-1

Query Match          72.4%; Score 21; DB 6; Length 414;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVFFA 6
Db 59 VMFFA 63

RESULT 75
US-11-194-246-308
; Sequence 308, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MEI
; FILE REFERENCE: 00592.US1 (M&R 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 308
; LENGTH: 432
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-308

Query Match          72.4%; Score 21; DB 7; Length 432;
Best Local Similarity 60.0%; Pred. No. 6.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
Db 4 KILFF 8

Search completed: December 29, 2005, 18:50:18
Job time : 4.29032 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds
(without alignments)
37.818 Million cell updates/sec

Title: US-10-009-122-9

Perfect score: 29

Sequence: 1 KVFPPA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	3	US-09-867-847-18
2	29	100.0	6	3	US-09-867-847-26
3	29	100.0	6	3	US-09-915-092-8
4	29	100.0	6	3	US-09-915-092-16
5	29	100.0	6	3	US-09-747-408-9
6	29	100.0	6	3	US-09-747-408-17
7	29	100.0	6	5	US-10-728-028-8
8	29	100.0	6	5	US-10-728-028-16
9	29	100.0	6	5	US-10-825-958-16
10	29	100.0	6	5	US-10-825-958-24
11	29	100.0	37	4	US-10-641-924-7
12	29	100.0	37	4	US-10-642-255-7
13	29	100.0	60	4	US-10-437-963-173619
14	29	100.0	87	4	US-10-437-963-133986
15	29	100.0	109	4	US-10-437-963-105773
16	29	100.0	135	4	US-10-437-963-141578
17	29	100.0	175	4	US-10-437-963-122124
18	29	100.0	186	5	US-10-481-032A-214
19	29	100.0	186	5	US-10-481-032A-228
20	29	100.0	188	4	US-10-437-963-172476
21	29	100.0	198	4	US-10-437-963-172452
22	29	100.0	416	6	US-10-055-475-14
23	29	100.0	416	6	US-11-042-922-14
24	29	100.0	514	4	US-10-055-475-13
25	29	100.0	514	6	US-11-042-922-13
26	29	100.0	925	4	US-10-408-765A-2031
27	29	100.0	925	4	US-10-755-889-234

28	29	100.0	925	5	US-10-370-7158-8	Sequence 8, Appli
29	29	100.0	925	5	US-10-631-467-680	Sequence 680, App
30	29	100.0	925	5	US-10-631-467-747	Sequence 747, App
31	29	100.0	1144	3	US-09-870-759-124	Sequence 124, App
32	29	100.0	1144	3	US-09-751-708A-124	Sequence 124, App
33	29	100.0	1144	4	US-10-428-817A-120	Sequence 120, App
34	29	100.0	1144	5	US-10-937-758A-101	Sequence 101, App
35	29	100.0	1144	5	US-10-631-467-1388	Sequence 1388, Ap
36	29	100.0	1144	5	US-10-631-467-1464	Sequence 1464, Ap
37	29	100.0	1640	4	US-10-437-963-109646	Sequence 109646,
38	28	96.6	6	3	US-09-867-847-11	Sequence 11, Appl
39	28	96.6	6	3	US-09-867-847-19	Sequence 19, Appl
40	28	96.6	6	3	US-09-915-092-1	Sequence 1, Appli
41	28	96.6	6	3	US-09-915-092-9	Sequence 9, Appli
42	28	96.6	6	3	US-09-747-408-1	Sequence 1, Appli
43	28	96.6	6	3	US-09-747-408-10	Sequence 10, Appl
44	28	96.6	6	5	US-10-728-028-1	Sequence 1, Appli
45	28	96.6	6	5	US-10-728-028-9	Sequence 9, Appli
46	28	96.6	6	5	US-10-825-958-9	Sequence 9, Appli
47	28	96.6	6	5	US-10-825-958-17	Sequence 17, Appl
48	28	96.6	58	4	US-10-425-115-280164	Sequence 280164,
49	28	96.6	90	4	US-10-424-599-165325	Sequence 165325,
50	28	96.6	93	4	US-10-424-599-240310	Sequence 240310,
51	28	96.6	99	5	US-10-450-763-56957	Sequence 56957, A
52	27	93.1	564	6	US-11-097-143-12723	Sequence 12723, A
53	27	93.1	1443	6	US-11-097-143-32208	Sequence 32208, A
54	26	89.7	6	3	US-09-867-847-7	Sequence 7, Appli
55	26	89.7	6	3	US-09-867-847-20	Sequence 20, Appl
56	26	89.7	6	3	US-09-972-475-9	Sequence 9, Appli
57	26	89.7	6	3	US-09-915-092-10	Sequence 10, Appl
58	26	89.7	6	3	US-09-915-092-28	Sequence 28, Appl
59	26	89.7	6	3	US-09-956-625-25	Sequence 25, Appl
60	26	89.7	6	3	US-09-747-408-3	Sequence 3, Appli
61	26	89.7	6	3	US-09-747-408-11	Sequence 11, Appl
62	26	89.7	6	4	US-10-463-729-9	Sequence 9, Appli
63	26	89.7	6	5	US-10-728-028-10	Sequence 10, Appl
64	26	89.7	6	5	US-10-728-028-27	Sequence 27, Appl
65	26	89.7	6	5	US-10-728-028-28	Sequence 28, Appl
66	26	89.7	6	5	US-10-825-958-7	Sequence 7, Appli
67	26	89.7	6	5	US-10-825-958-18	Sequence 18, Appl
68	26	89.7	6	5	US-10-666-095-3	Sequence 3, Appli
69	26	89.7	7	3	US-09-867-847-12	Sequence 12, Appl
70	26	89.7	7	3	US-09-867-847-27	Sequence 27, Appl
71	26	89.7	7	3	US-09-867-847-28	Sequence 28, Appl
72	26	89.7	7	3	US-09-972-475-7	Sequence 7, Appli
73	26	89.7	7	3	US-09-915-092-2	Sequence 2, Appli
74	26	89.7	7	3	US-09-915-092-17	Sequence 17, Appl
75	26	89.7	7	3	US-09-915-092-18	Sequence 18, Appl
76	26	89.7	7	3	US-09-747-408-2	Sequence 2, Appli
77	26	89.7	7	3	US-09-747-408-18	Sequence 18, Appl
78	26	89.7	7	3	US-09-747-408-19	Sequence 19, Appl
79	26	89.7	7	4	US-10-463-729-7	Sequence 7, Appli
80	26	89.7	7	5	US-10-728-028-2	Sequence 2, Appli
81	26	89.7	7	5	US-10-728-028-17	Sequence 17, Appl
82	26	89.7	7	5	US-10-728-028-18	Sequence 18, Appl
83	26	89.7	7	5	US-10-825-958-10	Sequence 10, Appl
84	26	89.7	7	5	US-10-825-958-25	Sequence 25, Appl
85	26	89.7	7	5	US-10-825-958-26	Sequence 26, Appl
86	26	89.7	7	5	US-10-810-881A-128	Sequence 128, App
87	26	89.7	8	3	US-10-505-313-269	Sequence 269, App
88	26	89.7	8	3	US-09-850-061A-44	Sequence 44, Appl
89	26	89.7	8	3	US-09-972-475-5	Sequence 5, Appli
90	26	89.7	8	4	US-10-235-483-1	Sequence 1, Appli
91	26	89.7	8	4	US-10-463-729-5	Sequence 5, Appli
92	26	89.7	8	4	US-10-281-092-42	Sequence 42, Appl
93	26	89.7	8	4	US-10-721-774-44	Sequence 44, Appl
94	26	89.7	8	5	US-10-810-881A-125	Sequence 125, App
95	26	89.7	8	5	US-10-817-979-73	Sequence 73, Appl
96	26	89.7	9	3	US-09-867-847-9	Sequence 9, Appli
97	26	89.7	9	3	US-09-899-815-2	Sequence 2, Appli
98	26	89.7	9	3	US-09-747-408-20	Sequence 20, Appl
99	26	89.7	9	4	US-10-235-483-64	Sequence 64, Appl
100	26	89.7	9	4	US-10-619-454-3	Sequence 3, Appli

101	26	89.7	9	4	US-10-619-454-25	Sequence 25, Appl	174	26	89.7	12	6	US-11-012-797A-33	Sequence 33, Appl
102	26	89.7	9	4	US-10-619-454-28	Sequence 28, Appl	175	26	89.7	13	4	US-10-281-458-1	Sequence 1, Appl
103	26	89.7	9	4	US-10-619-454-57	Sequence 57, Appl	176	26	89.7	13	5	US-10-625-854-127	Sequence 127, App
104	26	89.7	9	4	US-10-619-454-157	Sequence 157, Appl	177	26	89.7	13	5	US-10-625-854-140	Sequence 140, App
105	26	89.7	10	3	US-09-867-847-29	Sequence 29, Appl	178	26	89.7	14	3	US-09-992-800-5	Sequence 5, Appl
106	26	89.7	10	3	US-09-915-092-19	Sequence 19, Appl	179	26	89.7	14	3	US-09-992-994-5	Sequence 5, Appl
107	26	89.7	10	5	US-10-889-999-20	Sequence 20, Appl	180	26	89.7	14	4	US-10-385-065-5	Sequence 5, Appl
108	26	89.7	10	5	US-10-889-999-21	Sequence 21, Appl	181	26	89.7	14	5	US-10-810-801A-114	Sequence 114, App
109	26	89.7	10	5	US-10-889-999-22	Sequence 22, Appl	182	26	89.7	14	5	US-10-505-313-2	Sequence 2, Appl
110	26	89.7	10	5	US-10-889-999-23	Sequence 23, Appl	183	26	89.7	14	5	US-10-625-854-115	Sequence 115, App
111	26	89.7	10	5	US-10-889-999-24	Sequence 24, Appl	184	26	89.7	14	5	US-10-625-854-128	Sequence 128, App
112	26	89.7	10	5	US-10-890-070-20	Sequence 20, Appl	185	26	89.7	14	5	US-10-625-854-141	Sequence 141, App
113	26	89.7	10	5	US-10-890-070-21	Sequence 21, Appl	186	26	89.7	14	6	US-11-063-350-5	Sequence 5, Appl
114	26	89.7	10	5	US-10-890-070-22	Sequence 22, Appl	187	26	89.7	15	3	US-09-972-475-14	Sequence 14, Appl
115	26	89.7	10	5	US-10-890-070-23	Sequence 23, Appl	188	26	89.7	15	3	US-09-996-357-9	Sequence 9, Appl
116	26	89.7	10	5	US-10-890-070-24	Sequence 24, Appl	189	26	89.7	15	4	US-10-235-483-56	Sequence 56, Appl
117	26	89.7	10	5	US-10-890-000-20	Sequence 20, Appl	190	26	89.7	15	4	US-10-235-483-57	Sequence 57, Appl
118	26	89.7	10	5	US-10-890-000-21	Sequence 21, Appl	191	26	89.7	15	4	US-10-235-483-58	Sequence 58, Appl
119	26	89.7	10	5	US-10-890-000-22	Sequence 22, Appl	192	26	89.7	15	4	US-10-235-483-60	Sequence 60, Appl
120	26	89.7	10	5	US-10-890-000-23	Sequence 23, Appl	193	26	89.7	15	4	US-10-235-483-61	Sequence 61, Appl
121	26	89.7	10	5	US-10-890-000-24	Sequence 24, Appl	194	26	89.7	15	4	US-10-235-483-62	Sequence 62, Appl
122	26	89.7	10	5	US-10-823-463-20	Sequence 20, Appl	195	26	89.7	15	4	US-10-235-483-63	Sequence 63, Appl
123	26	89.7	10	5	US-10-823-463-21	Sequence 21, Appl	196	26	89.7	15	4	US-10-235-483-65	Sequence 65, Appl
124	26	89.7	10	5	US-10-823-463-22	Sequence 22, Appl	197	26	89.7	15	4	US-10-463-729-14	Sequence 14, Appl
125	26	89.7	10	5	US-10-823-463-23	Sequence 23, Appl	198	26	89.7	15	5	US-10-625-854-103	Sequence 103, App
126	26	89.7	10	5	US-10-823-463-24	Sequence 24, Appl	199	26	89.7	15	5	US-10-625-854-116	Sequence 116, App
127	26	89.7	10	5	US-10-728-028-19	Sequence 19, Appl	200	26	89.7	15	5	US-10-625-854-129	Sequence 129, App
128	26	89.7	10	5	US-10-822-968-20	Sequence 20, Appl	201	26	89.7	15	5	US-10-625-854-142	Sequence 142, App
129	26	89.7	10	5	US-10-822-968-21	Sequence 21, Appl	202	26	89.7	16	5	US-10-625-854-91	Sequence 91, Appl
130	26	89.7	10	5	US-10-822-968-22	Sequence 22, Appl	203	26	89.7	16	5	US-10-625-854-104	Sequence 104, App
131	26	89.7	10	5	US-10-822-968-23	Sequence 23, Appl	204	26	89.7	16	5	US-10-625-854-117	Sequence 117, App
132	26	89.7	10	5	US-10-822-968-24	Sequence 24, Appl	205	26	89.7	16	5	US-10-625-854-130	Sequence 130, App
133	26	89.7	10	5	US-10-777-792-20	Sequence 20, Appl	206	26	89.7	16	5	US-10-625-854-143	Sequence 143, App
134	26	89.7	10	5	US-10-777-792-21	Sequence 21, Appl	207	26	89.7	17	3	US-09-992-800-3	Sequence 3, Appl
135	26	89.7	10	5	US-10-777-792-22	Sequence 22, Appl	208	26	89.7	17	3	US-09-992-994-3	Sequence 3, Appl
136	26	89.7	10	5	US-10-777-792-23	Sequence 23, Appl	209	26	89.7	17	3	US-09-998-491-8	Sequence 8, Appl
137	26	89.7	10	5	US-10-777-792-24	Sequence 24, Appl	210	26	89.7	17	4	US-10-385-065-3	Sequence 3, Appl
138	26	89.7	10	5	US-10-825-958-27	Sequence 27, Appl	211	26	89.7	17	4	US-10-451-367-26	Sequence 26, Appl
139	26	89.7	10	5	US-10-890-071-20	Sequence 20, Appl	212	26	89.7	17	4	US-10-475-281-8	Sequence 8, Appl
140	26	89.7	10	5	US-10-890-071-21	Sequence 21, Appl	213	26	89.7	17	4	US-10-810-919-3	Sequence 3, Appl
141	26	89.7	10	5	US-10-890-071-22	Sequence 22, Appl	214	26	89.7	17	5	US-10-684-346-24	Sequence 24, Appl
142	26	89.7	10	5	US-10-890-071-23	Sequence 23, Appl	215	26	89.7	17	5	US-10-997-078-46	Sequence 46, Appl
143	26	89.7	10	5	US-10-890-071-24	Sequence 24, Appl	216	26	89.7	17	5	US-10-997-700-19	Sequence 19, Appl
144	26	89.7	10	5	US-10-890-024-20	Sequence 20, Appl	217	26	89.7	17	6	US-11-063-350-3	Sequence 3, Appl
145	26	89.7	10	5	US-10-890-024-21	Sequence 21, Appl	218	26	89.7	17	6	US-11-066-697-950	Sequence 950, App
146	26	89.7	10	5	US-10-890-024-22	Sequence 22, Appl	219	26	89.7	17	6	US-11-066-697-983	Sequence 983, App
147	26	89.7	10	5	US-10-890-024-23	Sequence 23, Appl	220	26	89.7	19	3	US-09-823-242-5	Sequence 5, Appl
148	26	89.7	10	5	US-10-890-024-24	Sequence 24, Appl	221	26	89.7	19	4	US-10-816-529-5	Sequence 5, Appl
149	26	89.7	10	5	US-10-928-926-20	Sequence 20, Appl	222	26	89.7	19	4	US-10-816-529-5	Sequence 5, Appl
150	26	89.7	10	5	US-10-928-926-21	Sequence 21, Appl	223	26	89.7	19	4	US-10-815-353-5	Sequence 5, Appl
151	26	89.7	10	5	US-10-928-926-22	Sequence 22, Appl	224	26	89.7	19	4	US-10-815-391-5	Sequence 5, Appl
152	26	89.7	10	5	US-10-928-926-23	Sequence 23, Appl	225	26	89.7	19	5	US-10-828-548-5	Sequence 5, Appl
153	26	89.7	10	5	US-10-928-926-24	Sequence 24, Appl	226	26	89.7	19	5	US-10-816-380-5	Sequence 5, Appl
154	26	89.7	10	6	US-11-058-757-20	Sequence 20, Appl	227	26	89.7	19	5	US-10-816-380-5	Sequence 5, Appl
155	26	89.7	10	6	US-11-058-757-21	Sequence 21, Appl	228	26	89.7	19	5	US-10-889-999-75	Sequence 75, Appl
156	26	89.7	10	6	US-11-058-757-22	Sequence 22, Appl	229	26	89.7	19	5	US-10-890-070-75	Sequence 75, Appl
157	26	89.7	10	6	US-11-058-757-23	Sequence 23, Appl	230	26	89.7	19	5	US-10-890-000-75	Sequence 75, Appl
158	26	89.7	10	6	US-11-058-757-24	Sequence 24, Appl	231	26	89.7	19	5	US-10-788-666-5	Sequence 5, Appl
159	26	89.7	11	3	US-09-988-842-9	Sequence 9, Appl	232	26	89.7	19	5	US-10-923-471-5	Sequence 5, Appl
160	26	89.7	11	3	US-09-988-842-25	Sequence 25, Appl	233	26	89.7	19	5	US-10-823-463-75	Sequence 75, Appl
161	26	89.7	11	4	US-10-235-483-14	Sequence 14, Appl	234	26	89.7	19	5	US-10-923-469-5	Sequence 5, Appl
162	26	89.7	11	4	US-10-050-200-33	Sequence 33, Appl	235	26	89.7	19	5	US-10-933-559-5	Sequence 5, Appl
163	26	89.7	11	4	US-10-237-673-20	Sequence 20, Appl	236	26	89.7	19	5	US-10-815-404-5	Sequence 5, Appl
164	26	89.7	11	5	US-10-464-117-13	Sequence 13, Appl	237	26	89.7	19	5	US-10-934-603-5	Sequence 5, Appl
165	26	89.7	11	5	US-10-772-230-9	Sequence 9, Appl	238	26	89.7	19	5	US-10-923-474-5	Sequence 5, Appl
166	26	89.7	12	3	US-09-772-230-25	Sequence 25, Appl	239	26	89.7	19	5	US-10-884-892-5	Sequence 5, Appl
167	26	89.7	12	3	US-09-867-847-8	Sequence 8, Appl	240	26	89.7	19	5	US-10-822-968-75	Sequence 75, Appl
168	26	89.7	12	4	US-10-481-180-671	Sequence 671, App	241	26	89.7	19	5	US-10-777-792-75	Sequence 75, Appl
169	26	89.7	12	5	US-10-810-881A-115	Sequence 115, App	242	26	89.7	19	5	US-10-890-071-75	Sequence 75, Appl
170	26	89.7	12	5	US-10-810-881A-117	Sequence 117, App	243	26	89.7	19	5	US-10-890-024-75	Sequence 75, Appl
171	26	89.7	12	5	US-10-508-586-2	Sequence 2, Appl	244	26	89.7	19	5	US-10-934-819-5	Sequence 5, Appl
172	26	89.7	12	5	US-10-508-586-3	Sequence 3, Appl	245	26	89.7	19	5	US-10-923-267-5	Sequence 5, Appl
173	26	89.7	12	5	US-10-625-854-139	Sequence 139, App	246	26	89.7	19	5	US-10-928-926-75	Sequence 75, Appl

247 26 89.7 19 6 US-11-058-757-75 Sequence 75, Appl
248 26 89.7 19 6 US-11-108-102-5 Sequence 5, Appl
249 26 89.7 20 3 US-09-908-943A-25 Sequence 25, Appl
250 26 89.7 20 4 US-10-481-180-710 Sequence 710, Appl
251 26 89.7 20 5 US-10-801-487-25 Sequence 25, Appl
252 26 89.7 20 5 US-10-801-938-25 Sequence 25, Appl
253 26 89.7 20 5 US-10-801-509-25 Sequence 25, Appl
254 26 89.7 20 5 US-10-801-486-25 Sequence 25, Appl
255 26 89.7 20 5 US-10-801-493-25 Sequence 25, Appl
256 26 89.7 24 5 US-10-728-246-5 Sequence 5, Appl
257 26 89.7 24 5 US-10-728-246-6 Sequence 6, Appl
258 26 89.7 25 4 US-10-481-180-724 Sequence 724, Appl
259 26 89.7 26 3 US-09-792-079-11 Sequence 11, Appl
260 26 89.7 26 4 US-10-159-279-11 Sequence 11, Appl
261 26 89.7 28 3 US-09-867-847-4 Sequence 4, Appl
262 26 89.7 28 3 US-09-865-294-66 Sequence 66, Appl
263 26 89.7 28 3 US-09-792-079-5 Sequence 5, Appl
264 26 89.7 28 4 US-10-159-279-5 Sequence 5, Appl
265 26 89.7 28 4 US-10-363-082-2 Sequence 2, Appl
266 26 89.7 28 4 US-10-433-385-7 Sequence 7, Appl
267 26 89.7 28 4 US-10-390-472-4 Sequence 4, Appl
268 26 89.7 28 4 US-10-741-205-36 Sequence 36, Appl
269 26 89.7 28 4 US-10-416-262B-7 Sequence 7, Appl
270 26 89.7 28 4 US-10-481-180-735 Sequence 735, Appl
271 26 89.7 28 4 US-10-478-308-4 Sequence 4, Appl
272 26 89.7 28 4 US-10-478-307-4 Sequence 4, Appl
273 26 89.7 28 5 US-10-861-614-66 Sequence 66, Appl
274 26 89.7 28 5 US-10-825-958-4 Sequence 4, Appl
275 26 89.7 28 6 US-11-091-309-3 Sequence 3, Appl
276 26 89.7 28 6 US-11-066-697-959 Sequence 959, Appl
277 26 89.7 28 6 US-11-066-697-965 Sequence 965, Appl
278 26 89.7 28 6 US-11-066-697-976 Sequence 976, Appl
279 26 89.7 28 6 US-11-066-697-992 Sequence 992, Appl
280 26 89.7 28 6 US-11-066-697-1003 Sequence 1003, Appl
281 26 89.7 30 3 US-09-861-847-1 Sequence 1, Appl
282 26 89.7 30 4 US-10-301-488A-1 Sequence 1, Appl
283 26 89.7 30 4 US-10-666-423-1 Sequence 1, Appl
284 26 89.7 30 4 US-10-617-876-9 Sequence 9, Appl
285 26 89.7 30 4 US-10-619-454-24 Sequence 24, Appl
286 26 89.7 30 4 US-10-301-448-1 Sequence 1, Appl
287 26 89.7 30 5 US-10-775-562-5 Sequence 5, Appl
288 26 89.7 32 4 US-10-732-862A-99 Sequence 99, Appl
289 26 89.7 33 3 US-09-930-915A-295 Sequence 295, Appl
290 26 89.7 33 4 US-10-082-014-84 Sequence 84, Appl
291 26 89.7 33 4 US-10-372-076-85 Sequence 85, Appl
292 26 89.7 33 4 US-10-732-862A-98 Sequence 98, Appl
293 26 89.7 33 4 US-10-806-006-295 Sequence 295, Appl
294 26 89.7 33 4 US-10-677-074-85 Sequence 85, Appl
295 26 89.7 33 4 US-10-805-913-295 Sequence 295, Appl
296 26 89.7 33 4 US-10-481-180-746 Sequence 746, Appl
297 26 89.7 35 3 US-09-867-847-3 Sequence 3, Appl
298 26 89.7 35 3 US-09-972-475-16 Sequence 16, Appl
299 26 89.7 35 4 US-10-463-729-16 Sequence 16, Appl
300 26 89.7 35 5 US-10-825-958-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-867-847-18
; Sequence 18, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-18

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 2

US-09-867-847-26
; Sequence 26, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-26

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 3

US-09-915-092-8
; Sequence 8, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert

4

```
;
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-8

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 8
US-10-728-028-16
; Sequence 16, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNERULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-16

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 9
US-10-825-958-16
; Sequence 16, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-825-958-16

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 10
US-10-825-958-24
; Sequence 24, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-24

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 11
US-10-641-924-7
; Sequence 7, Application US/10641924
; Publication No. US20040096881A1
; GENERAL INFORMATION:
; APPLICANT: Blasko, Eric
; APPLICANT: Kauser, Katalin
; APPLICANT: Parkinson, John
; TITLE OF INVENTION: eNOS Mutants Useful for Gene Therapy
; FILE REFERENCE: 53035AUSM1
; CURRENT APPLICATION NUMBER: US/10/641,924
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,638
; PRIOR FILING DATE: 2002-08-16
```

```
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-641-924-7

Query Match      100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      18 KVVFFA 23

RESULT 12
US-10-642-255-7
; Sequence 7, Application US/10642255
; Publication No. US20040120930A1
; GENERAL INFORMATION:
; APPLICANT: Dole, William P.
; APPLICANT: Kauser, Katalin
; APPLICANT: Qian, Hu Sheng
; APPLICANT: Rubanyi, Gabor
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant
; FILE REFERENCE: eNOS
; CURRENT APPLICATION NUMBER: US/10/642,255
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,637
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-642-255-7

Query Match      100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      18 KVVFFA 23

RESULT 13
US-10-437-963-173619
; Sequence 173619, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 104966
; SEQ ID NO 173619
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Oryza sativa
```

```
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_71639C.1.pep
US-10-437-963-173619

Query Match      100.0%; Score 29; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      4 KVVFFA 9

RESULT 14
US-10-437-963-133986
; Sequence 133986, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133986
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35803C.1.pep
US-10-437-963-133986

Query Match      100.0%; Score 29; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      6 KVVFFA 11

RESULT 15
US-10-437-963-105773
; Sequence 105773, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 105773
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
```


; OTHER INFORMATION: Clone ID: PAT_MRT4530_102988C.1.pep
US-10-437-963-105773

Query Match 100.0%; Score 29; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
| | | | |
Db 4 KVVFFA 9

RESULT 16

US-10-437-963-141578

; Sequence 141578, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 141578

; LENGTH: 135

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_42668C.1.pep

US-10-437-963-141578

Query Match 100.0%; Score 29; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
| | | | |
Db 4 KVVFFA 9

RESULT 17

US-10-437-963-122124

; Sequence 122124, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 122124

; LENGTH: 175

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)-(175)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_25081C.1.pep

US-10-437-963-122124

Query Match 100.0%; Score 29; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
| | | | |
Db 4 KVVFFA 9

RESULT 18

US-10-481-032A-214

; Sequence 214, Application US/10481032A

; Publication No. US20050177901A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Tong

; APPLICANT: Cheng, Wenglong

; APPLICANT: Briggs, Steven

; APPLICANT: Cooper, Bret

; APPLICANT: Goff, Stephen A.

; APPLICANT: Moughamer, Todd

; APPLICANT: Glazebrook, Jane

; APPLICANT: Katagiri, Fumiaki

; APPLICANT: Kreps, Joel

; APPLICANT: Provart, Nicolas

; APPLICANT: Rickes, Darrell

; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES

; FILE REFERENCE: 60148USPT

; CURRENT APPLICATION NUMBER: US/10/481,032A

; CURRENT FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: US 60/300,112

; PRIOR FILING DATE: 2001-06-22

; PRIOR APPLICATION NUMBER: US 60/325,277

; PRIOR FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: US 60/342,327

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: PCT/IB02/02450

; PRIOR FILING DATE: 2002-06-21

; NUMBER OF SEQ ID NOS: 1201

; SOFTWARE: PatentIn Ver. 2.2

; SEQ ID NO 214

; LENGTH: 186

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-481-032A-214

Query Match 100.0%; Score 29; DB 5; Length 186;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
| | | | |
Db 4 KVVFFA 9

RESULT 19

US-10-481-032A-228

; Sequence 228, Application US/10481032A

; Publication No. US20050177901A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Tong

; APPLICANT: Cheng, Wenglong

; APPLICANT: Briggs, Steven

; APPLICANT: Cooper, Bret

; APPLICANT: Goff, Stephen A.

; APPLICANT: Moughamer, Todd

; APPLICANT: Glazebrook, Jane

; APPLICANT: Katagiri, Fumiaki

```
/ APPLICANT: Kreps, Joel
/ APPLICANT: Provart, Nicolas
/ APPLICANT: Ricke, Darrell
/ TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
/ FILE REFERENCE: 60148USPCT
/ CURRENT APPLICATION NUMBER: US/10/481,032A
/ CURRENT FILING DATE: 2003-12-16
/ PRIOR APPLICATION NUMBER: US 60/300,112
/ PRIOR FILING DATE: 2001-06-22
/ PRIOR APPLICATION NUMBER: US 60/325,277
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: US 60/342,327
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: PCT/IB02/02450
/ PRIOR FILING DATE: 2002-06-21
/ NUMBER OF SEQ ID NOS: 1201
/ SOFTWARE: PatentIn Ver. 2.2
/ SEQ ID NO 228
/ LENGTH: 186
/ TYPE: PRT
/ ORGANISM: Oryza sativa
US-10-481-032A-228
```

```
Query Match 100.0%; Score 29; DB 5; Length 186;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVFFA 6
Db 4 KVVFFA 9
```

```
RESULT 20
US-10-437-963-172476
/ Sequence 172476, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 172476
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ NAME/KEY: unsure
/ LOCATION: (1)..(188)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_70608C.1.pep
US-10-437-963-172476
```

```
Query Match 100.0%; Score 29; DB 4; Length 188;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVFFA 6
Db 4 KVVFFA 9
```

RESULT 21

```
US-10-437-963-172452
/ Sequence 172452, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 172452
/ LENGTH: 198
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ NAME/KEY: unsure
/ LOCATION: (1)..(198)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_70597C.1.pep
US-10-437-963-172452
```

```
Query Match 100.0%; Score 29; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVFFA 6
Db 4 KVVFFA 9
```

```
RESULT 22
US-10-055-475-14
/ Sequence 14, Application US/10055475
/ Publication No. US20030022855A1
/ GENERAL INFORMATION:
/ APPLICANT: Fisher, Paul B.
/ APPLICANT: Kang, Dong-Chul
/ APPLICANT: Gopalakrishnan, Rahul V.
/ TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
/ FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
/ CURRENT APPLICATION NUMBER: US/10/055,475
/ CURRENT FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: PCT/US01/06960
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: 09/515,363
/ PRIOR FILING DATE: 2000-02-29
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 14
/ LENGTH: 416
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-10-055-475-14
```

```
Query Match 100.0%; Score 29; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KVVFFA 6
Db 57 KVVFFA 62
```

RESULT 23

US-11-042-922-14
 ; Sequence 14, Application US/11042922
 ; Publication No. US20050186211A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fisher, Paul B.
 ; APPLICANT: Kang, Dong-Chul
 ; APPLICANT: Gopalkrishnan, Rahul V.
 ; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
 ; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
 ; FILE REFERENCE: A34614-A-PCT-USA-A (070050.2689)
 ; CURRENT APPLICATION NUMBER: US/11/042,922
 ; CURRENT FILING DATE: 2005-01-24
 ; PRIOR APPLICATION NUMBER: 10/055,475
 ; PRIOR FILING DATE: 2002-01-22
 ; PRIOR APPLICATION NUMBER: PCT/US01/06960
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: 09/515,363
 ; PRIOR FILING DATE: 2000-02-29
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 416
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-11-042-922-14

Query Match 100.0%; Score 29; DB 6; Length 416;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
 |||||
 Db 57 KVVFPA 62

RESULT 24

US-10-055-475-13
 ; Sequence 13, Application US/10055475
 ; Publication No. US20030022855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fisher, Paul B.
 ; APPLICANT: Kang, Dong-Chul
 ; APPLICANT: Gopalkrishnan, Rahul V.
 ; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
 ; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
 ; FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
 ; CURRENT APPLICATION NUMBER: US/10/055,475
 ; CURRENT FILING DATE: 2002-01-22
 ; PRIOR APPLICATION NUMBER: PCT/US01/06960
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: 09/515,363
 ; PRIOR FILING DATE: 2000-02-29
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 514
 ; TYPE: PRT
 ; ORGANISM: sus scrofa
 US-10-055-475-13

Query Match 100.0%; Score 29; DB 4; Length 514;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
 |||||
 Db 57 KVVFPA 62

RESULT 25

US-11-042-922-13
 ; Sequence 13; Application US/11042922

; Publication No. US20050186211A1

; GENERAL INFORMATION:
 ; APPLICANT: Fisher, Paul B.
 ; APPLICANT: Kang, Dong-Chul
 ; APPLICANT: Gopalkrishnan, Rahul V.
 ; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
 ; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
 ; FILE REFERENCE: A34614-A-PCT-USA-A (070050.2689)
 ; CURRENT APPLICATION NUMBER: US/11/042,922
 ; CURRENT FILING DATE: 2005-01-24
 ; PRIOR APPLICATION NUMBER: 10/055,475
 ; PRIOR FILING DATE: 2002-01-22
 ; PRIOR APPLICATION NUMBER: PCT/US01/06960
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: 09/515,363
 ; PRIOR FILING DATE: 2000-02-29
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 514
 ; TYPE: PRT
 ; ORGANISM: sus scrofa
 US-11-042-922-13

Query Match 100.0%; Score 29; DB 6; Length 514;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
 |||||
 Db 57 KVVFPA 62

RESULT 26

US-10-408-765A-2031
 ; Sequence 2031, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.
 ; APPLICANT: Glenn, Gary M.
 ; APPLICANT: Warnock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
 ; FILE REFERENCE: 660088.465
 ; CURRENT APPLICATION NUMBER: US/10/408,765A
 ; CURRENT FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 3077
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2031
 ; LENGTH: 925
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-765A-2031

Query Match 100.0%; Score 29; DB 4; Length 925;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFPA 6
 |||||
 Db 292 KVVFPA 297

RESULT 27

US-10-755-889-234
 ; Sequence 234, Application US/10755889
 ; Publication No. US20040171823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 234
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-234

Query Match 100.0%; Score 29; DB 4; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 292 KVVFFA 297

RESULT 28
US-10-370-715B-8
; Sequence 8, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRIDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 8
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-8

Query Match 100.0%; Score 29; DB 5; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 292 KVVFFA 297

RESULT 29
US-10-631-467-680
; Sequence 680, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; FILE REFERENCE: 3462.1005-000
; FILE REFERENCE: disease
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212

; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 680
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-680

Query Match 100.0%; Score 29; DB 5; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 292 KVVFFA 297

RESULT 30
US-10-631-467-747
; Sequence 747, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive i
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 747
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-747

Query Match 100.0%; Score 29; DB 5; Length 925;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 292 KVVFFA 297

RESULT 31
US-09-870-759-124
; Sequence 124, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-870-759-124

Query Match 100.0%; Score 29; DB 3; Length 1144;

Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 32
US-09-751-708A-124
; Sequence 124, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751.708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-751-708A-124

Query Match 100.0%; Score 29; DB 3; Length 1144;
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 33
US-10-428-817A-120
; Sequence 120, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428.817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-428-817A-120

Query Match 100.0%; Score 29; DB 4; Length 1144;
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 34
US-10-937-758A-101
; Sequence 101, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-937-758A-101

Query Match 100.0%; Score 29; DB 5; Length 1144;
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 35
US-10-631-467-1388
; Sequence 1388, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1388
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1388

Query Match 100.0%; Score 29; DB 5; Length 1144;
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 36
US-10-631-467-1464
; Sequence 1464, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive

```
; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1464
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1464

Query Match 100.0%; Score 29; DB 5; Length 1144;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 37
US-10-437-963-109646
; Sequence 109646, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109646
; LENGTH: 1640
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_13784C.1.pep
US-10-437-963-109646

Query Match 100.0%; Score 29; DB 4; Length 1640;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1596 KVVFFA 1601

RESULT 38
US-09-867-847-11
; Sequence 11, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
```

```
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-11

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1 KIVFFA 6

RESULT 39
US-09-867-847-19
; Sequence 19, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-19

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1 KIVFFA 6

RESULT 40
US-09-915-092-1
; Sequence 1, Application US/09915092
; Publication No. US2002011517A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
```

```

; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-1

```

```

Query Match      96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVVFFA 6
        |:||||
Db      1 KVVFFA 6

```

```

RESULT 41
US-09-915-092-9
; Sequence 9, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-9

```

```

Query Match      96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVVFFA 6
        |:||||
Db      1 KVVFFA 6

```

```

RESULT 42
US-09-915-092-1
; Sequence 1, Application US/09747408
; Publication No. US2003003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877

```

```

; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-1

```

```

Query Match      96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVVFFA 6
        |:||||
Db      1 KVVFFA 6

```

```

RESULT 43
US-09-747-408-10
; Sequence 10, Application US/09747408
; Publication No. US2003003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-10

```

```

Query Match      96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KVVFFA 6
        |:||||
Db      1 KVVFFA 6

```

```

RESULT 44
US-10-728-028-1
; Sequence 1, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6

```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-1

Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      1 KIVFFA 6

RESULT 45
US-10-728-028-9
; Sequence 9, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xiangqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-9

Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      1 KIVFFA 6

RESULT 46
US-10-825-958-9
; Sequence 9, Application US/10825958
; Publication No. US20050050439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-10-825-958-17

Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      1 KIVFFA 6

RESULT 47
US-10-825-958-17
; Sequence 17, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-10-825-958-17

Query Match          96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      1 KIVFFA 6

RESULT 48
US-10-425-115-280164
; Sequence 280164, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
```



```
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 280164
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_187087C.1.pep
; US-10-425-115-280164

Query Match          96.6%; Score 28; DB 4; Length 58;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
       |:||||
Db      28 KIVFFA 33

RESULT 49
US-10-424-599-165325
; Sequence 165325, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 165325
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_120303C.1.pep
; US-10-424-599-165325

Query Match          96.6%; Score 28; DB 4; Length 90;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
       |:||||
Db      21 KIVFFA 26

RESULT 50
US-10-424-599-240310
; Sequence 240310, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240310
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59027C.1.pep
```

```
US-10-424-599-240310

Query Match          96.6%; Score 28; DB 4; Length 93;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
       |:||||
Db      34 KIVFFA 39

RESULT 51
US-10-450-763-56957
; Sequence 56957, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56957
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (13)..(62)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354Z, p-value=2.452e-13, raw score
; OTHER INFORMATION: 9.06
; NAME/KEY: misc feature
; LOCATION: (1)..(99)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
; US-10-450-763-56957

Query Match          96.6%; Score 28; DB 5; Length 99;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
       |:||||
Db      63 KIVFFA 68

RESULT 52
US-11-097-143-12723
; Sequence 12723, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
```

```
/ PRIOR APPLICATION NUMBER: 60/164,769
/ PRIOR FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: 60/173,383
/ PRIOR FILING DATE: 1999-12-28
/ PRIOR APPLICATION NUMBER: 60/175,693
/ PRIOR FILING DATE: 2000-01-12
/ PRIOR APPLICATION NUMBER: 60/184,831
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: 60/191,637
/ PRIOR FILING DATE: 2000-03-23
/ NUMBER OF SEQ ID NOS: 43008
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12723
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: DROSOPHILA
US-11-097-143-12723

Query Match      93.1%; Score 27; DB 6; Length 564;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
DB      53 KIIFFA 58

RESULT 53
US-11-097-143-32208
/ Sequence 32208, Application US/11097143
/ Publication No. US2005020858A1
/ GENERAL INFORMATION:
/ APPLICANT: Venter, J. Craig
/ APPLICANT: et al.
/ TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
/ TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
/ TITLE OF INVENTION: DROSOPHILA GENES.
/ FILE REFERENCE: CL000728
/ CURRENT APPLICATION NUMBER: US/11/097,143
/ CURRENT FILING DATE: 2005-04-04
/ PRIOR APPLICATION NUMBER: 60/157,832
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: 60/160,191
/ PRIOR FILING DATE: 1999-10-19
/ PRIOR APPLICATION NUMBER: 60/161,932
/ PRIOR FILING DATE: 1999-10-28
/ PRIOR APPLICATION NUMBER: 60/164,769
/ PRIOR FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: 60/173,383
/ PRIOR FILING DATE: 1999-12-28
/ PRIOR APPLICATION NUMBER: 60/175,693
/ PRIOR FILING DATE: 2000-01-12
/ PRIOR APPLICATION NUMBER: 60/184,831
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: 60/191,637
/ PRIOR FILING DATE: 2000-03-23
/ NUMBER OF SEQ ID NOS: 43008
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 32208
/ LENGTH: 1443
/ TYPE: PRT
/ ORGANISM: DROSOPHILA
US-11-097-143-32208

Query Match      93.1%; Score 27; DB 6; Length 1443;
Best Local Similarity 66.7%; Pred. No. 4.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
DB      1204 KIIFFA 1209

us-09-867-847-7
/ Sequence 7, Application US/09867847
/ Patent No. US20020094335A1
/ GENERAL INFORMATION:
/ APPLICANT: Chalifour, Robert
/ APPLICANT: Hebert, Lise
/ APPLICANT: Kong, Xiangqi
/ APPLICANT: Gervais, Francine
/ TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
/ TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
/ FILE REFERENCE: 14445-501 CIP
/ CURRENT APPLICATION NUMBER: US/09/867,847
/ CURRENT FILING DATE: 2001-09-20
/ PRIOR APPLICATION NUMBER: 60/168,594
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: 09/724,842
/ PRIOR FILING DATE: 2000-11-28
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 7
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: All D peptides
/ OTHER INFORMATION: or peptidomimetics
US-09-867-847-7

Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
DB      1 KLVFFA 6

RESULT 55
US-09-867-847-20
/ Sequence 20, Application US/09867847
/ Patent No. US20020094335A1
/ GENERAL INFORMATION:
/ APPLICANT: Chalifour, Robert
/ APPLICANT: Hebert, Lise
/ APPLICANT: Kong, Xiangqi
/ APPLICANT: Gervais, Francine
/ TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
/ TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
/ FILE REFERENCE: 14445-501 CIP
/ CURRENT APPLICATION NUMBER: US/09/867,847
/ CURRENT FILING DATE: 2001-09-20
/ PRIOR APPLICATION NUMBER: 60/168,594
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: 09/724,842
/ PRIOR FILING DATE: 2000-11-28
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 20
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: All D peptides
/ OTHER INFORMATION: or peptidomimetics
/ NAME/KEY: MOD RES
/ LOCATION: (6)
/ OTHER INFORMATION: AMIDATION
US-09-867-847-20

Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 56
US-09-972-475-9
; Sequence 9, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findexis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972.475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-972-475-9
Query Match 89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 57
US-09-915-092-10
; Sequence 10, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
```

```
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-915-092-10

Query Match 89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 58
US-09-915-092-28
; Sequence 28, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(6)
; OTHER INFORMATION: D-amino acids
; US-09-915-092-28

Query Match 89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 59
US-09-956-625-25
; Sequence 25, Application US/09956625
; Patent No. US20020119926A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Paul
; TITLE OF INVENTION: Inhibitors of IAPP Fibril Formation and Uses Thereof
; FILE REFERENCE: 14445-503
; CURRENT APPLICATION NUMBER: US/09/956,625
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,482
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
```

```

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Antifibrillogenic agents
US-09-956-625-25

Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
   |:|
Db 1 KLVFFA 6

RESULT 60
US-09-747-408-3
; Sequence 3, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-3

Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
   |:|
Db 1 KLVFFA 6

RESULT 61
US-09-747-408-11
; Sequence 11, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-11

Query Match      89.7%; Score 26; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KLVFFA 6
   |:|
Db 1 KLVFFA 6

RESULT 62
US-10-463-729-9
; Sequence 9, Application US/10463729
; Publication No. US20040005307A1
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/463,729
; FILING DATE: 17-JUNE-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-463-729-9

Query Match      89.7%; Score 26; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
   |:|
Db 1 KLVFFA 6

RESULT 63
US-10-728-028-10
; Sequence 10, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xiangl
; APPLICANT: CHALIFOUR, Robert

```

; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; US-10-728-028-10

Query Match 89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 64
US-10-728-028-27
; Sequence 27, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; US-10-728-028-27

Query Match 89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 65
US-10-728-028-28
; Sequence 28, Application US/10728028

; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; US-10-728-028-28

Query Match 89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 66
US-10-825-958-7
; Sequence 7, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; US-10-825-958-7

Query Match 89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 67
US-10-825-958-18
; Sequence 18, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-18

Query Match 89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 68
US-10-666-095-3
; Sequence 3, Application US/10666095
; Publication No. US2005019187A1
; GENERAL INFORMATION:
; APPLICANT: Hammer, Robert P.
; APPLICANT: Fu, Yanwen
; APPLICANT: Aucoin, Jed P.
; APPLICANT: Miller, Tod J.
; APPLICANT: McLaughlin, Mark L.
; APPLICANT: McCarley, Robin L.
; TITLE OF INVENTION: Anti-fibril Peptides
; FILE REFERENCE: 0212.1 Hammer
; CURRENT APPLICATION NUMBER: US/10/666,095
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,081
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-666-095-3

Query Match 89.7%; Score 26; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6

Db 1 KLVFFA 6
RESULT 69
US-09-867-847-12
; Sequence 12, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-12

Query Match 89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 70
US-09-867-847-27
; Sequence 27, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-27

Query Match 89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 71

US-09-867-847-28
; Sequence 28, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 28
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD RES
; LOCATION: (7)
; OTHER INFORMATION: AMIDATION
US-09-867-847-28

Query Match 89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 72

US-09-972-475-7
; Sequence 7, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267

; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-972-475-7

Query Match 89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 73

US-09-915-092-2
; Sequence 2, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NRI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-2

Query Match 89.7%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 74

US-09-915-092-17
; Sequence 17, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND

```
; TITLE OF INVENTION:  USES THEREOF
; FILE REFERENCE:  NBI-139
; CURRENT APPLICATION NUMBER:  US/09/915,092
; CURRENT FILING DATE:  2001-07-24
; PRIOR APPLICATION NUMBER:  60/220,808
; PRIOR FILING DATE:  2000-07-25
; NUMBER OF SEQ ID NOS:  28
; SOFTWARE:  FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH:  7
; TYPE:  PRT
; ORGANISM:  Homo sapiens
US-09-915-092-17
```

```
Query Match      89.7%;  Score 26;  DB 3;  Length 7;
Best Local Similarity  83.3%;  Pred. No. 1.7e+06;
Matches  5;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

QY      1  KVVFFA 6
      |:||||
Db      1  KLVFFA 6
```

```
RESULT 75
US-09-915-092-18
; Sequence 18, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT:  Gervais, Francine
; APPLICANT:  Kong, Xianqi
; APPLICANT:  Chalifour, Robert
; APPLICANT:  Migneault, David
; TITLE OF INVENTION:  AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION:  USES THEREOF
; FILE REFERENCE:  NBI-139
; CURRENT APPLICATION NUMBER:  US/09/915,092
; CURRENT FILING DATE:  2001-07-24
; PRIOR APPLICATION NUMBER:  60/220,808
; PRIOR FILING DATE:  2000-07-25
; NUMBER OF SEQ ID NOS:  28
; SOFTWARE:  FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH:  7
; TYPE:  PRT
; ORGANISM:  Homo sapiens
US-09-915-092-18
```

```
Query Match      89.7%;  Score 26;  DB 3;  Length 7;
Best Local Similarity  83.3%;  Pred. No. 1.7e+06;
Matches  5;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

QY      1  KVVFFA 6
      |:||||
Db      1  KLVFFA 6
```

Search completed: December 29, 2005, 18:49:45
Job time : 67.2903 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds
(without alignments)
24.763 Million cell updates/sec

Title: US-10-009-122-9
Perfect score: 29
Sequence: 1 KVVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- 1: /cgm2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgm2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgm2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgm2_6/ptodata/1/iaa/PCITUS_COMB.pep.*
- 5: /cgm2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	2	US-09-747-408-9
2	29	100.0	6	2	US-09-747-408-17
3	29	100.0	77	2	US-09-513-999C-6921
4	29	100.0	1144	1	US-08-147-812-5
5	29	100.0	1144	1	US-08-319-866-12
6	29	100.0	1144	2	US-09-123-708-2
7	29	100.0	1144	2	US-09-123-624-2
8	29	100.0	1144	2	US-09-661-258-5
9	29	100.0	1144	2	US-08-809-917-12
10	29	100.0	1144	2	US-09-419-371-12
11	28	96.6	6	2	US-09-747-408-1
12	28	96.6	6	2	US-09-747-408-10
13	28	96.6	123	2	US-09-902-540-13513
14	26	89.7	6	1	US-08-612-785B-9
15	26	89.7	6	2	US-08-703-675C-32
16	26	89.7	6	2	US-08-617-267C-9
17	26	89.7	6	2	US-09-747-408-3
18	26	89.7	6	2	US-09-747-408-11
19	26	89.7	7	1	US-08-127-904-14
20	26	89.7	7	1	US-08-612-785B-7
21	26	89.7	7	2	US-08-703-675C-30
22	26	89.7	7	2	US-08-617-267C-7
23	26	89.7	7	2	US-08-264-709A-13
24	26	89.7	7	2	US-09-747-408-2
25	26	89.7	7	2	US-09-747-408-18
26	26	89.7	7	2	US-09-747-408-19
27	26	89.7	7	4	PCT-US94-10475-14

28	26	89.7	8	1	US-08-612-785B-5	Sequence 5, Appli
29	26	89.7	8	1	US-08-630-645-1	Sequence 1, Appli
30	26	89.7	8	2	US-08-703-675C-28	Sequence 28, Appli
31	26	89.7	8	2	US-08-617-267C-5	Sequence 5, Appli
32	26	89.7	8	2	US-09-095-106A-44	Sequence 44, Appli
33	26	89.7	8	2	US-08-766-596A-1	Sequence 1, Appli
34	26	89.7	8	4	PCT-US96-10220-1	Sequence 73, Appli
35	26	89.7	8	4	PCT-US96-10220-1	Sequence 64, Appli
36	26	89.7	9	2	US-08-766-596A-64	Sequence 20, Appli
37	26	89.7	9	2	US-09-747-408-20	Sequence 3, Appli
38	26	89.7	10	2	US-08-970-833-3	Sequence 20, Appli
39	26	89.7	10	2	US-08-724-961-20	Sequence 21, Appli
40	26	89.7	10	2	US-09-724-961-21	Sequence 22, Appli
41	26	89.7	10	2	US-09-724-961-22	Sequence 23, Appli
42	26	89.7	10	2	US-09-724-961-23	Sequence 24, Appli
43	26	89.7	10	2	US-09-724-961-24	Sequence 20, Appli
44	26	89.7	10	2	US-09-580-018-20	Sequence 21, Appli
45	26	89.7	10	2	US-09-580-018-21	Sequence 22, Appli
46	26	89.7	10	2	US-09-580-018-22	Sequence 23, Appli
47	26	89.7	10	2	US-09-580-018-23	Sequence 24, Appli
48	26	89.7	10	2	US-09-580-018-24	Sequence 20, Appli
49	26	89.7	10	2	US-09-724-551-20	Sequence 21, Appli
50	26	89.7	10	2	US-09-724-551-21	Sequence 22, Appli
51	26	89.7	10	2	US-09-724-551-22	Sequence 23, Appli
52	26	89.7	10	2	US-09-724-551-23	Sequence 24, Appli
53	26	89.7	10	2	US-09-724-551-24	Sequence 20, Appli
54	26	89.7	10	2	US-09-724-940-20	Sequence 21, Appli
55	26	89.7	10	2	US-09-724-940-21	Sequence 22, Appli
56	26	89.7	10	2	US-09-724-940-22	Sequence 23, Appli
57	26	89.7	10	2	US-09-724-940-23	Sequence 24, Appli
58	26	89.7	10	2	US-09-724-940-24	Sequence 14, Appli
59	26	89.7	11	1	US-08-630-645-14	Sequence 9, Appli
60	26	89.7	11	2	US-08-766-596A-14	Sequence 9, Appli
61	26	89.7	11	2	US-09-988-842-9	Sequence 25, Appli
62	26	89.7	11	2	US-09-988-842-25	Sequence 14, Appli
63	26	89.7	11	4	PCT-US96-10220-14	Sequence 5, Appli
64	26	89.7	14	2	US-09-594-366-5	Sequence 5, Appli
65	26	89.7	14	2	US-09-992-800-5	Sequence 14, Appli
66	26	89.7	15	1	US-08-612-785B-14	Sequence 37, Appli
67	26	89.7	15	1	US-08-612-785B-37	Sequence 14, Appli
68	26	89.7	15	2	US-08-617-267C-14	Sequence 56, Appli
69	26	89.7	15	2	US-08-766-596A-56	Sequence 57, Appli
70	26	89.7	15	2	US-08-766-596A-57	Sequence 58, Appli
71	26	89.7	15	2	US-08-766-596A-58	Sequence 60, Appli
72	26	89.7	15	2	US-08-766-596A-60	Sequence 61, Appli
73	26	89.7	15	2	US-08-766-596A-61	Sequence 62, Appli
74	26	89.7	15	2	US-08-766-596A-62	Sequence 63, Appli
75	26	89.7	15	2	US-08-766-596A-63	Sequence 65, Appli
76	26	89.7	15	2	US-08-766-596A-65	Sequence 2, Appli
77	26	89.7	17	2	US-09-264-709A-2	Sequence 3, Appli
78	26	89.7	17	2	US-09-594-366-3	Sequence 950, Appli
79	26	89.7	17	2	US-09-623-548A-950	Sequence 983, Appli
80	26	89.7	17	2	US-09-623-548A-983	Sequence 3, Appli
81	26	89.7	17	2	US-09-992-800-3	Sequence 950, Appli
82	26	89.7	17	2	US-09-657-276-950	Sequence 983, Appli
83	26	89.7	17	2	US-09-657-276-983	Sequence 11, Appli
84	26	89.7	19	2	US-08-970-833-11	Sequence 5, Appli
85	26	89.7	19	2	US-09-723-384-5	Sequence 75, Appli
86	26	89.7	19	2	US-09-724-961-75	Sequence 5, Appli
87	26	89.7	19	2	US-09-724-552-5	Sequence 75, Appli
88	26	89.7	19	2	US-09-580-018-75	Sequence 5, Appli
89	26	89.7	19	2	US-09-723-927-5	Sequence 5, Appli
90	26	89.7	19	2	US-09-724-489-5	Sequence 5, Appli
91	26	89.7	19	2	US-09-724-477-5	Sequence 5, Appli
92	26	89.7	19	2	US-09-723-762-5	Sequence 5, Appli
93	26	89.7	19	2	US-09-201-430-5	Sequence 5, Appli
94	26	89.7	19	2	US-09-724-551-75	Sequence 75, Appli
95	26	89.7	19	2	US-10-815-353-5	Sequence 5, Appli
96	26	89.7	19	2	US-10-816-529-5	Sequence 5, Appli
97	26	89.7	19	2	US-10-815-391-5	Sequence 5, Appli
98	26	89.7	19	2	US-10-816-022-5	Sequence 5, Appli
99	26	89.7	19	2	US-09-724-940-75	Sequence 75, Appli
100	26	89.7	19	2	US-10-934-609-5	Sequence 5, Appli

101	26	89.7	19	2	US-10-884-892-5	Sequence 5, Appli	174	26	89.7	38	2	US-09-623-548A-1002	Sequence 1002, Ap
102	26	89.7	20	2	US-08-970-833-10	Sequence 10, Appli	175	26	89.7	38	2	US-09-657-276-975	Sequence 975, App
103	26	89.7	20	2	US-09-724-953-33	Sequence 33, Appl	176	26	89.7	38	2	US-09-657-276-1002	Sequence 1002, Ap
104	26	89.7	20	2	US-09-724-567-33	Sequence 33, Appl	177	26	89.7	39	1	US-08-304-585-5	Sequence 5, Appli
105	26	89.7	20	2	US-09-979-953-33	Sequence 33, Appl	178	26	89.7	39	1	US-08-302-808-2	Sequence 2, Appli
106	26	89.7	20	2	US-09-585-817-33	Sequence 33, Appl	179	26	89.7	39	1	US-08-609-090-7	Sequence 7, Appli
107	26	89.7	26	1	US-08-304-585-7	Sequence 7, Appli	180	26	89.7	39	1	US-08-682-245A-1	Sequence 1, Appli
108	26	89.7	28	1	US-08-346-849-4	Sequence 4, Appli	181	26	89.7	39	1	US-08-986-948-2	Sequence 2, Appli
109	26	89.7	28	1	US-08-302-808-7	Sequence 7, Appli	182	26	89.7	40	1	US-07-744-767A-1	Sequence 1, Appli
110	26	89.7	28	1	US-08-609-090-2	Sequence 2, Appli	183	26	89.7	40	1	US-08-235-400-2	Sequence 2, Appli
111	26	89.7	28	1	US-08-986-948-7	Sequence 7, Appli	184	26	89.7	40	1	US-08-476-464A-2	Sequence 2, Appli
112	26	89.7	28	1	US-08-293-284A-4	Sequence 4, Appli	185	26	89.7	40	1	US-08-304-585-1	Sequence 1, Appli
113	26	89.7	28	2	US-08-461-216-2	Sequence 2, Appli	186	26	89.7	40	1	US-08-304-585-8	Sequence 8, Appli
114	26	89.7	28	2	US-09-388-890-2	Sequence 2, Appli	187	26	89.7	40	1	US-08-302-808-3	Sequence 3, Appli
115	26	89.7	28	2	US-09-388-890-3	Sequence 3, Appli	188	26	89.7	40	1	US-08-433-734-1	Sequence 1, Appli
116	26	89.7	28	2	US-09-388-890-4	Sequence 4, Appli	189	26	89.7	40	1	US-08-609-090-8	Sequence 8, Appli
117	26	89.7	28	2	US-09-388-890-5	Sequence 5, Appli	190	26	89.7	40	1	US-07-737-371E-69	Sequence 69, Appli
118	26	89.7	28	2	US-09-388-890-6	Sequence 6, Appli	191	26	89.7	40	1	US-08-682-245A-2	Sequence 2, Appli
119	26	89.7	28	2	US-09-388-890-7	Sequence 7, Appli	192	26	89.7	40	1	US-08-986-948-3	Sequence 3, Appli
120	26	89.7	28	2	US-09-388-890-8	Sequence 8, Appli	193	26	89.7	40	1	US-08-461-216-1	Sequence 1, Appli
121	26	89.7	28	2	US-09-388-890-9	Sequence 9, Appli	194	26	89.7	40	2	US-08-959-148-1	Sequence 1, Appli
122	26	89.7	28	2	US-09-388-890-10	Sequence 10, Appl	195	26	89.7	40	2	US-09-242-724-22	Sequence 22, Appl
123	26	89.7	28	2	US-09-388-890-12	Sequence 12, Appl	196	26	89.7	40	2	US-08-723-661B-1	Sequence 1, Appli
124	26	89.7	28	2	US-09-388-890-13	Sequence 13, Appl	197	26	89.7	40	2	US-08-062-365-3	Sequence 3, Appli
125	26	89.7	28	2	US-09-388-890-14	Sequence 14, Appl	198	26	89.7	40	2	US-09-133-866-1	Sequence 1, Appli
126	26	89.7	28	2	US-09-264-709A-1	Sequence 1, Appli	199	26	89.7	40	2	US-09-861-847A-7	Sequence 7, Appli
127	26	89.7	28	2	US-08-723-661B-2	Sequence 2, Appli	200	26	89.7	40	2	US-09-861-847A-8	Sequence 8, Appli
128	26	89.7	28	2	US-09-660-954-2	Sequence 2, Appli	201	26	89.7	40	2	US-09-988-842-3	Sequence 3, Appli
129	26	89.7	28	2	US-09-660-954-3	Sequence 3, Appli	202	26	89.7	40	2	US-10-455-218-1	Sequence 1, Appli
130	26	89.7	28	2	US-09-660-954-4	Sequence 4, Appli	203	26	89.7	40	2	US-10-151-614-1	Sequence 1, Appli
131	26	89.7	28	2	US-09-660-954-5	Sequence 5, Appli	204	26	89.7	40	2	US-09-623-548A-956	Sequence 956, App
132	26	89.7	28	2	US-09-660-954-6	Sequence 6, Appli	205	26	89.7	40	2	US-09-623-548A-962	Sequence 962, App
133	26	89.7	28	2	US-09-660-954-7	Sequence 7, Appli	206	26	89.7	40	2	US-09-623-548A-968	Sequence 968, App
134	26	89.7	28	2	US-09-660-954-8	Sequence 8, Appli	207	26	89.7	40	2	US-09-623-548A-978	Sequence 978, App
135	26	89.7	28	2	US-09-660-954-9	Sequence 9, Appli	208	26	89.7	40	2	US-09-623-548A-989	Sequence 989, App
136	26	89.7	28	2	US-09-660-954-10	Sequence 10, Appl	209	26	89.7	40	2	US-09-623-548A-995	Sequence 995, App
137	26	89.7	28	2	US-09-660-954-12	Sequence 12, Appl	210	26	89.7	40	2	US-09-623-548A-1005	Sequence 1005, Ap
138	26	89.7	28	2	US-09-660-954-13	Sequence 13, Appl	211	26	89.7	40	2	US-09-657-276-956	Sequence 956, App
139	26	89.7	28	2	US-09-660-954-14	Sequence 14, Appl	212	26	89.7	40	2	US-09-657-276-962	Sequence 962, App
140	26	89.7	28	2	US-08-898-300-4	Sequence 4, Appli	213	26	89.7	40	2	US-09-657-276-968	Sequence 968, App
141	26	89.7	28	2	US-08-824-513-4	Sequence 4, Appli	214	26	89.7	40	2	US-09-657-276-978	Sequence 978, App
142	26	89.7	28	2	US-09-623-548A-959	Sequence 959, App	215	26	89.7	40	2	US-09-657-276-989	Sequence 989, App
143	26	89.7	28	2	US-09-623-548A-965	Sequence 965, App	216	26	89.7	40	2	US-09-657-276-995	Sequence 995, App
144	26	89.7	28	2	US-09-623-548A-976	Sequence 976, App	217	26	89.7	40	2	US-09-657-276-1005	Sequence 1005, Ap
145	26	89.7	28	2	US-09-623-548A-992	Sequence 992, App	218	26	89.7	40	2	US-09-962-955D-36	Sequence 36, Appl
146	26	89.7	28	2	US-09-623-548A-1003	Sequence 1003, Ap	219	26	89.7	40	4	PCT-US92-06700-1	Sequence 1, Appli
147	26	89.7	28	2	US-09-657-276-959	Sequence 959, App	220	26	89.7	41	1	US-07-819-361-1	Sequence 1, Appli
148	26	89.7	28	2	US-09-657-276-965	Sequence 965, App	221	26	89.7	41	1	US-08-302-808-4	Sequence 4, Appli
149	26	89.7	28	2	US-09-657-276-976	Sequence 976, App	222	26	89.7	41	1	US-08-682-245A-3	Sequence 3, Appli
150	26	89.7	28	2	US-09-657-276-992	Sequence 992, App	223	26	89.7	41	1	US-08-986-948-4	Sequence 4, Appli
151	26	89.7	28	2	US-09-657-276-1003	Sequence 1003, Ap	224	26	89.7	42	1	US-07-744-767A-2	Sequence 2, Appli
152	26	89.7	28	2	US-09-865-294A-66	Sequence 66, Appl	225	26	89.7	42	1	US-08-179-574-1	Sequence 1, Appli
153	26	89.7	30	1	US-08-609-090-3	Sequence 3, Appli	226	26	89.7	42	1	US-08-271-162-5	Sequence 5, Appli
154	26	89.7	30	2	US-09-861-847A-1	Sequence 1, Appli	227	26	89.7	42	1	US-08-347-144-1	Sequence 1, Appli
155	26	89.7	33	1	US-08-609-090-4	Sequence 4, Appli	228	26	89.7	42	1	US-08-462-859A-19	Sequence 19, Appl
156	26	89.7	35	1	US-08-475-579A-4	Sequence 4, Appli	229	26	89.7	42	1	US-08-123-659A-19	Sequence 19, Appl
157	26	89.7	34	1	US-08-304-585-6	Sequence 6, Appli	230	26	89.7	42	1	US-08-464-247A-19	Sequence 19, Appl
158	26	89.7	35	1	US-08-612-785B-16	Sequence 16, Appl	231	26	89.7	42	1	US-08-464-248A-19	Sequence 19, Appl
159	26	89.7	35	1	US-08-612-785B-36	Sequence 36, Appl	232	26	89.7	42	1	US-08-476-464A-1	Sequence 1, Appli
160	26	89.7	35	1	US-08-612-785B-38	Sequence 38, Appl	233	26	89.7	42	1	US-08-304-585-2	Sequence 2, Appli
161	26	89.7	35	1	US-08-612-785B-40	Sequence 40, Appl	234	26	89.7	42	1	US-08-302-808-5	Sequence 5, Appli
162	26	89.7	35	2	US-08-617-267C-16	Sequence 16, Appl	235	26	89.7	42	1	US-08-268-348A-1	Sequence 1, Appli
163	26	89.7	35	2	US-09-623-548A-979	Sequence 979, App	236	26	89.7	42	1	US-08-268-348A-2	Sequence 2, Appli
164	26	89.7	35	2	US-09-623-548A-1006	Sequence 1006, Ap	237	26	89.7	42	1	US-08-268-348A-3	Sequence 3, Appli
165	26	89.7	35	2	US-09-657-276-979	Sequence 979, App	238	26	89.7	42	1	US-08-268-348A-4	Sequence 4, Appli
166	26	89.7	35	2	US-08-609-090-6	Sequence 6, Appli	239	26	89.7	42	1	US-08-268-348A-5	Sequence 5, Appli
167	26	89.7	36	1	US-08-609-090-7	Sequence 7, Appli	240	26	89.7	42	1	US-08-268-348A-6	Sequence 6, Appli
168	26	89.7	36	2	US-09-861-847A-11	Sequence 11, Appl	241	26	89.7	42	1	US-08-433-734-2	Sequence 2, Appli
169	26	89.7	36	2	US-08-302-808-1	Sequence 1, Appli	242	26	89.7	42	1	US-08-609-090-9	Sequence 9, Appli
170	26	89.7	38	1	US-08-302-808-1	Sequence 1, Appli	243	26	89.7	42	1	US-07-737-371E-72	Sequence 72, Appl
171	26	89.7	38	1	US-07-737-371E-68	Sequence 68, Appl	244	26	89.7	42	1	US-08-422-333-4	Sequence 4, Appli
172	26	89.7	38	1	US-08-986-948-1	Sequence 1, Appli	245	26	89.7	42	1	US-08-682-245A-4	Sequence 4, Appli
173	26	89.7	38	2	US-09-623-548A-975	Sequence 975, App	246	26	89.7	42	1	US-08-986-948-5	Sequence 5, Appli

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 38 KVVFFA 43

RESULT 4

US-08-147-812-5
; Sequence 5, Application US/08147812
; Patent No. 5766909
; GENERAL INFORMATION:
; APPLICANT: Xie, Qiao-wen
; APPLICANT: Nathan, Carl F.
; APPLICANT: Mumford, Richard A.
; APPLICANT: Calaycay, Jimmy Ramos
; TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 East Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh Centris650
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,812
FILING DATE: No. 5766909 Available

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/841,841
FILING DATE: 02-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 186581A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1144 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-147-812-5

Query Match 100.0%; Score 29; DB 1; Length 1144;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 514 KVVFFA 519

RESULT 5

US-08-319-866-12
; Sequence 12, Application US/08319866
; Patent No. 5929223
; GENERAL INFORMATION:
; APPLICANT: Tully, Timothy P.
; APPLICANT: Yin, Jerry C.
; APPLICANT: Regulski, Michael
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,866
FILING DATE: 7-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 1144 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-319-866-12

Query Match 100.0%; Score 29; DB 1; Length 1144;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 514 KVVFFA 519

RESULT 6

US-09-123-708-2
; Sequence 2, Application US/09123708
; Patent No. 6146887
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Juergen
; APPLICANT: GOEDECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
; FILE REFERENCE: 51169-2003
; CURRENT APPLICATION NUMBER: US/09/123,708
; CURRENT FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: 08/553,503
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: P4411402.8
; EARLIER FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

US-09-123-708-2

Query Match 100.0%; Score 29; DB 2; Length 1144;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6

Db 1144

```
Db          514 KVVFFA 519

RESULT 7
US-09-123-624-2
; Sequence 2, Application US/09123624
; Patent No. 6149936
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Jurgen
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
; FILE REFERENCE: 511169-2004
; CURRENT APPLICATION NUMBER: US/09/123,624
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 08/553,503
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: 4411402.8
; PRIOR FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-123-624-2

Query Match      100.0%; Score 29; DB 2; Length 1144;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      |||||
Db      514 KVVFFA 519

RESULT 8
US-09-661-258-5
; Sequence 5, Application US/09661258
; Patent No. 6620616
; GENERAL INFORMATION:
; APPLICANT: Stuehr, Dennis J.
; TITLE OF INVENTION: Nucleic Acids Encoding Nitric Oxide Synthase Variants
; FILE REFERENCE: 26473/04028
; CURRENT APPLICATION NUMBER: US/09/661,258
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-661-258-5

Query Match      100.0%; Score 29; DB 2; Length 1144;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      |||||
Db      514 KVVFFA 519

RESULT 9
US-08-809-917-12
; Sequence 12, Application US/08809917
; Patent No. 6689557
; GENERAL INFORMATION:
; APPLICANT: APPLICANT
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
; FILE REFERENCE: 1994-10-07
; CURRENT APPLICATION NUMBER: 08/319,866
; PRIOR FILING DATE: 1994-10-07
; PRIOR APPLICATION NUMBER: 08/319,866
; PRIOR FILING DATE: 1995-10-06
; PRIOR APPLICATION NUMBER: PCT/US95/13198
; CURRENT FILING DATE: 1999-10-14
; CURRENT APPLICATION NUMBER: 08/809,917
; FILE REFERENCE: CSHL94-03A3Z
; TITLE OF INVENTION: Cloning and Characterizing of Genes
; APPLICANT: Tully, Timothy P.
; APPLICANT: Yin, Jerry Chi-Ping
; TITLE OF INVENTION: Cloning and Characterizing of Genes
; FILE REFERENCE: CSHL94-03A3Z
; CURRENT APPLICATION NUMBER: US/09/419,371
; CURRENT FILING DATE: 1999-10-14
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: PCT/US95/13198
; PRIOR FILING DATE: 1995-10-06
; PRIOR APPLICATION NUMBER: 08/361,063
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/319,866
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
```

```
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,917
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13198
; FILING DATE:
; APPLICATION NUMBER: US 08/361,063
; FILING DATE: 21-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,866
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-03A2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1144 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-917-12

Query Match      100.0%; Score 29; DB 2; Length 1144;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      |||||
Db      514 KVVFFA 519

RESULT 10
US-09-419-371-12
; Sequence 12, Application US/09419371
; Patent No. 6890516
; GENERAL INFORMATION:
; APPLICANT: Tully, Timothy P.
; APPLICANT: Yin, Jerry Chi-Ping
; TITLE OF INVENTION: Cloning and Characterizing of Genes
; FILE REFERENCE: CSHL94-03A3Z
; CURRENT APPLICATION NUMBER: US/09/419,371
; CURRENT FILING DATE: 1999-10-14
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: PCT/US95/13198
; PRIOR FILING DATE: 1995-10-06
; PRIOR APPLICATION NUMBER: 08/361,063
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/319,866
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
```

```
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: mouse
US-09-419-371-12

Query Match      100.0%; Score 29; DB 2; Length 1144;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 514 KVVFFA 519

RESULT 11
US-09-747-408-1
; Sequence 1, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-1

Query Match      96.6%; Score 28; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 12
US-09-747-408-10
; Sequence 10, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-10

Query Match      96.6%; Score 28; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 1 KVVFFA 6

RESULT 13
US-09-902-540-13513
; Sequence 13513, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; FILE REFERENCE: 38-10(15849)B
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13513
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13513

Query Match      96.6%; Score 28; DB 2; Length 123;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 52 KVVFFA 57

RESULT 14
US-08-612-785B-9
; Sequence 9, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Flindeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-785B-9

Query Match 89.7%; Score 26; DB 1; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 15
US-08-703-675C-32
Sequence 32, Application US/08703675C
Patent No. 6303567
GENERAL INFORMATION:
APPLICANT: Findexis, Mark A. et al.
TITLE OF INVENTION: Modulators of -Amyloid Peptide Aggregation Comprising D-
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-703-675C-32

Query Match 89.7%; Score 26; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 16
US-08-617-267C-9
Sequence 9, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findexis, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-617-267C-9

Query Match 89.7%; Score 26; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 17
US-09-747-408-3
Sequence 3, Application US/09747408
Patent No. 6670399
GENERAL INFORMATION:
APPLICANT: Green, Allan M.
TITLE OF INVENTION: Compounds And Methods For Modulating
Cerebral Amyloid Angiopathy
FILE REFERENCE: NEI-088
CURRENT APPLICATION NUMBER: US/09/747,408

```
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-3

Query Match      89.7%; Score 26; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
Db      1 KLVFFA 6
|:|||||

RESULT 18
US-09-747-408-11
; Sequence 11, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-11

Query Match      89.7%; Score 26; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
Db      1 KLVFFA 6
|:|||||

RESULT 19
US-08-127-904-14
; Sequence 14, Application US/08127904
; Patent No. 5470951
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For Antagonizing
; TITLE OF INVENTION: Amnestic Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving the
; TITLE OF INVENTION: Quality of Life in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4" diskette
; COMPUTER: Wang PC

; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,904
; FILING DATE: 29 September 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: No. 5470951e
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: No. 5470951e
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; TELEX: No. 5470951e
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown
US-08-127-904-14

Query Match      89.7%; Score 26; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
Db      1 KLVFFA 6
|:|||||

RESULT 20
US-08-612-785B-7
; Sequence 7, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
```


; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-7

Query Match 89.7%; Score 26; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 21
US-08-703-675C-30
; Sequence 30, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide Aggregation Comprising D-
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703.675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-703-675C-30

Query Match 89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6

Db 2 KLVFFA 7

RESULT 22
US-08-617-267C-7
; Sequence 7, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-617-267C-7

Query Match 89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 23
US-09-264-709A-13
; Sequence 13, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
; APPLICANT: Roberts, Eugene
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
; FILE REFERENCE: 2124-310
; CURRENT APPLICATION NUMBER: US/09/264,709A
; CURRENT FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 08/797,782
; PRIOR FILING DATE: 1997-02-07

```
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-264-709A-13

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 24
US-09-747-408-2
; Sequence 2, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-2

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |:||||
Db 2 KLVFFA 7

RESULT 25
US-09-747-408-18
; Sequence 18, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-18

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |:||||
Db 2 KLVFFA 7

RESULT 26
US-09-747-408-19
; Sequence 19, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-19

Query Match      89.7%; Score 26; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 27
PCT-US94-10475-14
; Sequence 14, Application PC/TUS9410475
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For
; TITLE OF INVENTION: Antagonizing Amnestic
; TITLE OF INVENTION: Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving
; TITLE OF INVENTION: the Quality of Life
; TITLE OF INVENTION: in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4"
; MEDIUM TYPE: diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10475
; FILING DATE: 16 September 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA: U. S. Application
; PRIOR APPLICATION DATA: Serial No.
; PRIOR APPLICATION DATA: 08/127,904; filed
; PRIOR APPLICATION DATA: 29 September 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
```

REGISTRATION NUMBER: 16,541
REFERENCE/DOCKET NUMBER: None
TELEPHONE: (202) 626-3564 or 783-6030
TELEFAX: (202) 783-6031
TELEX: None
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7
TYPE: Amino Acid
STRANDEDNESS:
TOPOLOGY: Unknown
PCT-US94-10475-14

Query Match 89.7%; Score 26; DB 4; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 28
US-08-612-785B-5
; Sequence 5, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612.785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PFI-002CP3
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-785B-5

Query Match 89.7%; Score 26; DB 1; Length 8;

Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 29
US-08-630-645-1
; Sequence 1, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,645
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-630-645-1

Query Match 89.7%; Score 26; DB 1; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 30
US-08-703-675C-28
; Sequence 28, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
Aggregation Comprising D-

```
; ADDRESS: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-703-675C-28

Query Match 89.7%; Score 26; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 3 KLVFFA 8

RESULT 31
US-08-617-267C-5
; Sequence 5, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSES: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
```

```
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-617-267C-5

Query Match 89.7%; Score 26; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 3 KLVFFA 8

RESULT 32
US-09-095-106A-44
; Sequence 44, Application US/09095106A
; Patent No. 6331440
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TJERNBERG, Lars O.
; APPLICANT: TERENIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 000500-124
; CURRENT APPLICATION NUMBER: US/09/095,106A
; CURRENT FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 44
; LENGTH: 8
; TYPE: PPT
; ORGANISM: Amyloidosis
; US-09-095-106A-44

Query Match 89.7%; Score 26; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 33
US-08-766-596A-1
; Sequence 1, Application US/08766596A
; Patent No. 6462171
```

;; GENERAL INFORMATION:
;; APPLICANT: SOTO-JARA, Claudio
;; APPLICANT: BAUMANN, Marc
;; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
;; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
;; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
;; NUMBER OF SEQUENCES: 69
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEIMARK
;; STREET: 419 Seventh Street, N.W., Suite 400
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/766,596A
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/630,645
;; FILING DATE: 10-APR-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/478,326
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: YUN, Allen C.
;; REGISTRATION NUMBER: 37,971
;; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-766-596A-1

Query Match 89.7%; Score 26; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 34
US-09-668-314C-73
;; Sequence 73, Application US/09668314C
;; Patent No. 6844148
;; GENERAL INFORMATION:
;; APPLICANT: Guiney, et al
;; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;; FILE REFERENCE: 28341/6280NCP
;; CURRENT APPLICATION NUMBER: US/09/668,314C
;; CURRENT FILING DATE: 2000-09-22
;; PRIOR APPLICATION NUMBER: US 60/169,232
;; PRIOR FILING DATE: 1999-12-06
;; PRIOR APPLICATION NUMBER: US 09/416,901
;; PRIOR FILING DATE: 1999-10-13
;; PRIOR APPLICATION NUMBER: US 60/155,493
;; PRIOR FILING DATE: 1999-09-23

;; PRIOR APPLICATION NUMBER: US 09/404,133
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: PCT/US99/20881
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: US 60/101,594
;; PRIOR FILING DATE: 1998-09-24
;; NUMBER OF SEQ ID NOS: 84
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 73
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURES:
;; OTHER INFORMATION: Synthetic peptide
US-09-668-314C-73

Query Match 89.7%; Score 26; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
Db 1 KLVFFA 6

RESULT 35
PCT-US96-10220-1
;; Sequence 1, Application PC/TUS9610220
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
;; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEIMARK
;; STREET: 419 Seventh Street, N.W., Suite 400
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/10220
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/478,326
;; FILING DATE: 06-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/630,645
;; FILING DATE: 10-APR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
PCT-US96-10220-1

Query Match 89.7%; Score 26; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;

```

Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1 KVVFFA 6
Db      1 KLVFFA 6

RESULT 36
US-08-766-596A-64
; Sequence 64, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-64

Query Match      89.7%; Score 26; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1 KVVFFA 6
Db      2 KLVFFA 7

RESULT 37
US-09-747-408-20
; Sequence 20, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.

```

```

; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-20

Query Match      89.7%; Score 26; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1 KVVFFA 6
Db      4 KLVFFA 9

RESULT 38
US-08-970-833-3
; Sequence 3, Application US/08970833
; Patent No. 6022859
; GENERAL INFORMATION:
; APPLICANT: Kiessling, Laura L.
; APPLICANT: Murphy, Regina M.
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,833
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 960296.94291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-970-833-3

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1 KVVFFA 6
Db      1 KLVFFA 6

```

```
RESULT 39
US-09-724-961-20
; Sequence 20, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-20
Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      |:||||
Db      5 KLVFFA 10

RESULT 40
US-09-724-961-21
; Sequence 21, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-21
Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      |:||||
Db      5 KLVFFA 10

RESULT 41
US-09-724-961-22
; Sequence 22, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-22
Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      |:||||
Db      3 KLVFFA 8

RESULT 42
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
```

```
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-21
```

```
Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      |:||||
Db      4 KLVFFA 9
```

```
RESULT 41
US-09-724-961-22
; Sequence 22, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-22
```

```
Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      |:||||
Db      3 KLVFFA 8
```

```
RESULT 42
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
```

; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US 09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-23

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:|||||
Db 2 KLVFFA 7

RESULT 43
US-09-724-961-24
; Sequence 24, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US 09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide

; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-24

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:|||||
Db 1 KLVFFA 6

RESULT 44
US-09-580-018-20
; Sequence 20, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US 09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-20

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:|||||
Db 5 KLVFFA 10

RESULT 45
US-09-580-018-21
; Sequence 21, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US 09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-21

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 46
US-09-580-018-22
; Sequence 22, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-22

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 47
US-09-580-018-23
; Sequence 23, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-23

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 48
US-09-580-018-24
; Sequence 24, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-24

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 49
US-09-724-551-20
; Sequence 20, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-20

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 KVVFFA 6
Db      5 KLVFFA 10

RESULT 50
US-09-724-551-21
; Sequence 21, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-21

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      4 KLVFFA 9

RESULT 51
US-09-724-551-22
; Sequence 22, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-22

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      3 KLVFFA 8

RESULT 52
US-09-724-551-23
; Sequence 23, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-23

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      2 KLVFFA 7

RESULT 53
US-09-724-551-24
; Sequence 24, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-24

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Best Local Similarity 83.3%; Pred. No. 8.4; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 54

US-09-724-940-20
; Sequence 20, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/724,940
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US/09/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US/09/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-20

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 56

US-09-724-940-22
; Sequence 22, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/724,940
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US/09/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US/09/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-22

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 3 KLVFFA 8

Best Local Similarity 83.3%; Pred. No. 8.4; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KVVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 55

US-09-724-940-21
; Sequence 21, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/724,940
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US/09/201,430
; PRIOR FILING DATE: 1998-11-30

Query Match 89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 3 KLVFFA 8

```

RESULT 57
US-09-724-940-23
; Sequence 23, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-23

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
       |:|||||
Db      2 KLVFFA 7

RESULT 58
US-09-724-940-24
; Sequence 24, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-24

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
       |:|||||
Db      2 KLVFFA 7

```

```

; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-24

Query Match      89.7%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 8.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
       |:|||||
Db      1 KLVFFA 6

RESULT 59
US-08-630-645-14
; Sequence 14, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,645
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-630-645-14

Query Match      89.7%; Score 26; DB 1; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVFFA 6
       |:|||||
Db      2 KLVFFA 7

```

RESULT 60
US-08-766-596A-14
; Sequence 14, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-14
Query Match 89.7%; Score 26; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
DB 2 KLVFFA 7
RESULT 61
US-09-988-842-9
; Sequence 9, Application US/09988842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25
Query Match 89.7%; Score 26; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
DB 2 KLVFFA 7
RESULT 62
US-09-988-842-25
; Sequence 25, Application US/09988842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25
Query Match 89.7%; Score 26; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
DB 2 KLVFFA 7
RESULT 63
PCT-US96-10220-14
; Sequence 14, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: PCT/US96/10220
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US96-10220-14

```

```

Query Match      89.7%; Score 26; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KVVFFA 6
       |:|||||
Db      2 KLVFFA 7

```

```

RESULT 64
US-09-594-366-5
; Sequence 5, Application US/09594366
; Patent No. 6582945
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2004
; CURRENT APPLICATION NUMBER: US/09/594,366
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-594-366-5

```

```

Query Match      89.7%; Score 26; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KVVFFA 6
       |:|||||
Db      4 KLVFFA 9

```

```

RESULT 65
US-09-992-800-5
; Sequence 5, Application US/09992800
; Patent No. 6872554
; GENERAL INFORMATION:

```

```

; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2006
; CURRENT APPLICATION NUMBER: US/09/992,800
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-992-800-5

```

```

Query Match      89.7%; Score 26; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 KVVFFA 6
       |:|||||
Db      4 KLVFFA 9

```

```

RESULT 66
US-08-612-785B-14
; Sequence 14, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

```

; FRAGMENT TYPE: internal
US-08-612-785B-14

Query Match 89.7%; Score 26; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 67

US-08-612-785B-37
; Sequence 37, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-612-785B-37

Query Match 89.7%; Score 26; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 6 KLVFFA 11

RESULT 68

US-08-617-267C-14

; Sequence 14, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-617-267C-14

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 69

US-08-766-596A-56
; Sequence 56, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.

```
/
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/766,596A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/630,645
/ FILING DATE: 10-APR-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/478,326
/ FILING DATE: 06-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: YUN, Allen C.
/ REGISTRATION NUMBER: 37,971
/ REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ INFORMATION FOR SEQ ID NO: 56:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-766-596A-56

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 5 KLVFFA 10

RESULT 70
US-08-766-596A-57
; Sequence 57, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
```

```
/
/ FILING DATE: 10-APR-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/478,326
/ FILING DATE: 06-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: YUN, Allen C.
/ REGISTRATION NUMBER: 37,971
/ REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 57:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-766-596A-57

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 5 KLVFFA 10

RESULT 71
US-08-766-596A-58
; Sequence 58, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
```


; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-58

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 5 KLVFFA 10

RESULT 72

US-08-766-596A-60
; Sequence 60, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-60

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 5 KLVFFA 10

Db 5 KLVFFA 10

RESULT 73

US-08-766-596A-61
; Sequence 61, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-61

Query Match 89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 5 KLVFFA 10

RESULT 74

US-08-766-596A-62
; Sequence 62, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

```

Query Match      89.7%; Score 26; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVVFFA 6
      ||:||
Db      5 KVLFFA 10

RESULT 75
US-08-766-596A-63
; Sequence 63, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds
(without alignments)
32.238 Million cell updates/sec

Title: US-10-009-122-9
Perfect score: 29
Sequence: 1 KVVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	4	AAB48482
2	29	100.0	6	4	AAB48490
3	29	100.0	6	4	AAB82630
4	29	100.0	6	4	AAB82638
5	29	100.0	6	5	AAU96818
6	29	100.0	6	5	AAU96826
7	29	100.0	6	5	AAU11664
8	29	100.0	6	5	AAU11656
9	29	100.0	6	6	AAE35452
10	29	100.0	6	8	ADQ37277
11	29	100.0	6	8	ADQ37321
12	29	100.0	6	8	ADQ37329
13	29	100.0	6	9	ADY37928
14	29	100.0	6	9	ADY37936
15	29	100.0	22	8	ADQ09761
16	29	100.0	23	8	ADT93984
17	29	100.0	37	3	AAB05910
18	29	100.0	37	8	ADK34080
19	29	100.0	37	8	ADL70727
20	29	100.0	77	3	AAQ02840
21	29	100.0	175	4	AAQ11219
22	29	100.0	186	7	ADC07962
23	29	100.0	186	7	ADC07948
24	29	100.0	190	4	AAW83792

98	26	89.7	7	2	AAW89376	AAW89376 Beta-amyl	171	26	89.7	9	9	AEA51417	AAE51417 C-A 16-23
99	26	89.7	7	4	AA567281	Aab67281 Residues	172	26	89.7	9	9	AEA62825	AAE62825 Immunoon
100	26	89.7	7	4	AA484475	Aab48475 Antifibri	173	26	89.7	9	9	AAE62828	AAE62828 Immunoon
101	26	89.7	7	4	AA484492	Aab48492 Antifibri	174	26	89.7	10	3	AAV79338	AAV79338 Beta-amyl
102	26	89.7	7	4	AA484491	Aab48491 Antifibri	175	26	89.7	10	4	AA462226	AA462226 Human APP
103	26	89.7	7	4	AA482624	Aab82624 All-D pep	176	26	89.7	10	4	AA462225	AA462225 Human APP
104	26	89.7	7	4	AA482640	Aab82640 All-D pep	177	26	89.7	10	4	AA462228	AA462228 Human APP
105	26	89.7	7	4	AA482639	Aab82639 All-D pep	178	26	89.7	10	4	AA462224	AA462224 Human APP
106	26	89.7	7	5	ABG71007	Abg71007 Long form	179	26	89.7	10	4	AA462227	AA462227 Human APP
107	26	89.7	7	5	AB505155	Ab505155 Beta amyl	180	26	89.7	10	4	AA462227	AA462227 Human APP
108	26	89.7	7	5	AAU96827	Aau96827 Amyloid t	181	26	89.7	10	4	AA462227	AA462227 Human APP
109	26	89.7	7	5	AAU96812	Aau96812 Amyloid t	182	26	89.7	10	4	AA462227	AA462227 Human APP
110	26	89.7	7	5	AAU96828	Aau96828 Amyloid t	183	26	89.7	10	6	ABP57511	ABP57511 Different
111	26	89.7	7	5	AAU96828	Aau96828 Amyloid t	184	26	89.7	10	6	AAE35455	AAE35455 Beta pep
112	26	89.7	7	5	AAU11665	Aau11665 Peptide #	185	26	89.7	10	8	ADQ37280	ADQ37280 Vaccine a
113	26	89.7	7	5	AAU11649	Aau11649 Peptide #	186	26	89.7	10	8	ADQ37371	ADQ37371 Amyloid-b
114	26	89.7	7	5	AAU11666	Aau11666 Peptide #	187	26	89.7	10	8	ADQ37374	ADQ37374 Amyloid-b
115	26	89.7	7	6	AB882630	Aab82630 Beta fib	188	26	89.7	10	9	ADY37939	ADY37939 Amyloid-c
116	26	89.7	7	6	AAE35439	Aae35439 Abeta pep	189	26	89.7	11	2	AAW32560	AAW32560 Anti-amyl
117	26	89.7	7	6	AAE35454	Aae35454 Abeta pep	190	26	89.7	11	4	AAW32586	AAW32586 Peptide #
118	26	89.7	7	6	AAE35453	Aae35453 Abeta pep	191	26	89.7	11	5	AAU99431	AAU99431 Human amy
119	26	89.7	7	6	ADA90937	Ada90937 Solid-pha	192	26	89.7	11	5	AAE29504	AAE29504 Amyloid b
120	26	89.7	7	6	ADA90154	Ada90154 Anti-Abet	193	26	89.7	11	6	ABU79013	ABU79013 Amyloidog
121	26	89.7	7	7	ADD20746	Add20746 Human bet	194	26	89.7	11	7	ABR84683	ABR84683 Aggrekana
122	26	89.7	7	7	ADF50855	Adf50855 Human cal	195	26	89.7	11	7	ABW00147	ABW00147 Amyloid-b
123	26	89.7	7	8	ADJ64058	Adj64058 Human bet	196	26	89.7	12	6	ABR91837	ABR91837 P. papata
124	26	89.7	7	8	ADP64922	Adp64922 Beta-amyl	197	26	89.7	12	6	AAE35464	AAE35464 Abeta pep
125	26	89.7	7	8	ADQ37278	Adq37278 Vaccine a	198	26	89.7	12	6	AAE35466	AAE35466 Abeta pep
126	26	89.7	7	8	ADQ37314	Adq37314 Antifibri	199	26	89.7	12	6	AAE35466	AAE35466 Abeta pep
127	26	89.7	7	8	ADQ37263	Adq37263 Vaccine a	200	26	89.7	12	7	ADD20745	ADD20745 Human bet
128	26	89.7	7	8	ADQ37279	Adq37279 Vaccine a	201	26	89.7	12	7	ADD20744	ADD20744 Human bet
129	26	89.7	7	8	ADQ37330	Adq37330 Antifibri	202	26	89.7	12	8	ADJ71476	ADJ71476 N-termina
130	26	89.7	7	8	ADQ37331	Adq37331 Antifibri	203	26	89.7	12	8	ADQ37407	ADQ37407 Amyloid-b
131	26	89.7	7	8	ADQ37351	Adq37351 Beta-amyl	204	26	89.7	12	8	ADQ37289	ADQ37289 Vaccine a
132	26	89.7	7	9	ADQ37922	Adq37922 Amyloid-t	205	26	89.7	12	8	ADQ37259	ADQ37259 Vaccine a
133	26	89.7	7	9	ADQ37938	Adq37938 Amyloid-t	206	26	89.7	12	9	ADZ08890	ADZ08890 Human bet
134	26	89.7	7	9	ADQ37937	Adq37937 Amyloid-t	207	26	89.7	12	9	ADZ08892	ADZ08892 Human bet
135	26	89.7	7	9	ADZ08903	Adz08903 Human bet	208	26	89.7	13	6	AAE35465	AAE35465 Abeta pep
136	26	89.7	8	2	AAW02310	Aaw02310 Beta-amyl	209	26	89.7	13	6	AAE35467	AAE35467 Abeta pep
137	26	89.7	8	2	AAW45967	Aaw45967 Peptide d	210	26	89.7	13	6	ADA37467	ADA37467 Human amy
138	26	89.7	8	2	AAW32551	Aaw32551 Amyloidog	211	26	89.7	13	8	ADJ71477	ADJ71477 N-termina
139	26	89.7	8	2	AAW89374	Aaw89374 Beta-amyl	212	26	89.7	13	8	ADJ71464	ADJ71464 N-termina
140	26	89.7	8	4	AAE10663	Aae10663 Human amy	213	26	89.7	13	8	ADQ37408	ADQ37408 Amyloid-b
141	26	89.7	8	4	AAE02615	Aae02615 Human amy	214	26	89.7	13	8	ADQ37290	ADQ37290 Vaccine a
142	26	89.7	8	5	ABG71005	Abg71005 Long form	215	26	89.7	14	6	ADA89887	ADA89887 Beta-A4 s
143	26	89.7	8	5	ABR78624	Ab78624 Human alp	216	26	89.7	14	6	ADJ71452	ADJ71452 N-termina
144	26	89.7	8	5	ABR05153	Abb05153 Beta amyl	217	26	89.7	14	8	ADJ71465	ADJ71465 N-termina
145	26	89.7	8	5	ABU09765	Abu09765 Amyloidog	218	26	89.7	14	8	ADJ71478	ADJ71478 N-termina
146	26	89.7	8	6	ABR61959	Ab61959 Human amy	219	26	89.7	14	9	ADZ08889	ADZ08889 Human bet
147	26	89.7	8	7	ABW00134	Abw00134 Beta-amyl	220	26	89.7	15	2	AAW02334	AAW02334 Beta-amyl
148	26	89.7	8	8	ADJ64056	Adj64056 Human bet	221	26	89.7	15	2	AAW89354	AAW89354 Beta-amyl
149	26	89.7	8	8	ADQ37385	Adq37385 Antifibri	222	26	89.7	15	2	AAW89354	AAW89354 Beta-amyl
150	26	89.7	8	8	ADQ37349	Adq37349 Beta-amyl	223	26	89.7	15	5	ABW05162	ABW05162 Long form
151	26	89.7	8	9	ADZ08900	Adz08900 Human bet	224	26	89.7	15	5	ABW05162	ABW05162 Beta amyl
152	26	89.7	8	9	AEA51423	Aea51423 C-Abeta 1	225	26	89.7	15	5	ABU79057	ABU79057 Aggregati
153	26	89.7	8	9	AEA51420	Aea51420 A 16-22-C	226	26	89.7	15	6	ABU79064	ABU79064 Aggregati
154	26	89.7	8	9	AEA62831	Aea62831 Immunoon	227	26	89.7	15	6	ABU79059	ABU79059 Aggregati
155	26	89.7	8	9	AEA62834	Aea62834 Immunoon	228	26	89.7	15	6	ABU79060	ABU79060 Aggregati
156	26	89.7	9	2	AAK45239	Aar45239 Mutant am	229	26	89.7	15	6	ABU79055	ABU79055 Aggregati
157	26	89.7	9	4	AA484493	Aab48493 Antifibri	230	26	89.7	15	6	ABU79056	ABU79056 Aggregati
158	26	89.7	9	5	AAU11667	Aau11667 Peptide #	231	26	89.7	15	6	ABU79062	ABU79062 Aggregati
159	26	89.7	9	6	ABP57517	Abp57517 Different	232	26	89.7	15	6	ABU79061	ABU79061 Aggregati
160	26	89.7	9	6	ABU79063	Abu79063 Aggregati	233	26	89.7	15	7	ABW00190	ABW00190 Peptide #
161	26	89.7	9	6	AAE35436	Aae35436 Abeta pep	234	26	89.7	15	7	ABW00198	ABW00198 Peptide #
162	26	89.7	9	7	ABW00197	Abw00197 Peptide #	235	26	89.7	15	7	ABW00189	ABW00189 Peptide #
163	26	89.7	9	8	ADI36003	Adi36003 Amyloid b	236	26	89.7	15	7	ABW00193	ABW00193 Peptide #
164	26	89.7	9	8	ADI35849	Adi35849 Amyloid b	237	26	89.7	15	7	ABW00191	ABW00191 Peptide #
165	26	89.7	9	8	ADI35874	Adi35874 Amyloid b	238	26	89.7	15	7	ABW00196	ABW00196 Peptide #
166	26	89.7	9	8	ADI35871	Adi35871 Amyloid b	239	26	89.7	15	7	ABW00195	ABW00195 Peptide #
167	26	89.7	9	8	ADI35903	Adi35903 Amyloid b	240	26	89.7	15	7	ABW00194	ABW00194 Peptide #
168	26	89.7	9	8	ADQ37260	Adq37260 Vaccine a	241	26	89.7	15	7	ADK82695	ADK82695 Beta-amyl
169	26	89.7	9	8	ADQ37332	Adq37332 Antifibri	242	26	89.7	15	7	ADK82697	ADK82697 Beta-amyl
170	26	89.7	9	9	AEA51414	Aea51414 A 16-23-C	243	26	89.7	15	7	ADK82700	ADK82700 Beta-amyl

244	26	89.7	15	7	ADK92698	Adk92698 Beta-amyl
245	26	89.7	15	7	ADK92699	Adk92699 Beta-amyl
246	26	89.7	15	8	ADJ71466	Adj71466 N-termina
247	26	89.7	15	8	ADJ71453	Adj71453 N-termina
248	26	89.7	15	8	ADJ71479	Adj71479 N-termina
249	26	89.7	15	8	ADJ71440	Adj71440 N-termina
250	26	89.7	15	8	ADJ64065	Adj64065 Human bet
251	26	89.7	16	5	AAE26330	AAE26330 Human bet
252	26	89.7	16	8	ADJ71454	Adj71454 N-termina
253	26	89.7	16	8	ADJ71480	Adj71480 N-termina
254	26	89.7	16	8	ADJ71441	Adj71441 N-termina
255	26	89.7	16	8	ADJ71467	Adj71467 N-termina
256	26	89.7	16	8	ADJ71428	Adj71428 N-termina
257	26	89.7	17	2	AAE54703	AAE54703 Beta-amyl
258	26	89.7	17	2	AAW18880	AAW18880 Beta-amyl
259	26	89.7	17	4	AAW18880	AAW18880 Beta-amyl
260	26	89.7	17	4	AAW18880	AAW18880 Beta-amyl
261	26	89.7	17	4	AAW18880	AAW18880 Beta-amyl
262	26	89.7	17	5	ABB04911	ABB04911 Human amyl
263	26	89.7	17	6	AAE35468	AAE35468 Abeta pep
264	26	89.7	17	6	AAE35468	AAE35468 Abeta pep
265	26	89.7	17	8	ADG93165	ADG93165 Novel exp
266	26	89.7	17	8	ADJ65843	ADJ65843 Amyloid B
267	26	89.7	17	8	ADN02827	ADN02827 Mammalian
268	26	89.7	17	8	ADQ37291	ADQ37291 Vaccine a
269	26	89.7	17	8	ADL18447	ADL18447 Amyloid-b
270	26	89.7	18	3	AAW10963	AAW10963 Beta-amyl
271	26	89.7	18	3	AAW18882	AAW18882 AEDANS-be
272	26	89.7	19	2	AAW18881	AAW18881 Txp-Beta-
273	26	89.7	19	2	AAW18881	AAW18881 Txp-Beta-
274	26	89.7	19	4	AAW18881	AAW18881 Txp-Beta-
275	26	89.7	19	4	AAW18881	AAW18881 Txp-Beta-
276	26	89.7	19	4	AAW18881	AAW18881 Txp-Beta-
277	26	89.7	19	8	ADU24440	ADU24440 Novel glu
278	26	89.7	19	8	ADU24442	ADU24442 Novel glu
279	26	89.7	19	8	ADU46714	ADU46714 Amyloid b
280	26	89.7	19	8	ADU46716	ADU46716 Gln3 amyl
281	26	89.7	19	9	ADZ71366	ADZ71366 Human bet
282	26	89.7	19	9	ADZ71368	ADZ71368 Human bet
283	26	89.7	19	9	AEA35401	AEA35401 Novel QC
284	26	89.7	19	9	AEA35399	AEA35399 Novel QC
285	26	89.7	19	9	AEA35399	AEA35399 Novel QC
286	26	89.7	19	9	AEA35399	AEA35399 Novel QC
287	26	89.7	20	3	AAE2574	AAE2574 Glutamine
288	26	89.7	20	5	ABB06431	ABB06431 Beta-secr
289	26	89.7	20	6	ABR91876	ABR91876 P. papata
290	26	89.7	21	2	AAE30941	AAE30941 Human sec
291	26	89.7	21	8	ADU24439	ADU24439 Novel glu
292	26	89.7	21	8	ADU46713	ADU46713 Amyloid b
293	26	89.7	21	9	ADV86872	ADV86872 Beta-amyl
294	26	89.7	21	9	ADZ71365	ADZ71365 Human bet
295	26	89.7	21	9	AEA35398	AEA35398 Novel QC
296	26	89.7	21	9	AEA35398	AEA35398 Novel QC
297	26	89.7	22	2	ADR83670	ADR83670 Amyloidog
298	26	89.7	24	2	AAE35669	AAE35669 Alzheimer
299	26	89.7	24	9	ADW88085	ADW88085 T668 phos
300	26	89.7	24	9	AEBO9195	AEBO9195 Human bet
						AEBO9194 Human bet

ALIGNMENTS

RESULT 1
 ID AAB48482 standard; peptide; 6 AA.
 AC AAB48482;
 XX
 DT 02-MAR-2001 (first entry)
 DE Antifibrillogenic peptide #9.
 XX
 KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;

KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX Homo sapiens.
 XX WO200068263-A2.
 XX 16-NOV-2000.
 XX 04-MAY-2000; 2000WO-CA0000515.
 XX 05-MAY-1999; 99US-0132592P.
 XX (NEUR-) NEUROCHEM INC.
 XX Chalfour R, Gervais F, Gupta A;
 XX WPI; 2001-031852/04.
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 XX cytoprotection for treating amyloidosis disorders, comprises a peptide,
 XX its isomer or peptidomimetic.
 XX Claim 7; Page 25; 46pp; English.
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 XX for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 XX AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 XX useful for treating amyloidosis disorders such as Alzheimer's disease.
 XX Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 XX binding region and the prot-prot interaction region of the human amyloid
 XX protein
 XX Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFFFA 6
 Db 1 KVFFFA 6
 RESULT 2
 AAB48490
 ID AAB48490 standard; peptide; 6 AA.
 XX
 AC AAB48490;
 XX
 DT 02-MAR-2001 (first entry)
 DE Antifibrillogenic peptide #17.
 XX
 KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 6
 FT /note= "C-terminal amide"
 XX
 XX WO200068263-A2.
 XX 16-NOV-2000.
 XX 04-MAY-2000; 2000WO-CA0000515.
 XX 05-MAY-1999; 99US-0132592P.
 XX (NEUR-) NEUROCHEM INC.
 PA

XX Chalifour R, Gervais F, Gupta A;
 XX WPI; 2001-031852/04.
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 XX Claim 7; Page 25; 46pp; English.
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 XX Sequence 6 AA;
 SQ Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 1 KVVFFA 6
 RESULT 3
 AAB82630
 ID AAB82630 standard; peptide; 6 AA.
 AC AAB82630;
 XX 02-OCT-2001 (first entry)
 DE All-D peptide used in Alzheimer's disease vaccine.
 KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 1..6 /note= "all D-form residues"
 FT
 FT
 XX WO200139796-A2.
 XX 07-JUN-2001.
 XX 29-NOV-2000; 2000WO-CA001413.
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 PA Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.
 XX Disclosure; Page 11; 31pp; English.
 PS The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and

CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self',
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX Sequence 6 AA;
 SQ Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 1 KVVFFA 6
 RESULT 4
 AAB82638
 ID AAB82638 standard; peptide; 6 AA.
 AC AAB82638;
 XX 02-OCT-2001 (first entry)
 DE All-D peptide used in Alzheimer's disease vaccine.
 KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 1..6 /note= "all D-form residues"
 FT
 FT Modified-site 6 /note= "C-terminal amide"
 FT
 XX WO200139796-A2.
 XX 07-JUN-2001.
 XX 29-NOV-2000; 2000WO-CA001413.
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 PA Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,

PT which elicits production of antibodies to prevent fibrillogenesis and
 FT associated cellular toxicity.

XX Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use in
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see A882622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in A882623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis, and
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 Db 1 KVVFFA 6

RESULT 5
 AAU96818
 ID AAU96818 standard; peptide; 6 AA.

XX

AC AAU96818;

XX 30-JUL-2002 (first entry)

DE Amyloid targeting peptide #8.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

OS Key Location/Qualifiers

XX Key Misc-difference 1. .6

FT Key Misc-difference 1. .6

XX WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX

PR 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

DR New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 FT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A₁-_n-_k-_z-A₁-_a-_b (1) where z = 0 - 1;
 CC A₁ = an amyloid targeting moiety; A₁-_n-_k = a linker moiety; and A₁-_a-_b
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (I) to the patient, and ultrasound imaging (I) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 Db 1 KVVFFA 6

RESULT 6
 AAU96826
 ID AAU96826 standard; peptide; 6 AA.

XX

AC AAU96826;

XX 30-JUL-2002 (first entry)

DE Amyloid targeting peptide #16.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

OS Key Location/Qualifiers

XX Key Misc-difference 1. .6

XX PA (NEUR-) NEUROCHEM INC.
 XX PI Green AM, Gervais F;
 XX XX WPI; 2002-075222/10.
 XX XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.
 XX XX Disclosure; Page 10; 68pp; English.
 XX XX The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVVFFA 6
 Db 1 KVVFFA 6

RESULT 9
 AAE35452
 ID AAE35452 standard; peptide; 6 AA.

XX AC AAE35452;
 XX DT 17-JUN-2003 (first entry)
 XX DE Abeta peptide #23.
 KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX OS Unidentified.
 XX XX Key Location/Qualifiers
 FT Misc-difference 1. .6 /note= "D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT WO200296937-A2.
 XX PD 05-DEC-2002.
 XX XX 29-MAY-2002; 2002WO-CA000763.
 XX PR 29-MAY-2001; 2001US-00867847.
 XX PA (NEUR-) NEUROCHEM INC.
 XX PI Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX Claim 1; Page 59; 44pp; English.
 XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 XX invention
 XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVVFFA 6
 Db 1 KVVFFA 6

RESULT 10
 ADQ37277

XX ID ADQ37277 standard; peptide; 6 AA.
 XX AC ADQ37277;
 XX DT 07-OCT-2004 (first entry)
 XX DE Vaccine antigen amyloid-beta related amino acid sequence.
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; nontropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antichyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 XX vaccine antigen.
 XX OS Synthetic.
 XX XX Key Location/Qualifiers
 FT Misc-difference 1. .6 /note= "D-form residues"
 FT Modified-site 6 /note= "amidated"
 XX

PN	WO2004058239-A1.	ID	ADQ37321 standard; peptide; 6 AA.
XX		XX	
PD	15-JUL-2004.	AC	ADQ37321;
XX		XX	
PF	24-DEC-2003; 2003WO-CA002021.	DT	07-OCT-2004 (first entry)
XX		XX	
PR	24-DEC-2002; 2002US-0436379P.	DE	Antifibrillogenic amyloidosis inhibiting peptide.
PR	23-JUN-2003; 2003US-0482214P.	XX	
XX		XX	
PA	(NEUR-) NEUROCHEM INT LTD.	KW	amyloid-beta; amyloid-beta related disease;
XX		KW	amyloid-beta fibril formation; immune response; nootropic;
PI	Gervais F, Bellini F;	KW	neuroprotective; cerebroprotective; haemostatic; ophthalmological;
XX		KW	antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
XX		KW	anticongulant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
DR	WPI; 2004-543342/52.	KW	cardiant; antidepressant; endocrine; hypnotic;
XX		KW	amyloid-beta fibril formation modulator; immune system modulator;
XX		KW	Alzheimer's disease; mild cognitive impairment;
PT	Composition for treating e.g. Alzheimer's disease comprises first agent	KW	mild-to-moderate cognitive impairment; vascular dementia;
PT	that prevents or treats amyloid-beta related disease and second agent	KW	cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
PT	that is either a peptide or peptidomimetic or an immune system modulator.	KW	senile dementia; Down's syndrome; inclusion body myositis;
XX		KW	age-related macular degeneration; hypothyroidism;
PS	Disclosure; Page 67; 143pp; English.	KW	cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
XX		KW	behavioural dysfunction; neurological condition; psychological condition;
CC	The present invention describes compositions (C) comprising: (a) a first	KW	vaccine antigen.
CC	agent (a1) that prevents or treats amyloid-beta related disease; and (b)	XX	Synthetic.
CC	a second agent (a2) that is: (i) a peptide or peptidomimetic that	OS	
CC	modulates amyloid-beta fibril formation or induces a prophylactic or	XX	
CC	therapeutic immune response against amyloid-beta fibril formation; or	XX	
CC	(ii) an immune system modulator that prevents or inhibits amyloid-beta	PN	WO2004058239-A1.
CC	fibril formation. Also described is a kit comprising (C). (C) have	XX	
CC	nootropic, neuroprotective, cerebroprotective, haemostatic,	PD	15-JUL-2004.
CC	ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,	XX	
CC	uropathic, anticongulant, anti-HIV, antiparkinsonian, muscular,	XX	
CC	neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,	PF	24-DEC-2003; 2003WO-CA002021.
CC	and can be used as amyloid-beta fibril formation modulators, and as	XX	
CC	immune system modulators. (C) can be used for preventing or treating an	XX	
CC	amyloid-beta related disease e.g. Alzheimer's disease (including sporadic	PR	24-DEC-2002; 2002US-0436379P.
CC	(non-hereditary) or familial (hereditary)), mild cognitive impairment,	PR	23-JUN-2003; 2003US-0482214P.
CC	mild-to-moderate cognitive impairment, vascular dementia, cerebral	XX	
CC	amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,	XX	(NEUR-) NEUROCHEM INT LTD.
CC	Down's syndrome, inclusion body myositis, age-related macular	PA	
CC	degeneration, or a condition associated with Alzheimer's disease	XX	
CC	(including hypothyroidism, cerebrovascular disease, cardiovascular	PI	Gervais F, Bellini F;
CC	disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,	XX	
CC	aggression, or incontinence), a neurological condition (e.g. Huntington's	DR	WPI; 2004-543342/52.
CC	disease, amyotrophic lateral sclerosis, acquired immunodeficiency,	XX	
CC	Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia	XX	
CC	with Lewy bodies, altered muscle tone, seizures, sensory loss, visual	XX	
CC	field deficits, incoordination, gait disturbance, transient ischaemic	XX	
CC	attack or stroke, transient alertness, attention deficit, frequent falls,	XX	
CC	syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural	XX	
CC	haematoma, brain tumour, posttraumatic brain injury, or posthypoxic	XX	
CC	damage), or a psychological condition (e.g. depression, delusions,	XX	
CC	illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep	XX	
CC	disturbance, insomnia, behavioural disinhibition, poor insight, suicidal	XX	
CC	ideation, depressed mood, irritability, anhedonia, social withdrawal, or	XX	
CC	excessive guilt)) in a subject e.g. human having a genomic mutation in an	XX	
CC	amyloid precursor protein gene, an ApoE gene, or a presenilin gene;	XX	
CC	having amyloid-beta deposits. The present sequence represents a peptide	XX	
CC	that can be used as a vaccine antigen in the exemplification of the	XX	
CC	present invention.	XX	
XX		XX	
SQ	Sequence 6 AA;	XX	
	Query Match 100.0%; Score 29; DB 8; Length 6;		
	Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;		
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 KVVFFA 6		
Db	1 KVVFFA 6		
RESULT 11			
ADQ37321			

CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

Db 1 KVVFFA 6

RESULT 12

ADQ37329

ID ADQ37329 standard; peptide; 6 AA.

AC ADQ37329;

DT 07-OCT-2004 (first entry)

XX Antifibrillogenic amyloidosis inhibiting peptide.

XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antihypertoid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.

XX Synthetic.

Key Location/Qualifiers
 FT Modified-site 6 /note= "amidated"

XX WO2004058239-A1.

XX 15-JUL-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2003; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent
 FT that prevents or treats amyloid-beta related disease and second agent

PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX Disclosure; Page 70; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

Db 1 KVVFFA 6

RESULT 13

ADY37928

ID ADY37928 standard; peptide; 6 AA.

XX ADY37928;

XX 19-MAY-2005 (first entry)

XX Amyloid-targeting peptide, SEQ ID NO:8, for use in imaging agent.

XX Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;

XX transmissible spongiform encephalopathy; scrapie; BSE;

XX Alzheimer's disease; neurological disease; amyloidosis;

XX non-insulin dependent diabetes; metabolic disorder.

XX Synthetic.

XX US2005048000-A1.

PD 03-MAR-2005.
 XX 03-DEC-2003; 2003US-00728028.
 XX 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.
 PR 29-JAN-2003; 2003US-0443291P.
 XX (NEUR-) NEUROCHEM INT LTD.
 XX Gervais F, Kong X, Chalifour R, Migneault D;
 PI WPI; 2005-212201/22.
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
 PT related condition, e.g. Creutzfeldt-Jakob disease, bovine spongiform
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.
 XX Disclosure; SEQ ID NO 8; 34pp; English.
 XX The invention relates to an amyloid-targeting imaging agent. The imaging
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
 CC a labeling moiety via a linking moiety, and is preferably able to cross
 CC the blood-brain barrier. The invention also relates to a kit for
 CC preparing a radiopharmaceutical preparation from the imaging agent of the
 CC invention, a method for imaging amyloid deposition in a patient and a
 CC method for diagnosing an amyloid-related condition in a patient. The
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
 CC related conditions such as Creutzfeldt-Jakob disease (CJD), Kuru,
 CC transmissible cerebral amyloidoses (also known as transmissible virus
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
 CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
 CC mediated diseases, dialysis-related amyloidosis, light chain-related
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
 CC patient. The agent does not exhibit excessive toxicity or irritation,
 CC does not induce an allergic response, and permits an earlier diagnosis of
 CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.
 XX Sequence 6 AA;
 SQ Query Match 100.0%; Score 29; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 1 KVVFFA 6
 RESULT 14
 ADY37936
 ID ADY37936 standard; peptide; 6 AA.
 XX
 AC ADY37936;
 XX
 XX 19-MAY-2005 (first entry)
 XX Amyloid-targeting peptide, SEQ ID NO:16, for use in imaging agent.
 XX
 XX Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
 KW transmissible spongiform encephalopathy; scrapie; BSE;
 KW Alzheimers disease; neurological disease; amyloidosis;
 KW non-insulin dependent diabetes; metabolic disorder.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 6
 FT

FT XX /note= "C-terminal amide"
 XX US2005048000-A1.
 XX 03-MAR-2005.
 PD 03-DEC-2003; 2003US-00728028.
 XX 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.
 PR 29-JAN-2003; 2003US-0443291P.
 XX (NEUR-) NEUROCHEM INT LTD.
 XX Gervais F, Kong X, Chalifour R, Migneault D;
 PI WPI; 2005-212201/22.
 XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
 PT related condition, e.g. Creutzfeldt-Jakob disease, bovine spongiform
 PT encephalopathy, primary amyloidosis or Alzheimer's disease.
 XX Disclosure; SEQ ID NO 16; 34pp; English.
 XX The invention relates to an amyloid-targeting imaging agent. The imaging
 CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
 CC a labeling moiety via a linking moiety, and is preferably able to cross
 CC the blood-brain barrier. The invention also relates to a kit for
 CC preparing a radiopharmaceutical preparation from the imaging agent of the
 CC invention, a method for imaging amyloid deposition in a patient and a
 CC method for diagnosing an amyloid-related condition in a patient. The
 CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
 CC related conditions such as Creutzfeldt-Jakob disease (CJD), Kuru,
 CC transmissible cerebral amyloidoses (also known as transmissible virus
 CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
 CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
 CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
 CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
 CC mediated diseases, dialysis-related amyloidosis, light chain-related
 CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
 CC patient. The agent does not exhibit excessive toxicity or irritation,
 CC does not induce an allergic response, and permits an earlier diagnosis of
 CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.
 XX Sequence 6 AA;
 SQ Query Match 100.0%; Score 29; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 1 KVVFFA 6
 RESULT 15
 ADQ09761
 ID ADQ09761 standard; peptide; 22 AA.
 XX
 AC ADQ09761;
 XX
 XX 23-SEP-2004 (first entry)
 XX Rice 26kDa globulin signal sequence SEQ ID NO:117.
 DE
 XX prolamine; rice; plant; seed; transgenic plant; signal.
 KW
 XX Oryza sativa.
 OS
 XX WO2004056993-A1.
 PN

XX PD 08-JUL-2004.

XX PF 09-DEC-2003; 2003WO-JP015753.

XX PR 20-DEC-2002; 2002JP-00369700.

XX PA (NAG-) NAT AGRIC & BIO-ORIENTED RES ORG.

XX PI Kuroda M;

XX DR WPI; 2004-525439/50.

XX DR N-PSDB; ADQ09760.

XX PT Novel nucleic acid molecule antisense to nucleic acid sequence encoding

PT prolamine, useful for reducing expression dose of protein in seed, and

PT for producing transgenic plant, preferably rice plant having reduced

PT storage protein.

XX Example 13; SEQ ID NO 117; 272pp; Japanese.

XX The present invention describes a nucleic acid molecule (I) comprising a

CC consecutive nucleic acid sequence (S1) of at least 15 bp in length and

CC complementary with a nucleic acid sequence encoding a prolamine

CC polypeptide or a nucleic acid sequence having a homology of at least

CC about 70% to (S1). Also described: (1) a nucleic acid molecule (N1)

CC comprising a nucleic acid sequence (A) having about 70% homology to a

CC nucleic acid sequence encoding a prolamine polypeptide and a nucleic acid

CC sequence (B) having about 70% homology to the complement of the nucleic

CC acid sequence encoding a prolamine polypeptide; (2) a factor (II) capable

CC of causing RNA interference of the gene sequence encoding a prolamine

CC polypeptide; (3) a nucleic acid cassette (III) containing (1); (4)

CC producing (III); (5) a vector (IV) comprising (1); (6) a plant cell (V)

CC comprising (1); (7) a plant tissue (VI) comprising (V); (8) a plant (VII)

CC containing (1) or (V); (9) a seed (VIII) produced by (VII); (10) starch

CC preparation produced from (VII) or (VIII); and (11) a composition

CC containing gene product of foreign gene produced from (VII) or (VIII).

CC (I) is useful for decreasing the expression level of a protein in the

CC seed of a plant, for expressing a foreign gene in the seed of a plant and

CC for decreasing the expression of a natural protein in the seed of a

CC plant. The method of decreasing the amount of expression level of a

CC protein in the seed of a plant involves providing (I), introducing (I)

CC into the cell of the plant, redifferentiating the cell, producing a

CC transgenic plant, and obtaining the seed from the transgenic plant. The

CC method after the step of introduction, further involves selecting the

CC cell introduced with (I), by determining resistance with respect to

CC antibiotics. The method of expressing a foreign gene in the seed of a

CC plant, involves providing (I) and the nucleic acid molecule encoding a

CC foreign gene product, introducing (I) and the nucleic acid molecule

CC encoding a foreign gene product into cell of the plant, re-

CC differentiating the cell, producing a transgenic plant, and obtaining the

CC seed from the transgenic plant. The method further involves isolating the

CC gene product of the foreign gene from the seed. (I) is useful for

CC producing transgenic plants having reduced expression of storage proteins

CC and for reducing the expression dose of a protein in a seed of a plant.

CC The present sequence represents a rice 26kDa globulin signal sequence,

XX which is used in the exemplification of the present invention.

XX SQ Sequence 22 AA;

Query Match 100.0%; Score 29; DB 8; Length 22;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6

Db |||||

4 KVVFFA 9

RESULT 16

ADT93984

ID ADT93984 standard; peptide; 23 AA.

XX

AC ADT93984;

XX 27-JAN-2005 (first entry)

DT XX

DE XX

DE XX

XX Rice 26 kDa peptide.

XX Storage protein; allergen specific T cell epitope;

KW vesicle anchoring signal; transgenic plant; rice albumen;

KW T cell epitope-attached peptide; 7crp; seed; glutelin; edible vaccine;

KW Japanese cedar pollen antigen; Cry11; Cry12; allergic disease; hay fever;

KW antiallergic; plant; 26 kDa.

XX Oryza sativa.

OS

XX WO2004094637-A1.

XX 04-NOV-2004.

PD

XX 23-APR-2004; 2004WO-JP005938.

PF

XX 24-APR-2003; 2003JP-00120639.

PR

XX (NORQ) NAT INST AGROBIOLOGICAL SCI.

PA Takaiwa F, Takagi H;

PI WPI; 2004-784905/77.

XX Novel DNA having sequence encoding allergen specific T-cell epitope

XX peptide, useful for accumulating T-cell epitope peptide in plants and for

PT treating allergic diseases such as pollinosis.

PT Disclosure; SEQ ID NO 5; 79pp; Japanese.

PS This invention relates to a DNA (I) having a sequence under the control

XX of a storage protein promoter, chosen from a sequence encoding storage

CC protein signal sequence at the 5' end of a sequence encoding allergen

CC specific T cell epitope peptide and/or a sequence encoding vesicle

CC anchoring signal sequence at the 3' end, and a DNA sequence encoding a

CC polypeptide having allergen specific T-cell epitope peptide inserted in

CC the variable region of a storage protein. Also disclosed is a vector (II)

CC for T-cell epitope accumulated plant preparation, and a method of

CC accumulating allergen specific T-cell epitope in a plant. The method

CC involves introducing (I) or (II) to a plant, obtaining DNA encoding

CC allergen specific T-cell epitope peptide, adding a DNA encoding a storage

CC protein signal sequence to the 5' end and/or a vesicle anchoring signal

CC sequence to the 3' end of the obtained DNA, and expressing the DNA in a

CC plant under the control of a storage protein promoter, or obtaining DNA

CC encoding allergen specific T-cell epitope peptide, inserting a DNA into

CC the variable region of storage protein of the plant and expressing the

CC peptide in the transgenic plant. The invention describes the accumulation

CC of human T cell epitope in rice albumen, a method of accumulating T cell

CC epitope-attached peptide (7crp) in seeds, a method of inserting the 7crp

CC into the variable region of glutelin (the major storage protein of rice),

CC and expressing and accumulating 7crp as part of the glutelin. The rice

CC capable of producing the 7crp is useful as an edible vaccine against

CC Japanese (Cryptomeria japonica) cedar pollen antigen. The pollen allergen

CC is Cryj1 or Cryj2. The T-cell epitope is integrated on an edible region

CC such as the seed of a plant. The method of the invention is useful for

CC producing a plant accumulated with allergen specific T-cell epitope, and

CC manufacturing a transgenic plant, preferably rice, integrated with T-cell

CC epitope. The method is useful for preventing or treating allergic disease

CC such as hay fever. The method enables the production of allergen specific

CC T-cell epitope at a low cost and also reduces the amount for

CC administration. The allergen specific T-cell epitope accumulated in a

CC seed is stable for storage. This sequence represents rice 26 kDa peptide.

XX SQ Sequence 23 AA;

Query Match 100.0%; Score 29; DB 8; Length 23;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 KVVFFA 6
Db      4 KVVFFA 9

RESULT 17
AAB05910
ID AAB05910 standard; peptide; 37 AA.
XX
XX
AC AAB05910;
XX
DT 16-OCT-2000 (first entry)
XX
DE Mouse inducible nitric oxide synthase calmodulin-binding region.
XX
XX Mouse; inducible nitric oxide synthase; iNOS;
KW endothelial nitric oxide synthase; eNOS; vasotropic; hypertensive;
KW AMP-activated protein kinase; AMPK; calmodulin; CaM;
KW eNOS phosphorylation; ischaemic heart disease; pulmonary hypertension;
KW obstructive airways disease.
XX
OS Mus sp.
XX
PN WO200028076-A1.
XX
PD 18-MAY-2000.
XX
PF 05-NOV-1999; 99WO-AU000968.
XX
PR 06-NOV-1998; 98AU-0006976.
XX
PA (SVIN-) ST VINCENTS INST MEDICAL RES.
XX
PI Stapleton DI, Chen Z, Michell BJ, Kemp BE, Mitchellhill KT;
XX
DR WPI; 2000-376583/32.
XX
PT Identifying modulators of AMP-activated protein kinase-mediated
PT activation of a nitric oxide synthase (NOS), for use in ischemic heart
PT disease, comprises testing for the increase or decrease in
PT phosphorylation of NOS.
XX
XX Example 4; Fig 5; 4lpp; English.
XX
CC The present sequence is the calmodulin (CaM)-binding region of mouse
CC inducible nitric oxide synthase (iNOS). iNOS is one of three isoforms of
CC the enzyme NOS, which synthesises nitric oxide from the amino acid L-
CC arginine. The sequence is provided for comparison with endothelial nitric
CC oxide synthase (eNOS). The threonine residue at position 495 of eNOS is
CC phosphorylated by AMP-activated protein kinase (AMPK) in the absence of
CC Ca2+-CaM. Phosphorylation results in inhibition of eNOS. In the presence
CC of Ca2+-CaM, phosphorylation by AMPK occurs predominantly at Ser-117 and
CC eNOS is activated. Modulators which activate AMPK may be used in the
CC treatment of ischemic heart disease by promoting glucose and fatty acid
CC metabolism, and improving nutrient and oxygen supply to the myocytes.
CC They may also be used for the treatment of pulmonary hypertension and
CC obstructive airways disease
XX
XX Sequence 37 AA;

Query Match 100.0%; Score 29; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      18 KVVFFA 23

RESULT 18
ADK34080
ID ADK34080 standard; peptide; 37 AA.
XX
XX

```

```

AC ADK34080;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human nNOS calmodulin binding domain peptide seqid 7.
XX
KW vasotropic; antiangiogenic; gene therapy; critical limb ischaemia; CLI;
KW eNOS; endothelial nitric oxide synthase; angiogenesis;
KW microvascular dysfunction; human; calmodulin binding domain;
KW neuronal nitric oxide; nNOS.
XX
OS Homo sapiens.
XX
PN WO2004016761-A2.
XX
PD 26-FEB-2004.
XX
PF 15-AUG-2003; 2003WO-US025626.
XX
PR 16-AUG-2002; 2002US-0403637P.
XX
PA (SCHD ) SCHERING AG.
XX
PI Dole WP, Kauser K, Qian HS, Rubanyi G;
XX
DR WPI; 2004-203789/19.
XX
PT Treating critical limb ischemia (CLI), or angiogenesis comprises
PT administering to a patient a polynucleotide encoding a mammalian
PT endothelial nitric oxide synthase (eNOS) polypeptide.
XX
XX Example 1; SEQ ID NO 7; 82pp; English.
XX
CC The invention describes a method of creating critical limb ischaemia
CC (CLI) comprising administering to a patient a polynucleotide encoding a
CC mammalian eNOS (endothelial nitric oxide synthase) polypeptide. Also
CC described are: a method for treating angiogenesis by administering to a
CC patient a polynucleotide encoding eNOS; and ameliorating microvascular
CC dysfunction by administering to the patient the polynucleotide encoding
CC the eNOS polypeptide. The method is useful for treating critical limb
CC ischaemia or angiogenesis, or ameliorating a microvascular dysfunction.
CC This is the amino acid sequence of a human neuronal nitric synthase
CC (nNOS) calmodulin binding domain peptide.
XX
XX Sequence 37 AA;

Query Match 100.0%; Score 29; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVVFFA 6
Db      18 KVVFFA 23

RESULT 19
ADL70727
ID ADL70727 standard; peptide; 37 AA.
XX
XX ADL70727;
XX
DT 20-MAY-2004 (first entry)
XX
DE Mouse iNOS calmodulin-binding site amino acid sequence SEQ ID NO:7.
XX
KW mouse; endothelial nitric oxide synthase; eNOS; enzyme; mutant;
KW calmodulin-binding domain; vasotropic; antiarteriosclerotic; hypotensive;
KW antidiabetic; vulnery; antilipemic; anorectic;
KW reduced calcium dependence; ischaemia; atherosclerosis; hypertension;
KW diabetes; Raynaud's phenomenon; poor wound healing; hyperlipidaemia;
KW obesity; iNOS.
XX
OS Mus musculus.

```

XX	WO2004016764-A2.
PN	
XX	26-FEB-2004.
PD	
XX	
PP	15-AUG-2003; 2003WO-US025745.
XX	
PR	16-AUG-2002; 2002US-0403638P.
XX	(SCHD) SCHERING AG.
PA	
PI	Blasko E, Kauser K, Parkinson J;
XX	WPI; 2004-203792/19.
DR	
XX	
PT	New isolated endothelial nitric oxide synthase polypeptide mutant, useful
PT	for diagnosing or treating ischemia, atherosclerosis, hypertension,
PT	diabetes, Raynaud's phenomenon, poor wound healing, hyperlipidemia or
PT	obesity.
XX	
PS	Example 1; SEQ ID NO 7; 57pp; English.
XX	
CC	The present sequence represents the calmodulin-binding site of mouse eNOS
CC	amino acid sequence. The present invention describes endothelial nitric
CC	oxide synthase (eNOS) mutants having one or more mutations in an amino
CC	acid sequence corresponding to a functional domain of a mammalian eNOS.
CC	At least one of the mutations is at a position corresponding to an amino
CC	acid residue in a calmodulin-binding domain that is phosphorylated in
CC	mammalian cells, and not an amino acid substitution to Ala or Asp. Also
CC	described: (1) an isolated eNOS polypeptide mutant that is substantially
CC	homologous, or has a 95-99% sequence identity to the amino acid sequence
CC	of the novel eNOS polypeptide mutant; (2) an isolated polynucleotide
CC	encoding the polypeptide mutant; (3) a recombinant vector comprising the
CC	polynucleotide operably linked to at least one regulatory sequence; (4) a
CC	pharmaceutical composition comprising the polypeptide mutant or the
CC	polynucleotide; (5) a binding partner of the polypeptide mutant; (6)
CC	modulating eNOS activity in a cell by administering to the cell the
CC	polypeptide mutant; (7) modulating eNOS activity in a cell by
CC	administering the polypeptide mutant or the polynucleotide to the cell,
CC	such that the polypeptide mutant is expressed in the cell; (8) diagnosing
CC	a condition associated with aberrant eNOS activity by contacting a cell
CC	of a patient with the polynucleotide, and detecting a level of eNOS
CC	activity indicative of the medical condition; and (9) prophylactic and
CC	therapeutic methods of treating a condition associated with aberrant eNOS
CC	activity by administering the polypeptide mutant or polynucleotide to the
CC	patient. The eNOS mutant has vasotropic, antiarteriosclerotic,
CC	hypotensive, antidiabetic, vulnerable, antilipemic and anorectic
CC	activities, and has reduced calcium dependence and increased activity.
CC	The polypeptide mutant, polynucleotide and methods are useful for
CC	diagnosing or treating a condition associated with aberrant eNOS
CC	activity, e.g. ischaemia, atherosclerosis, hypertension, diabetes,
CC	Raynaud's phenomenon, poor wound healing, hyperlipidaemia or obesity.
XX	
SQ	Sequence 37 AA;
Query Match	100.0%; Score 29; DB 8; Length 37;
Best Local Similarity	100.0%; Pred. No. 22;
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1 KVVFPA 6
Dbb	18 KVVFPA 23
RESULT 20	
AAG02840	ID AAG02840 standard; protein; 77 AA.
XX	AAG02840;
AC	
XX	
DT	06-OCT-2000 (first entry)
DE	Human secreted protein. SEO ID NO: 6921.

PI	Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
XX	WPI; 2003-229341/22.
XX	N-PSDB; ADC07961.
XX	
XX	New plant genes encoding polypeptides having an activity involved in or
PT	associated with the synthesis, metabolism or degradation of carbohydrates
PT	in the plant grain useful in generating plants having improved
PT	nutritional properties.
XX	
XX	Claim 15; SEQ ID NO 228; 130pp; English.
PS	
XX	This invention, in the area of plant biotechnology, relates to novel
CC	polynucleotides comprising a nucleotide sequence encoding a protein which
CC	is involved in or associated with the synthesis, metabolism or
CC	degradation of carbohydrates in the plant grain and the expression of
CC	which is up-regulated during grain filling. The plant is selected from
CC	corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
CC	sugarbeet, wheat, and rice. The invention may be useful for the
CC	improvement of protein, oil, starch, fibre and moisture content of the
CC	cereal grains. In addition, carbohydrate levels may be modified to a more
CC	desirable level using the present invention. The present sequence is the
CC	amino acid sequence of a rice protein of the invention. Note: The
CC	sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/publishedpct_sequences.
XX	
XX	Sequence 186 AA;
SQ	
	Query Match 100.0%; Score 29; DB 7; Length 186;
	Best Local Similarity 100.0%; Pred. No. 1.1e+02;
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1 KVVFFA 6
Dd	4 KVVFFA 9
RESULT 23	
ADC07948	
ID	ADC07948 standard; protein; 186 AA.
XX	
AC	ADC07948;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	Rice protein sequence Seq ID214 related to grain filling.
XX	
XX	plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
KW	carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
KW	tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
KW	wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
KW	gene; ds; plant.
XX	
OS	Oryza sativa.
XX	
PN	WO2003000905-A2.
XX	
PD	03-JAN-2003.
XX	
PF	21-JUN-2002; 2002WO-IB002450.
XX	
PR	22-JUN-2001; 2001US-0300112P.
PR	26-SEP-2001; 2001US-0325277P.
PR	20-DEC-2001; 2001US-0342327P.
XX	
	(SYGN) SYNGENTA PARTICIPATIONS AG.
PA	
XX	
PI	Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
PI	Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
XX	
XX	WPI; 2003-229341/22.
DR	N-PSDB; ADC07947.

XX New plant genes encoding polypeptides having an activity involved in or
PT associated with the synthesis, metabolism or degradation of carbohydrates
PT in the plant grain useful in generating plants having improved
PT nutritional properties.
XX
PS Claim 15; SEQ ID NO 214; 130pp; English.
XX
CC This invention, in the area of plant biotechnology, relates to novel
CC polynucleotides comprising a nucleotide sequence encoding a protein which
CC is involved in or associated with the synthesis, metabolism or
CC degradation of carbohydrates in the plant grain and the expression of
CC which is up-regulated during grain filling. The plant is selected from
CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
CC sugarbeet, wheat, and rice. The invention may be useful for the
CC improvement of protein, oil, starch, fibre and moisture content of the
CC cereal grains. In addition, carbohydrate levels may be modified to a more
CC desirable level using the present invention. The present sequence is the
CC amino acid sequence of a rice protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences.

SQ Sequence 186 AA;

Query Match 100.0%; Score 29; DB 7; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 4 KVVFFA 9

RESULT 24

AAW83792
ID AAW83792 standard; protein; 190 AA.

XX
AC AAW83792;

XX
DT 07-NOV-2001 (first entry)

XX
DE Human immune/haematopoietic antigen SEQ ID NO:11385.

XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.

XX
OS Homo sapiens.

XX
PN WO200157182-A2.

XX
PD 09-AUG-2001.

XX
PF 17-JAN-2001; 2001WO-US001354.

XX
31-JAN-2000; 2000US-0179065P.

XX
04-FEB-2000; 2000US-0180628P.

XX
24-FEB-2000; 2000US-0184664P.

XX
02-MAR-2000; 2000US-0186350P.

XX
16-MAR-2000; 2000US-0189874P.

XX
17-MAR-2000; 2000US-0190076P.

XX
18-APR-2000; 2000US-0198123P.

XX
19-MAY-2000; 2000US-0205515P.

XX
07-JUN-2000; 2000US-0209467P.

XX
28-JUN-2000; 2000US-0214886P.

XX
30-JUN-2000; 2000US-0215135P.

XX
07-JUL-2000; 2000US-0216647P.

XX
07-JUL-2000; 2000US-0216880P.

XX
11-JUL-2000; 2000US-0217487P.

XX
11-JUL-2000; 2000US-0217496P.

XX
14-JUL-2000; 2000US-0218290P.

XX
26-JUL-2000; 2000US-0220963P.

XX
26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.

PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 11-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 DR WPI; 2001-483426/52.
 DR N-PSDB; AAK56573.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides;
 PT useful for preventing, diagnosing and/or treating cancers and metastasis.
 XX
 PS Claim 1; SEQ ID NO 11385; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic

CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 190 AA;
 Query Match 100.0%; Score 29; DB 4; Length 190;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVPFFA 6
 Db 14 KVPFFA 19
 |||||
 |||||
 RESULT 25
 ADQ66704
 ID ADQ66704 standard; protein; 854 AA.
 XX
 AC ADQ66704;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DB Novel human protein sequence #1677.
 XX
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KW gene therapy; diagnostic marker; morbid state; osteoporosis;
 KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN EP1440981-A2.
 XX
 PD 28-JUL-2004.
 XX
 PP 21-JAN-2004; 2004EP-00001196.
 PR 21-JAN-2003; 2003JP-00102206.
 PR 09-MAY-2003; 2003JP-00131392.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Nagai K, Irie R;
 PI WPI; 2004-535376/52.
 DR N-PSDB; ADQ64516.
 XX
 PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 XX
 PS Claim 1; SEQ ID NO 3865; 2449pp; English.
 XX
 CC The invention relates to 2495 novel polynucleotides (I) and their encoded
 CC polypeptides, sequences hybridizing to these nucleotides, sequences
 CC encoding partial polypeptides and sequences having 70% or 90% identity to
 CC the nucleotide and protein sequences. The nucleotides and polypeptides
 CC are useful as diagnostic markers or therapeutic target for the diseases
 CC or morbid states. They are also useful for treating osteoporosis,
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
 CC dementia and various cancers. This sequence corresponds to a protein
 CC sequence of the invention.
 XX
 SQ Sequence 854 AA;
 Query Match 100.0%; Score 29; DB 8; Length 854;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVPFFA 6
 Db 221 KVPFFA 226
 |||||
 |||||

RESULT 26
ABM83252
ID ABM83252 standard; protein; 922 AA.
XX
AC ABM83252;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3501.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2002; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN41904.
XX

New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.

Claim 27; Page; 190pp; English.

This invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

Sequence 922 AA;

Query Match 100.0%; Score 29; DB 8; Length 922;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|||||
Db 291 KVVFFA 296

RESULT 27

ADF76335
ID ADF76335 standard; protein; 925 AA.
XX
AC ADF76335;
XX
DT 26-FEB-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein SeqID 8.
XX
KW human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neurotrophic factor; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
XX
OS Homo sapiens.
XX
PN WO2003072035-A2.
XX
PD 04-SEP-2003.
XX
PF 21-FEB-2003; 2003WO-US005241.
XX
PR 22-FEB-2002; 2002US-0359461P.
XX
PA (GETH) GENENTECH INC.
XX
PI Bodary SC, Clark HI, Hunte B, Jackman JK, Schoenfeld JR;
PI Williams PM, Wood WI, Wu TD;
XX
XX WPI; 2003-721702/68.
DR N-PSDB; ADF76334.
XX
PT New PRO polypeptides, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or diabetes mellitus.
XX
PS Claim 10; SEQ ID NO 8; 918pp; English.

This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neurotrophic factors and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the invention.

Sequence 925 AA;

Query Match 100.0%; Score 29; DB 7; Length 925;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|||||
Db 292 KVVFFA 297

RESULT 28
ADJ70225
ID ADJ70225 standard; protein; 925 AA.
XX AC ADJ70225;
XX DT 06-MAY-2004 (first entry)
XX DE Human heat mitochondrial protein as a therapeutic target SeqID2031.
XX KW mitochondrial; human; screening assay; diabetes mellitus;
XX KW Huntington's disease; osteoarthritis;
XX KW Leber's hereditary optic neuropathy; LHON;
XX KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
XX KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
XX KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
XX KW osteopathic; ophthalmological; cytostatic.
XX OS Homo sapiens.
XX PN WO2003087768-A2.
XX PD 23-OCT-2003.
XX PF 04-APR-2003; 2003WO-US010870.
XX PR 12-APR-2002; 2002US-0372843P.
XX PR 17-JUN-2002; 2002US-0389987P.
XX PR 20-SEP-2002; 2002US-0411418P.
XX PA (MITO-) MITOKOR.
XX PA (BUCK-) BUCK INST AGE RES.
XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX WPI; 2003-845369/78.
XX PT Identifying a mitochondrial target for drug screening assays and for
XX PT treating diseases associated with altered mitochondrial function,
XX PT comprises detecting a modified polypeptide in a sample and correlating
XX PT with the disease.
XX PS Claim 1; SEQ ID NO 2031; 180pp; English.
XX CC This invention relates to novel mitochondrial targets that can be used
XX CC for therapeutic intervention in treating a disease associated with
XX CC altered mitochondrial function. Specifically, it refers to a method for
XX CC identifying proteins of the human heart mitochondrial proteome that are
XX CC useful for drug screening assays, as well as therapeutic targets. The
XX CC present invention describes a method for identifying such proteins that
XX CC can be used in the treatment of various diseases associated with altered
XX CC mitochondrial function including diabetes mellitus, Huntington's disease,
XX CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
XX CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
XX CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
XX CC compositions have neuroprotective, neurotropic, antidiabetic,
XX CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
XX CC cytostatic activities. This polypeptide sequence is a human heart
XX CC mitochondrial protein of the invention.
XX SQ Sequence 925 AA;

Query Match 100.0%; Score 29; DB 7; Length 925;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
|||

Db 292 KVVFFA 297

RESULT 29
ADJ75428
ID ADJ75428 standard; protein; 925 AA.
XX AC ADJ75428;
XX DT 20-MAY-2004 (first entry)
XX DE Marker gene related amino acid sequence SEQ ID NO:680.
XX KW bronchial asthma; chronic obstructive pulmonary disease;
XX KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
XX KW gene therapy; marker.
XX OS Homo sapiens.
XX PN EPI394274-A2.
XX PD 03-MAR-2004.
XX PF 04-AUG-2003; 2003EP-00254857.
XX PR 06-AUG-2002; 2002JP-00229312.
XX PR 20-MAR-2003; 2003JP-00077212.
XX PA (GENO-) GENOX RES INC.
XX PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuohara K;
XX WPI; 2004-193155/19.
XX PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
XX PT comparing the expression level of a marker gene in a biological sample
XX PT from a subject with the expression level of the gene in a sample from a
XX PT healthy subject.
XX PS Example 11; SEQ ID NO 680; 241pp; English.
XX CC The present invention describes a method of testing for bronchial asthma
XX CC or chronic obstructive pulmonary disease. The method comprises
XX CC determining the expression level of a marker gene in a biological sample
XX CC from a subject, comparing the expression level determined with the
XX CC expression level of the marker gene in a biological sample from a healthy
XX CC subject, and judging whether the subject has bronchial asthma or chronic
XX CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
XX CC genes (S1) whose expression levels increase when respiratory epithelial
XX CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
XX CC whose expression levels decrease when respiratory epithelial cells are
XX CC stimulated with interleukin-13. Also described: (1) a reagent (1) for
XX CC testing for bronchial asthma or chronic obstructive pulmonary disease;
XX CC (2) a kit for screening for a candidate compound for a therapeutic agent
XX CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
XX CC an animal model for bronchial asthma or chronic obstructive pulmonary
XX CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
XX CC method for producing an animal model for bronchial asthma or chronic
XX CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
XX CC asthma or chronic obstructive pulmonary disease, comprising the compound,
XX CC a marker gene or an antisense nucleic acid corresponding to a portion of
XX CC the marker gene, a ribozyme, a polynucleotide that suppresses the
XX CC expression of the gene through an RNAi effect or an antibody recognising
XX CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
XX CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
XX CC probe has been immobilised to assay a marker gene. (1) has respiratory
XX CC and antiasthmatic activities, and can be used in gene therapy. The method
XX CC is useful for testing for or screening for a therapeutic agent for
XX CC bronchial asthma or chronic obstructive pulmonary disease. The present
XX CC sequence is used in the exemplification of the present invention.
XX SQ Sequence 925 AA;

Query Match 100.0%; Score 29; DB 8; Length 925;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 Db 292 KVVFFA 297

RESULT 30
 ADJ75495
 ID ADJ75495 standard; protein; 925 AA.
 XX
 AC ADJ75495;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Marker gene related amino acid sequence SEQ ID NO:747.
 XX
 KW bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.
 XX
 OS Homo sapiens.
 XX
 PN EP1394274-A2.
 XX
 PD 03-MAR-2004.
 XX
 XX 04-AUG-2003; 2003EP-00254857.
 XX
 PF 06-AUG-2003; 2002JP-00229312.
 PR 20-MAR-2003; 2003JP-00077212.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuohara K;
 XX WPI; 2004-193155/19.
 DR
 XX
 XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.
 XX
 XX Example 11; SEQ ID NO 747; 241pp; English.

The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (1) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene; a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (1) has respiratory and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.

XX
 SQ Sequence 925 AA;
 Query Match 100.0%; Score 29; DB 8; Length 925;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVVFFA 6
 Db 292 KVVFFA 297

RESULT 31
 ADN04860
 ID ADN04860 standard; protein; 925 AA.
 XX
 AC ADN04860;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Antipsoriatic protein sequence #610.
 XX
 KW antipsoriatic; gene therapy; psoriasis; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2004028479-A2.
 XX
 PD 08-APR-2004.
 XX
 PF 25-SEP-2003; 2003WO-US030907.
 XX
 PR 25-SEP-2002; 2002US-0414006P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
 PI Wu TB;
 XX
 XX WPI; 2004-305105/28.
 DR N-PSDB; ADN04859.
 XX
 XX New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.
 XX
 PS Claim 9; SEQ ID NO 1254; 3069pp; English.
 XX
 CC The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.
 XX
 SQ Sequence 925 AA;
 Query Match 100.0%; Score 29; DB 8; Length 925;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVVFFA 6
 Db 292 KVVFFA 297

RESULT 32
 ADR14233
 ID ADR14233 standard; protein; 925 AA.
 XX
 AC ADR14233;
 XX
 DT 21-OCT-2004 (first entry)
 XX

DE Human NF-kappaB pathway-associated protein SeqID234.

XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;

KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;

KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;

KW immunosuppressive; vulnery; gene therapy; immune disorder;

KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;

KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;

KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;

KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;

KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;

KW viral replication; host cell survival; evasion of immune response;

KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;

KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;

KW autoimmune disorder; hyper immune activity;

KW aberrant acute phase response; hypercongenital condition; birth defect;

KW necrotic lesion; wound; organ transplant rejection;

KW aberrant signal transduction; proliferating disorder; cancer;

KW HIV propagation; human.

OS Homo sapiens.

XX WO2004065577-A2.

XX 05-AUG-2004.

XX 13-JAN-2004; 2004WO-US000798.

XX 14-JAN-2003; 2003US-0440068P.

PR 12-MAY-2003; 2003US-0469757P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

PA Nadler SG, Neubauer MG, Feder JN, Carman J;

XX WPI; 2004-562168/54.

XX N-PSDB; ADRL4232.

DR New isolated polynucleotides and polypeptides associated with NF-kappaB

PT pathway, useful for diagnosing, treating, or preventing disorders or

PT diseases associated with NF-kappaB pathway.

XX Claim 6; SEQ ID NO 234; 237pp; English.

XX This invention relates to the novel association of protein sequences (and

CC the genes which encode them) to the NF-kappaB pathway. The invention may

CC be useful for the production of compounds with an antiinflammatory,

CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,

CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,

CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or

CC vulnery activity or for gene therapy. The proteins and nucleotides are

CC useful for diagnosing, preventing, treating, or ameliorating conditions

CC or diseases associated with the NF-kappaB pathway. The condition is an

CC immune disorder, an inflammatory disorder, an inflammatory disorder

CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,

CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM

CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic

CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,

CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell

CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory

CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick

CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper

CC immune activity, disorders related to aberrant acute phase responses,

CC hypercongenital conditions, birth defects, necrotic lesions, wounds,

CC organ transplant rejection, conditions related to organ transplant

CC rejection, disorders related to aberrant signal transduction,

CC proliferating disorders, cancers and HIV propagation in cells infected

CC with other viruses. The present sequence is that of a human protein which

CC is subject to the novel association with the NF-kappaB pathway of the

CC invention. Note: This sequence does not appear in the specification but

CC was obtained by the indexer from Genbank.

XX Sequence 925 AA;

Query Match 100.0%; Score 29; DB 8; Length 925;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFPPA 6

DB 292 KVFPPA 297

|||||

RESULT 33

ADP25011

ID ADP25011 standard; protein; 925 AA.

XX AC ADP25011;

XX 18-NOV-2004 (first entry)

XX PRO polypeptide SEQ ID NO:2189.

DE PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;

XX KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;

XX KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

XX OS Unidentified.

XX WO2004041170-A2.

XX 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034312.

XX 01-NOV-2002; 2002US-0423394P.

XX (GETH) GENENTECH INC.

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;

PI Wu TD;

XX WPI; 2004-419628/39.

DR N-PSDB; ADP25010.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.

PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated

PT renal disease, or demyelinating diseases of the central or peripheral

XX nervous system.

PS Claim 7; SEQ ID NO 2189; 2940pp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO

CC polypeptide encoded by it. A protein of the invention has

CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,

CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,

CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide

CC of the invention may have a use in gene therapy. The PRO polypeptide, its

CC agonist, antagonist, or antibody that specifically binds to the

CC polypeptide is useful for treating an immune related disorder such as

CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an

CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic

CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune

CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal

CC disease, a demyelinating disease of the central or peripheral nervous

CC system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome,

CC a chronic inflammatory demyelinating polynuropathy, a hepatobiliary

CC disease, infectious or autoimmune chronic active hepatitis, primary

CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,

CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's

CC disease, an autoimmune or immune-mediated skin disease, a bullous skin

CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic

CC disease, asthma, allergic rhinitis, atopic dermatitis, food

CC hypersensitivity, urticaria, an immunologic disease of the lung,

CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity

CC pneumonia, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 XX
 SQ Sequence 925 AA;

Query Match 100.0%; Score 29; DB 8; Length 925;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 Db 292 KVVFFA 297

RESULT 34
 ADR97294
 ID ADR97294 standard; protein; 925 AA.

XX AC ADR97294;

XX XX 02-DEC-2004 (first entry)

XX XX Human RIG-I-DEAD/H box protein, an apoptosis related target Seq 2.

XX KW human; enzyme; apoptosis; cancer; inflammation; autoimmune;
 KW neurodegenerative disorder; cytostatic; antiinflammatory;
 KW immunosuppressive; neuroprotective; gene therapy; RIG-I-DEAD/H box.

XX OS Homo sapiens.

XX PN WO2004078783-A2.

XX PD 16-SEP-2004.

XX PF 05-MAR-2004; 2004WO-GB000957.

XX PR 07-MAR-2003; 2003GB-00005267.

XX PA (BIRX-) BIRX THERAPEUTICS LTD.

XX PI Murphy FU, Sheehan DE, Keating KE, Hayes I, Seera L;

XX DR WPI; 2004-662402/64.

XX DR N-PSDB; ADR97293.

XX PT Identifying an agent that modulates the function of an apoptosis-
 PT associated polypeptide, useful for diagnosing or treating e.g. cancer,
 PT comprises comparing the binding of the polypeptide to the candidate agent
 PT and to a control agent.

XX PS Claim 1; SEQ ID NO 2; 304pp; English.

XX CC This invention relates to novel agents that modulates the function of
 CC human apoptosis-associated proteins specified within the specification.
 CC Specifically, it refers to a method for the identification of target
 CC genes whose expression is correlated with an early stage in the
 CC regulation of apoptosis. The present invention describes a method of
 CC contacting either candidate agents or control agents to the target genes
 CC and assessing the difference of binding and inhibitory activity, where
 CC the candidate agent is selected from a low molecular weight organic
 CC molecule, an antibody or fragment thereof, an antisense oligonucleotide,
 CC a small inhibitory dsRNA, or a ribozyme. As such, the compositions and
 CC methods are useful for diagnosing and treating diseases or conditions
 CC associated with abnormal apoptosis in mammalian tissue, such as cancer,
 CC inflammation, autoimmune or neurodegenerative disorders. Accordingly,
 CC they exhibit cytostatic, antiinflammatory, immunosuppressive and
 CC neuroprotective activities. These may also be used for drug screening
 CC purposes and in gene therapy. This polypeptide sequence is a human target
 CC protein, an enzyme associated with the regulation of apoptosis whose
 CC expression is modulated by novel agents of the invention.

XX Sequence 925 AA;

Query Match 100.0%; Score 29; DB 8; Length 925;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 Db 292 KVVFFA 297

RESULT 35
 ADY17516
 ID ADY17516 standard; protein; 925 AA.

XX AC ADY17516;

XX XX 05-MAY-2005 (first entry)

XX DE PRO polypeptide SEQ ID NO 3322.

XX KW Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
 KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
 KW Antichyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
 KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
 KW Antiallergic; diagnosis.

XX OS Homo sapiens.

XX PN WO2005016962-A2.

XX PD 24-FEB-2005.

XX PF 11-AUG-2004; 2004WO-US026249.

XX PR 11-AUG-2003; 2003US-0493546P.

XX PA (GETH) GENENTECH INC.

XX PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX DR WPI; 2005-182330/19.

XX PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

XX PS Claim 8; SEQ ID NO 3322; 158pp; English.

XX CC The invention relates to an isolated nucleic acid encoding a PRO
 CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
 CC composition, and method are useful for diagnosing and treating an immune
 CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
 CC arthritis. The present sequence represents a PRO polypeptide.

XX SQ Sequence 925 AA;

Query Match 100.0%; Score 29; DB 9; Length 925;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 Db 292 KVVFFA 297

RESULT 36
 AEA23525
 ID AEA23525 standard; protein; 925 AA.

XX AC AEA23525;

XX XX 11-AUG-2005 (first entry)

XX DT

DE Human PRO polypeptide SEQ ID NO 67.
 XX immune disorder; PRO; Antiinflammatory; Dermatological;
 KW Immunosuppressive; Anti-rheumatic; Antiarthritic; Osteopathic;
 KW Muscular-Gen.; Vasootropic; Antianemic; Antipsoriatic; Immunostimulant.
 XX Homo sapiens.
 XX WO2005051988-A2.
 PN 09-JUN-2005.
 PD 02-MAR-2004; 2004WO-US006460.
 XX 03-MAR-2003; 2003US-0451884P.
 XX (GETH) GENENTECH INC.
 XX Abbas A, Bodary S, Clark H, Schoenfeld J, Williams PM, Wood WI;
 PI Wu TD;
 PI WPI: 2005-417958/42.
 DR N-PSDB; AEA23524.
 DR New nucleic acid encoding PRO polypeptide, useful for diagnosing and
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, autoimmune hemolytic anemia, or
 PT psoriasis.
 XX Disclosure; SEQ ID NO 67; 966pp; English.
 XX The invention relates to an isolated nucleic acid. The polypeptide,
 CC compound or composition, and methods are useful for diagnosing and
 CC treating an immune related disorder, e.g. systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis,
 CC spondyloarthropathies, systemic sclerosis, idiopathic inflammatory
 CC myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
 CC autoimmune hemolytic anemia, autoimmune or immune-mediated skin diseases
 CC including bullous skin diseases, erythema multiforme and contact
 CC dermatitis, psoriasis, lymphadenopathy, splenomegaly and leukopenia. The
 CC present sequence represents the amino acid sequence of a human PRO
 CC polypeptide.
 XX Sequence 925 AA;
 SQ Query Match 100.0%; Score 29; DB 9; Length 925;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02; Mismatches 0; Gaps 0;
 Matches 6; Conservative 0; Indels 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 292 KVVFFA 297
 |||||
 RESULT 37
 AAR77360
 ID AAR77360 standard; protein; 1144 AA.
 XX AAR77360;
 AC 10-MAY-1996 (first entry)
 DT Inducible nitrogen monoxide synthase.
 DE nitrogen monoxide synthase; inducible; treatment; prevention;
 KW vascular disease; restenosis.
 XX Mus musculus.
 XX DE4411402-A1.
 PN 05-OCT-1995.
 PD
 XX

PF 31-MAR-1994; 94DE-04411402.
 XX 31-MAR-1994; 94DE-04411402.
 XX (SCHR/) SCHRADER J.
 XX Schrader J, Goedecke A;
 XX WPI: 1995-345550/45.
 DR N-PSDB; AAQ94252.
 XX Eukaryotic expression vector for nitrogen-mon:oxide synthase gene -
 PT useful in the treatment and prevention of diseases of blood vessels by
 PT gene therapy.
 XX Claim 5; Fig 1; 28pp; German.
 XX Inducible nitrogen monoxide synthase (iNOS) was isolated from mice, and
 CC is encoded by AAQ94252. iNOS is homodimer with a mol. wt. of 130 kDa per
 CC subunit. The activity of iNOS is independent of calmodulin and cellular
 CC calcium levels. Vectors contg. the DNA are used in the treatment or
 CC prevention of vascular diseases, high blood pressure, arteriosclerosis,
 CC stenosis or restenosis of blood vessels, esp. coronary vessels after
 CC percutane transluminal coronary angioplasty. See AAR77363 and AAR77362
 CC for endothelial and brain-derived NOS
 XX Sequence 1144 AA;
 SQ Query Match 100.0%; Score 29; DB 2; Length 1144;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 514 KVVFFA 519
 |||||
 RESULT 38
 AAW51246
 ID AAW51246 standard; protein; 1144 AA.
 XX AAW51246;
 AC 25-MAR-2003 (revised)
 DT 12-AUG-1998 (first entry)
 DE Inducible nitric oxide synthase, long isoform.
 XX Inducible nitric oxide synthase; iNOS; recombinant protein; cDNA library;
 KW isoform.
 XX Mus sp.
 XX US5766909-A.
 PN 16-JUN-1998.
 PD 05-NOV-1993; 93US-00147812.
 PF 04-FEB-1992; 92US-00841641.
 PR (MERI) MERCK & CO INC.
 PA Mumford RA, Calaycay JR, Xie Q, Nathan CF;
 PI WPI: 1998-361696/31.
 DR N-PSDB; AAV07247.
 XX DNA encoding inducible nitric oxide synthase proteins - useful for
 PT producing recombinant proteins.
 XX Claim 1; Col 25-32; 39pp; English.
 PS

CC The invention relates to two DNA molecules encoding inducible nitric
 CC oxide synthase (iNOS) proteins, where the DNA molecules comprise defined
 CC sequences of 4041 and 4165 base pairs given in the specification and the
 CC proteins have 1144 amino acids. Also claimed are expression vectors
 CC containing the DNA molecules, and recombinant host cells containing the
 CC vectors. The DNA molecules are useful for producing the recombinant
 CC proteins. The present sequence represents inducible nitric oxide, long
 CC isoform. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 2; Length 1144;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |||||
 Db 514 KVVFFA 519

RESULT 39
 AAG64500
 ID AAG64500 standard; protein; 1144 AA.
 XX
 AC AAG64500;
 XX
 DT 02-OCT-2001 (first entry)
 XX
 DE Mouse inducible nitric oxide synthase 2.
 XX
 KW Antisense oligonucleotide; inducible nitric oxide synthase;
 KW modulate expression; immunomodulator; antidiabetic; cardiovascular;
 KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;
 KW 2'-O-methoxyethyl; phosphorothioate; mouse.
 XX
 OS Mus sp.
 XX
 PN WO200152902-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 15-JAN-2001; 2001WO-US001381.
 XX
 PF 24-JAN-2000; 2000US-00490208.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Bennett CP, Dean NM, Cowseert LM;
 XX
 XX WPI; 2001-465340/50.
 DR
 DR N-PSDB; AAH47974.
 XX
 XX New antisense oligonucleotides for modulating the expression of inducible
 PT nitric oxide synthase in cells or tissues, particularly useful for
 PT treating e.g. immunological, cardiovascular or neurological disorders, or
 PT ischemia.
 XX
 XX Example 17; Page 110-114; 144pp; English.
 PS
 XX The invention relates to antisense compounds, especially
 CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
 CC nitric oxide synthase and which specifically hybridise to and modulate
 CC expression of inducible nitric oxide synthase. The antisense compounds
 CC have immunomodulator, antidiabetic, cardiovascular, cardiant,
 CC neuroprotective, disorder and vasotropic activity. The antisense
 CC oligonucleotides are useful for inhibiting the expression of inducible
 CC nitric oxide synthase in cells or tissues. In particular, the antisense
 CC oligonucleotides are useful for treating diseases or disorders associated
 CC with inducible nitric oxide synthase, e.g. diabetes, immunological
 CC disorder, cardiovascular disorder, neurological disorder or
 CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
 CC useful for research and diagnostics. The present sequence is that of
 CC mouse inducible nitric oxide synthase

XX
 SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 4; Length 1144;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
 |||||
 Db 514 KVVFFA 519

RESULT 40
 ABU79138
 ID ABU79138 standard; protein; 1144 AA.
 XX
 AC ABU79138;
 XX
 DT 18-JUN-2003 (first entry)
 XX
 DE Inducible nitric oxide synthase protein.
 XX
 KW Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 KW gene therapy; mammalian cell receptor; cytostatic;
 KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
 KW tumouricidal immunocyte; antitumour.
 XX
 OS Unidentified.
 XX
 PN US2002177551-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 30-MAY-2001; 2001US-00870759.
 XX
 XX 31-MAY-2000; 2000US-0208128P.
 XX
 XX (TERM/) Terman D S.
 XX
 XX Terman DS;
 XX
 XX WPI; 2003-361759/34.
 DR
 DR N-PSDB; ACA64740.
 XX
 XX A mammalian cell receptor, useful in the treatment of cancer by binding
 PT to tumor associated lipids where the binding induces anergy or apoptosis
 PT in T cells and antigen presenting cells.
 XX
 XX Example 2; Page; 167pp; English.
 PS
 XX The invention relates to a mammalian cell receptor, useful in the
 CC treatment of cancer, which binds to tumour associated lipids and induces
 CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).
 CC Also included are a mammalian cell useful in the treatment of cancer
 CC where the receptor which binds tumour associated lipids and induces
 CC cellular inactivation or death is deleted or functionally deactivated,
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 CC (by allowing tumour associated lipids to contact immunocytes in which
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 CC deleted), a construct useful in the treatment of cancer comprising a
 CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 CC useful in the treatment of cancer (where an adaptor protein which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidal
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to

CC contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidally activated population,
 CC and administering APCs to the host), producing a tumouricidal T cell
 CC population ex vivo in a mammal) by allowing a tumour associated lipids to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC administering the tumouricidally activated T cells to the host, or
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidally activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC receptors, methods and compositions are useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents an anti-tumour protein which is co-administered with
 CC or incorporated into a fusion construct with a superantigen. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from the US patent
 CC office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"
 XX
 SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 6; Length 1144;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 Db 514 KVVFFA 519

RESULT 41
 ADF43404
 ID ADF43404 standard; protein; 1144 AA.

AC ADF43404;

DT 12-FEB-2004 (first entry)

DE iNOS polypeptide seqid 124.

KW receptor; lipid-based tumour associated antigen; cytostatic;
 KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
 KW infectious disease; iNOS.

OS Unidentified.

PN US2003157113-A1.

PD 21-AUG-2003.

PF 28-DEC-2000; 2000US-00751708.

PR 28-DEC-1999; 99US-0173371P.

PA (TERM/) Terman D S.

PI Terman DS;

XX WPI; 2003-787326/74.

DR N-PSDB; ADF43403.

XX New receptor in a mammalian cell that inhibits regular activation by
 PT receptors specific for lipid-based tumor associated antigens, useful for
 PT treating a neoplastic disease or tumor, and infectious diseases.

XX

PS Example 3; SEQ ID NO 124; 151pp; English.

XX The invention describes a receptor in a mammalian cell that inhibits
 CC regular activation by receptors specific for lipid-based tumour
 CC associated antigen. The receptor has cytostatic and antimicrobial
 CC properties and is suitable for use in gene therapy. The receptors,
 CC methods and compositions are useful for treating a neoplastic disease or
 CC tumour (cancer), and infectious diseases. This sequence represents iNOS
 CC polypeptide, a cell surface moiety, the DNA of which can be transfected
 CC into a cell with superantigen DNA to generate antitumour immunity.

XX Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 7; Length 1144;

Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 Db 514 KVVFFA 519

RESULT 42

ADFF7432

ID ADF77432 standard; protein; 1144 AA.

XX ADF77432;

DT 26-FEB-2004 (first entry)

DE Mouse inducible nitric oxide synthase, iNOS.

KW Mouse; inducible nitric oxide synthase; iNOS; cardiant; vasodilator;
 KW cytostatic; gynaecological; restenotic response; angioplasty;
 KW vasodilation; angina; cancer; cell death; premature labour; tumour;
 KW nervous system; brain; erectile dysfunction; uterus; lung; vascular tone;
 KW regional blood flow.

OS Mus musculus.

PN US6620616-B1.

PD 16-SEP-2003.

PF 13-SEP-2000; 2000US-00661258.

PR 13-SEP-2000; 2000US-00661258.

PA (CLEV-) CLEVELAND CLINIC FOUND.

PI Stuehr DJ, Adak S;

DR WPI; 2003-895427/82.

XX New isolated polynucleotide encoding a variant of a corresponding wild-
 PT type nitric oxide synthase, useful for reducing the restenotic response
 PT after angioplasty, or for inhibiting the development or onset of
 PT premature labor.

PS Disclosure; SEQ ID NO 5; 35pp; English.

XX The invention relates to an isolated polynucleotide encoding a variant of
 CC a corresponding wild-type nitric oxide synthase (NOS). The variant has
 CC the tryptophan in the alpha 3 helix substituted by tyrosine or
 CC phenylalanine. Also included are a nucleic acid construct comprising the
 CC nucleotide sequence that encodes a variant of a corresponding wild-type
 CC nitric oxide synthase and a promoter operably linked to the encoding
 CC sequence of the variant and a transformed cell comprising the construct,
 CC where the cell expresses the nitric oxide synthase variant. The variant
 CC has an in vitro enzymatic activity that is greater than the in vitro
 CC enzymatic activity of the corresponding wild-type nitric oxide synthase.
 CC The variant can preferably be of a corresponding wild-type endothelial
 CC nitric oxide synthase (eNOS), neuronal nitric oxide synthase (nNOS), or

CC inducible nitric oxide synthase (iNOS). The polynucleotides are useful
 CC for reducing the restenotic response after angioplasty, or related
 CC interventional procedures, or to enhance the vasodilation response in
 CC treating angina, for anticancer therapy to promote cell death, and for
 CC inhibiting the development or onset of premature labour. The
 CC polynucleotides are useful to achieve or augment expression of NOS
 CC variant proteins or polypeptides in vivo to increase NOS production in
 CC target tissue, tumour tissue, tissue of the nervous system, including
 CC brain, penis (e.g. in erectile dysfunction) and uterine tissue, and lung
 CC tissue. NOS is useful for maintaining vascular tone and regulating
 CC regional blood flow. The present sequence is wild-type mouse iNOS.
 XX
 SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 7; Length 1144;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 Db 514 KVVFFA 519

RESULT 43

ADJ76212
 ID ADJ76212 standard; protein; 1144 AA.

AC ADJ76212;

XX 20-MAY-2004 (first entry)

DE Marker gene related amino acid sequence SEQ ID NO:1464.

XX bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.

XX Mus musculus.

XX EPI394274-A2.

XX 03-MAR-2004.

XX 04-AUG-2003; 2003EP-00254857.

XX 06-AUG-2002; 2002JP-00229312.

XX 20-MAR-2003; 2003JP-00077212.

XX (GENO-) GENOX RES INC.

XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

XX WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.

XX Claim 16; SEQ ID NO 1464; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;

CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (I) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 8; Length 1144;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 Db 514 KVVFFA 519

RESULT 44

ADJ76136
 ID ADJ76136 standard; protein; 1144 AA.

XX AC ADJ76136;

XX 20-MAY-2004 (first entry)

DE Marker gene related amino acid sequence SEQ ID NO:1388.

XX bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.

XX Mus musculus.

XX EPI394274-A2.

XX 03-MAR-2004.

XX 04-AUG-2003; 2003EP-00254857.

XX 06-AUG-2002; 2002JP-00229312.

XX 20-MAR-2003; 2003JP-00077212.

XX (GENO-) GENOX RES INC.

XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

XX WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.

XX Claim 16; SEQ ID NO 1388; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic

CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (I) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.

SQ Sequence 1144 AA;
 Query Match 100.0%; Score 29; DB 8; Length 1144;
 Best Local Similarity 100.0%; Pred. No. 7e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0;

QY 1 KVVFFA 6
 |||||
 DB 514 KVVFFA 519

RESULT 45
 AEA03075
 ID AEA03075 standard; protein; 1144 AA.

AC AEA03075;

DT 28-JUL-2005 (first entry)

DE VEGF amino acid sequence SEQ ID NO:101.

KW tumor; neoplasm; gene therapy; immunotherapy; cytostatic;
 KW vascular endothelial cell growth factor.

OS Unidentified.

PN US2005112141-A1.

PD 26-MAY-2005.

PF 08-SEP-2004; 2004US-00937758.

PR 30-AUG-2000; 2000US-00650884.

PA (TERM/) TERMAN D S.

PI Terman DS;

DR WPI; 2005-394926/40.
 DR N-PGDB; AEA03074.

PT New composition for treating a tumor or neoplastic disease in a subject
 PT comprises conjugates comprising superantigen polypeptides or nucleic
 PT acids with other molecules that produce a tumoricidal response.

PS Example 3; SEQ ID NO 101; 125pp; English.

XX The invention relates to a composition for treating a tumor or neoplastic
 CC disease in a subject. Also described: (1) a mammalian cell comprising an

CC exogenous nucleic acid encoding a superantigen expressed in the cell,
 CC which cell also produces or expresses all alpha-anomers of
 CC monoglycosylceramide or diglycosylceramide, where expression of the
 CC superantigen and the mono- or diglycosylceramide is capable of eliciting
 CC an antitumor immune response in a mammal into which the cell is
 CC introduced; (2) treating a tumor or neoplastic disease in a subject; (3)
 CC preparing a population of immunotherapeutic T or natural killer T (NKT)
 CC cells useful to treat a tumor or neoplastic disease in a subject; (4) an
 CC apoptotic cell preparation or lysate useful for treating a tumor or
 CC neoplastic disease in a subject, comprising a cell population that has
 CC been transfected with naked DNA encoding a superantigen, and treated to
 CC undergo apoptosis or lysis; and (5) a cell that has ingested or been
 CC transfected with the above apoptotic preparation or lysate, thus,
 CC rendering the cell effective in presenting material expressed from
 CC transfecting nucleic acid or material ingested to the immune system of a
 CC mammal to elicit an anti-tumor immune response. The composition and
 CC methods are useful for treating tumors or neoplastic diseases. The
 CC present sequence represents a VEGF protein sequence, which is used in an
 CC example from the present invention. Note - The sequence data for this
 CC patent is not represented in the printed specification, but was obtained
 CC in electronic format directly from the USPTO web site.

SQ Sequence 1144 AA;

Query Match 100.0%; Score 29; DB 9; Length 1144;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |||||
 DB 514 KVVFFA 519

RESULT 46

AAB48483
 ID AAB48483 standard; peptide; 6 AA.

AC AAB48483;

DT 02-MAR-2001 (first entry)

DE Antifibrillogenic peptide #10.

KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.

OS Homo sapiens.

PH Key Location/Qualifiers
 FT Modified-site 6
 FT /note= "C-terminal amide"

XX WO200068263-A2.

PN 16-NOV-2000.

PF 04-MAY-2000; 2000WO-CA000515.

PR 05-MAY-1999; 99US-0132592P.

PA (NEUR-) NEUROCHEM INC.

PI Chalifour R, Gervais P, Gupta A;

XX WPI; 2001-031852/04.

XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.

XX Claim 7; Page 25; 46pp; English.

CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KVVFFA 6
 |:||||
 Db 1 KIVFFA 6

RESULT 47
 AAB48474
 ID AAB48474 standard; peptide; 6 AA.

XX AAB48474;
 AC
 XX 02-MAR-2001 (first entry)
 DT
 XX Antifibrillogenic peptide #1.

XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.

XX Homo sapiens.
 XX WO200068263-A2.
 XX 16-NOV-2000.
 PD
 XX 04-MAY-2000; 2000WO-CA000515.
 PF
 XX 05-MAY-1999; 99US-0132592P.
 PR
 XX (NEUR-) NEUROCHEM INC.

XX Chalifour R, Gervais F, Gupta A;
 PI
 XX WPI; 2001-031852/04.
 DR
 XX

PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.

XX Claim 7; Page 25; 46pp; English.

CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KVVFFA 6
 |:||||
 Db 1 KIVFFA 6

RESULT 48
 AAB82623

ID AAB82623 standard; peptide; 6 AA.

XX AAB82623;
 AC

XX 02-OCT-2001 (first entry)
 DT

XX All-D peptide used in Alzheimer's disease vaccine.

XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..6

PT /note= "all D-form residues"

XX WO200139796-A2.

XX 07-JUN-2001.
 PD

XX 29-NOV-2000; 2000WO-CA001413.
 PF

XX 29-NOV-1999; 99US-0168594P.
 PR

XX 28-NOV-2000; 2000US-00724842.
 PR

XX (NEUR-) NEUROCHEM INC.

XX Chalifour R, Hebert L, Kong X, Gervais F;
 PI

XX WPI; 2001-441458/47.

XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.

XX Disclosure; Page 10; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC CAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
XX : : : :
SQ 1 KIVFFA 6

Db

RESULT 49
AAB82631

ID AAB82631 standard; peptide; 6 AA.

XX

AC AAB82631;

XX

DT 02-OCT-2001 (first entry)

XX

DE All-D peptide used in Alzheimer's disease vaccine.

XX

KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
KW therapy; antigen.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1..6
FT /note= "all D-form residues"
FT Modified-site 6
FT /note= "C-terminal amide"

XX

PN WO200139796-A2.

XX

PD 07-JUN-2001.

XX

XX

PF 29-NOV-2000; 2000WO-CA001413.

XX

PR 29-NOV-1999; 99US-0168594P.

PR 28-NOV-2000; 2000US-00724842.

XX

PA (NEUR-) NEUROCHEM INC.

XX

PI Chalifour R, Hebert L, Kong X, Gervais F;
PI WPI; 2001-441458/47.

DR

XX

XX

PT Preventing/treating amyloid-related disease, especially Alzheimer's
PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
PT which elicits production of antibodies to prevent fibrillogenesis and
PT associated cellular toxicity.

XX

PS Disclosure; Page 11; 31pp; English.

XX

CC The present sequence is that of an all-D peptide suitable for use for
CC preparing vaccines for preventing or treating Alzheimer's disease and
CC other amyloid related disorders in humans. It is based on a portion of
CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
CC inserting 1 or more amino acid residues, or by substituting 1 or more
CC amino acid residues with other amino acid residues or non-amino acid
CC fragments. Vaccines of the invention are produced using 'non-self',
CC peptides synthesised from the unnatural D-configuration amino acids to
CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
CC aggregated to be operative or immunogenic. They preferably interact with
CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
CC fragments, protein conjugates, immunogenic derivative peptides and
CC immunogenic peptidomimetics. Examples include all-D peptides
CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
CC related diseases may be localised amyloidosis, e.g. diabetes type II,
CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
CC prion protein related disorders, or systemic amyloidosis associated with
CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic

CC amyloidosis found in long-term haemodialysis patients

XX

SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
XX : : : :
Db 1 KIVFFA 6

RESULT 50
AAU96819

ID AAU96819 standard; peptide; 6 AA.

XX

AC AAU96819;

XX

DT 30-JUL-2002 (first entry)

XX

DE Amyloid targeting peptide #9.

XX

KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
KW transmissible cerebral amyloidosis; transmissible virus dementia;
KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
KW bovine spongiform encephalopathy; inflammation associated amyloid;
KW primary amyloidosis; feline spongiform encephalopathy;
KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
KW dialysis-related amyloidosis; light chain-related amyloidosis;
KW cerebral amyloid angiopathy.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1..6
FT /note= "Preferably D-form residue"
FT Modified-site 6
FT /note= "Ala is amidated"

XX

PN WO200207781-A2.

XX

XX

PD 31-JAN-2002.

XX

XX

PF 25-JUL-2001; 2001WO-CA001071.

XX

PR 25-JUL-2000; 2000US-0220808P.

PR 24-JUL-2001; 2001US-00915092.

XX

PA (NEUR-) NEUROCHEM INC.

XX

PI Gervais F, Kong X, Chalifour R, Migneault D;
PI WPI; 2002-371447/40.

DR

XX

PT New amyloid-targeting imaging agents useful for in vivo imaging amyloid
PT plaques and/or for the treatment of amyloidosis disorders.

XX

PS Claim 49; Page 21; 57pp; English.

XX

CC The invention relates to an amyloid-targeting imaging agent comprising an
CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
CC agent is of general formula A.t-(A.l.n.k)z-A.l.a.b (t) where z = 0 - 1;
CC A.t = an amyloid targeting moiety; A.l.n.k = a linker moiety; and A.l.a.b
CC = a labelling moiety. Also included are imaging amyloid deposition or
CC diagnosing an amyloid-related condition in a patient involving
CC administering (i) to the patient, and ultrasound imaging (i) in the
CC patient to determine the presence of amyloid or amyloid-related condition
CC ; and a kit for preparing a radiopharmaceutical preparation comprising
CC (i) a reducing agent, a buffering agent, a transchelating agent, and
CC instructions for the preparation and use of the radiopharmaceutical in
CC the imaging of amyloid or an amyloid-related condition. The agents are
CC used for imaging amyloid deposition and for diagnosing an amyloid related

CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementias), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention
 XX
 XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 Db 1 KIVFFA 6

RESULT 51
 AAU96811
 ID AAU96811 standard; peptide; 6 AA.

XX
 AC AAU96811;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Amyloid targeting peptide #1.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementias;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers
 FH Misc-difference 1. .6
 FT /note= "Preferably D-form residue"

XX WO200207781-A2.
 XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX 25-JUL-2000; 2000US-0220808P.

XX 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalfour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 XX plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A_t-(A₁)_n(A₂)_m-(A₃)_k-(A₄)_l where z = 0 - 1;
 CC A_t = an amyloid targeting moiety; A₁ = a linker moiety; and A₄ = a
 CC = a labelling moiety. Also included are imaging amyloid deposition or

CC diagnosing an amyloid-related condition in a patient involving
 CC administering (I) to the patient, and ultrasound imaging (I) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementias), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC cerebral amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention
 XX
 XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 Db 1 KIVFFA 6

RESULT 52
 AAU11657
 ID AAU11657 standard; peptide; 6 AA.

XX
 AC AAU11657;

XX 09-APR-2002 (first entry)

XX Peptide #10, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.

XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 6
 FT /note= "C-terminal amide"

XX WO200185093-A2.

XX 15-NOV-2001.

XX 23-DEC-2000; 2000WO-IB002078.

XX 23-DEC-1999; 99US-0171877P.

XX (NEUR-) NEUROCHEM INC.

XX Green AM, Gervais F;

XX WPI; 2002-075222/10.

XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 XX disease comprises contacting blood vessel wall cell with amyloid-beta 40
 XX inhibitor.

XX Disclosure; Page 10; 68pp; English.

XX The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a

CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 XX
 SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KWVFFA 6
 Db 1 KIVFFA 6

RESULT 53

AAU11648
 ID AAU11648 standard; peptide; 6 AA.

AC AAU11648;

XX 09-APR-2002 (first entry)

XX Peptide #1, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.

XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX Synthetic.

XX WO200185093-A2.

XX 15-NOV-2001.

XX 22-DEC-2000; 2000WO-IB002078.

XX 23-DEC-1999; 99US-0171877P.

XX (NEUR-) NEUROCHEM INC.

XX Green AM, Gervais F;

XX WPI; 2002-075222/10.

XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.

XX Disclosure; Page 10; 68pp; English.

XX The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KWVFFA 6
 Db 1 KIVFFA 6

RESULT 54

AAE35446
 ID AAE35446 standard; peptide; 6 AA.

XX AAE35446;

XX 17-JUN-2003 (first entry)

XX Abeta peptide #17.

XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.

XX Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 1..6 /note= "D-form residues"

FT Modified-site 6 /note= "C-terminal amide"

XX WO200296937-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-CA000763.

XX 29-MAY-2001; 2001US-00867847.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.

XX Prevention and/or treatment of an amyloid-related disease e.g.

XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.

XX Claim 1; Page 59; 44pp; English.

XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |:|||||
 Db 1 KIVFFA 6

RESULT 55
 AAE35438
 ID AAE35438 standard; peptide; 6 AA.

AC AAE35438;

DT 17-JUN-2003 (first entry)

DE Abeta peptide #9.

KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.

XX Unidentified.

PH Key Location/Qualifiers

FT Misc-difference 1. .6 /note= "D-form residues"

XX WO200296937-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-CA000763.

XX 29-MAY-2001; 2001US-00867847.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.

XX Prevention and/or treatment of an amyloid-related disease e.g.

XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.

XX Claim 1; Page 58; 44pp; English.

XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention

SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |:|||||
 Db 1 KIVFFA 6

RESULT 56

ADQ37322

ID ADQ37322 standard; peptide; 6 AA.

XX ADQ37322;

XX 07-OCT-2004 (first entry)

XX Antifibrillogenic amyloidosis inhibiting peptide.

XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antichyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 6 /note= "amidated"

XX WO2004058239-A1.

XX 15-JUL-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/S2.

XX Composition for treating e.g. Alzheimer's disease comprises first agent
 CC that prevents or treats amyloid-beta related disease and second agent
 CC that is either a peptide or peptidomimetic or an immune system modulator.

XX Disclosure; Page 69; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,

CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators' and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0;

QY 1 KVVFFA 6
 |:||||
 Db 1 KIVFFA 6

RESULT 57

ADQ37270
 ID ADQ37270 standard; peptide; 6 AA.

AC ADQ37270;

DT 07-OCT-2004 (first entry)

DE Vaccine antigen amyloid-beta related amino acid sequence.

KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.

XX Synthetic.

OS Key Location/Qualifiers

FH Misc-difference 1..6

FT /note= "D-form residues"

FT Modified-site 6

/note= "amidated"

FT WO2004058239-A1.

XX 15-JUL-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.

XX Disclosure; Page 67; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.

SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
 |:||||

Db 1 KIVFFA 6

RESULT 58
ADQ37313
ID ADQ37313 standard; peptide; 6 AA.
XX
AC ADQ37313;
XX
DT 07-OCT-2004 (first entry)
XX
DE Antifibrillogenic amyloidosis inhibiting peptide.
XX
KW amyloid-beta; amyloid-beta related disease;
KW amyloid-beta fibril formation; immune response; nootropic;
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
KW cardiant; antidepressant; endocrine; hypnotic;
KW amyloid-beta fibril formation modulator; immune system modulator;
KW Alzheimer's disease; mild cognitive impairment;
KW mild-to-moderate cognitive impairment; vascular dementia;
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
KW senile dementia; Down's syndrome; inclusion body myositis;
KW age-related macular degeneration; hypothyroidism;
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
KW behavioural dysfunction; neurological condition; psychological condition;
KW vaccine antigen.
XX
OS Synthetic.
XX
PN WO2004058239-A1.
XX
PD 15-JUL-2004.
XX
PF 24-DEC-2003; 2003WO-CA002021.
XX
PR 24-DEC-2002; 2002US-0436379P.
PR 23-JUN-2003; 2003US-0482214P.
XX
XX (NEUR-) NEUROCHEM INT LTD.
XX
PI Gervais F, Bellini F;
XX
XX WPI; 2004-543342/52.
XX
XX Composition for treating e.g. Alzheimer's disease comprises first agent that prevents or treats amyloid-beta related disease and second agent that is either a peptide or peptidomimetic or an immune system modulator.
XX
PS Disclosure; Page 69; 143pp; English.
XX
XX The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have nootropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser, uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia

CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic CC damage), or a psychological condition (e.g. depression, delusions, CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or CC excessive guilt)) in a subject e.g. human having a genomic mutation in an CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
CC having amyloid-beta deposits. The present sequence represents a peptide CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide CC in the exemplification of the present invention.
XX
XX Sequence 6 AA;
SQ

Query Match 96.6%; Score 28; DB 8; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
DB 1 KIVFFA 6

RESULT 59

ADQ37262

ID ADQ37262 standard; peptide; 6 AA.

XX

AC ADQ37262;

XX

DT 07-OCT-2004 (first entry)

XX

DE Vaccine antigen amyloid-beta related amino acid sequence.

XX

XX amyloid-beta; amyloid-beta related disease;

KW amyloid-beta fibril formation; immune response; nootropic;

KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;

KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;

KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;

KW cardiant; antidepressant; endocrine; hypnotic;

KW amyloid-beta fibril formation modulator; immune system modulator;

KW Alzheimer's disease; mild cognitive impairment;

KW mild-to-moderate cognitive impairment; vascular dementia;

KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;

KW senile dementia; Down's syndrome; inclusion body myositis;

KW age-related macular degeneration; hypothyroidism;

KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;

KW behavioural dysfunction; neurological condition; psychological condition;

KW vaccine antigen.

XX

OS Synthetic.

XX

XX Key Location/Qualifiers

XX Misc-difference 1. .6

FT /note= "D-form residues"

XX

XX WO2004058239-A1.

XX

PD 15-JUL-2004.

XX

XX 24-DEC-2003; 2003WO-CA002021.

XX

XX 24-DEC-2002; 2002US-0436379P.

XX

XX 23-JUN-2003; 2003US-0482214P.

XX

XX (NEUR-) NEUROCHEM INT LTD.

XX

XX Gervais F, Bellini F;

XX

XX WPI; 2004-543342/52.

XX

PT Composition for treating e.g. Alzheimer's disease comprises first agent
PT that prevents or treats amyloid-beta related disease and second agent
PT that is either a peptide or peptidomimetic or an immune system modulator.

XX Disclosure; Page 67; 143pp; English.

CC The present invention describes compositions (C) comprising: (a) a first
CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
CC modulates amyloid-beta fibril formation or induces a prophylactic or
CC therapeutic immune response against amyloid-beta fibril formation; or
CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
CC fibril formation. Also described is a kit comprising (C). (C) have
CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,
CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
CC neuroleptic, cardiac, antidepressant, endocrine and hypnotic activities,
CC and can be used as amyloid-beta fibril formation modulators, and as
CC immune system modulators. (C) can be used for preventing or treating an
CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
CC Down's syndrome, inclusion body myositis, age-related macular
CC degeneration, or a condition associated with Alzheimer's disease
CC (including hypothyroidism, cerebrovascular disease, cardiovascular
CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
CC aggression, or incontinence), a neurological condition (e.g. Huntington's
CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
CC field deficits, incoordination, gait disturbance, transient ischaemic
CC attack or stroke, transient alertness, attention deficit, frequent falls,
CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
CC damage), or a psychological condition (e.g. depression, delusions,
CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
CC having amyloid-beta deposits. The present sequence represents a peptide
CC that can be used as a vaccine antigen in the exemplification of the
CC present invention.

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;
Best Local Similarity 83.3%; Pred. NO. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 1 KIVFFA 6

RESULT 60

ADY37921
ID ADY37921 standard; peptide; 6 AA.

XX AC ADY37921;

XX DT 19-MAY-2005 (first entry)

DE Amyloid-targeting peptide, SEQ ID NO:1, for use in imaging agent.

XX Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimer's disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.

XX OS Synthetic.

XX

PN US2005048000-A1.

XX PD 03-MAR-2005.

XX PF 03-DEC-2003; 2003US-00728028.

XX PR 25-JUL-2000; 2000US-0220808P.

XX PR 24-JUL-2001; 2001US-00915092.

XX PR 29-JAN-2003; 2003US-0443291P.

XX PA (NEUR-) NEUROCHEM INT LTD.

XX PI Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2005-212201/22.

XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
XX related condition, e.g. Creutzfeldt-Jakob disease, bovine spongiform
XX encephalopathy, primary amyloidosis or Alzheimer's disease.

XX Disclosure; SEQ ID NO 1; 34pp; English.

CC The invention relates to an amyloid-targeting imaging agent. The imaging
CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
CC the labeling moiety via a linking moiety, and is preferably able to cross
CC the blood-brain barrier. The invention also relates to a kit for
CC preparing a radiopharmaceutical preparation from the imaging agent and a
CC invention, a method for imaging amyloid deposition in a patient and a
CC method for diagnosing an amyloid-related condition in a patient. The
CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
CC related conditions such as Creutzfeldt-Jakob disease (CJD), Kuru,
CC transmissible cerebral amyloidosis (also known as transmissible virus
CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
CC patient. The agent does not exhibit excessive toxicity or irritation,
CC does not induce an allergic response, and permits an earlier diagnosis of
CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. NO. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|:||||
Db 1 KIVFFA 6

RESULT 61

ADY37929
ID ADY37929 standard; peptide; 6 AA.

XX AC ADY37929;

XX DT 19-MAY-2005 (first entry)

DE Amyloid-targeting peptide, SEQ ID NO:9, for use in imaging agent.

XX Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimer's disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.

XX OS Synthetic.

XX

XX 21-DEC-2004.
XX 10-JUL-2001; 2001US-00902540.
XX 10-JUL-2000; 2000US-0217883P.
XX (MONS) MONSANTO TECHNOLOGY LLC.
XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
XX WPI; 2005-028716/03.
XX New substantially purified Myxococcus xanthus nucleic acid molecule
XX encoding a nitrite reductase, useful for determining gene expression,
XX identifying mutations in a gene of interest, and for constructing
XX mutations in a gene of interest.
XX Example 2; SEQ ID NO 13513; 25pp; English.
XX The invention relates to a substantially purified nucleic acid molecule
XX encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
XX recombinant DNA construct for expression of a nitrite reductase gene in a
XX plant cell, and a plant cell comprising the recombinant DNA construct.
XX The nucleic acid is useful for determining gene expression, identifying
XX mutations in a gene of interest, and for constructing mutations in a gene
XX of interest. Sequences given in records for SEQ IDs 9692-16825 represent
XX a group of 7134 Myxococcus xanthus proteins and peptides. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from USPTO
XX Sequence 123 AA;
Query Match 96.6%; Score 28; DB 9; Length 123;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
Db 52 KVIFFA 57
RESULT 64
ADM16726
ID ADM16726 standard; protein; 393 AA.
XX ADM16726;
XX 17-JUN-2004 (first entry)
XX PERL-P7-G8 protein.
XX Phlebotomus ariasi; Phlebotomus perniciosus; Vaccine;
XX Leishmania infection.
XX Phlebotomus perniciosus.
XX WO2004027041-A2.
XX 01-APR-2004.
XX 18-SEP-2003; 2003WO-US029833.
XX 19-SEP-2002; 2002US-0412327P.
XX 12-NOV-2002; 2002US-0425852P.
XX (MERI-) MERIAL LTD.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Valenzuela JG, Ribiero JMC, Kamhawi S, Belkaid Y, Fischer L;
XX Audonnet J, Milward F;
XX WPI; 2004-295410/27.
XX 01-APR-2004.
XX 18-SEP-2003; 2003WO-US029833.
XX 19-SEP-2002; 2002US-0412327P.
XX 12-NOV-2002; 2002US-0425852P.
XX (MERI-) MERIAL LTD.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Valenzuela JG, Ribiero JMC, Kamhawi S, Belkaid Y, Fischer L;
XX Audonnet J, Milward F;
XX WPI; 2004-295410/27.

DR N-PSDB; ADM16727.
XX New substantially purified salivary Phlebotomus ariasi or Phlebotomus
XX perniciosus polypeptide, useful for inhibiting, treating or preventing
XX Leishmania infection in a subject.
XX Claim 40; SEQ ID NO 49; 200pp; English.
XX The present invention relates to a substantially purified salivary
XX Phlebotomus ariasi or Phlebotomus perniciosus polypeptide. The
XX composition comprising the polypeptide or the nucleic acid encoding the
XX polypeptide is useful for manufacture of a medicament. The polypeptides
XX and nucleic acids are useful for inducing an immune response to a P.
XX ariasi or P. perniciosus polypeptide. It is also useful for inhibiting a
XX symptom of a Leishmania infection or preventing a Leishmania infection in
XX a subject. The present sequence represents a purified Phlebotomus ariasi
XX protein.
XX SQ Sequence 393 AA;
Query Match 96.6%; Score 28; DB 8; Length 393;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
Db 299 KVIFFA 304
RESULT 65
ADM16684
ID ADM16684 standard; protein; 393 AA.
XX ADM16684;
XX 17-JUN-2004 (first entry)
XX PRL-P4-D6 protein.
XX Phlebotomus ariasi; Phlebotomus perniciosus; Vaccine;
XX Leishmania infection.
XX Phlebotomus ariasi.
XX WO2004027041-A2.
XX 01-APR-2004.
XX 18-SEP-2003; 2003WO-US029833.
XX 19-SEP-2002; 2002US-0412327P.
XX 12-NOV-2002; 2002US-0425852P.
XX (MERI-) MERIAL LTD.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Valenzuela JG, Ribiero JMC, Kamhawi S, Belkaid Y, Fischer L;
XX Audonnet J, Milward F;
XX WPI; 2004-295410/27.
XX N-PSDB; ADM16685.
XX New substantially purified salivary Phlebotomus ariasi or Phlebotomus
XX perniciosus polypeptide, useful for inhibiting, treating or preventing
XX Leishmania infection in a subject.
XX Claim 1; SEQ ID NO 7; 200pp; English.
XX The present invention relates to a substantially purified salivary
XX Phlebotomus ariasi or Phlebotomus perniciosus polypeptide. The
XX composition comprising the polypeptide or the nucleic acid encoding the
XX polypeptide is useful for manufacture of a medicament. The polypeptides
XX and nucleic acids are useful for inducing an immune response to a P.

CC ariasi or P. perniciosus polypeptide. It is also useful for inhibiting a
CC symptom of a Leishmania infection or preventing a Leishmania infection in
CC a subject. The present sequence represents a purified Phlebotomus ariasi
CC protein.

XX SQ Sequence 393 AA;

Query Match 96.6%; Score 28; DB 8; Length 393;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||:||||
Db 298 KVIFFA 303

RESULT 66

ADO43456
ID ADO43456 standard; protein; 399 AA.

XX AC ADO43456;

XX DT 29-JUL-2004 (first entry)

XX DE Lutzomyia longipalpis (sand fly) salivary protein LJM11.

XX LJM11; sand fly; leishmaniasis; diagnosis; vaccine; genetic immunisation.
XX Lutzomyia longipalpis.

XX FH Key Location/Qualifiers
FT Peptide 1..24
FT Protein /label= Signal_peptide
FT 25..399
FT /label= Mature_protein

XX PN WO2004039958-A2.

XX PD 13-MAY-2004.

XX PF 29-OCT-2003; 2003WO-US034453.

XX PR 29-OCT-2002; 2002US-0422303P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (PESQ-) CENT PESQUISAS GONCALO MONIZ.

XX PI Valenzuela JG, Ribeiro JMC, Barral A, Netto M, Brodekyn C;
PI Gomes R;

XX WPI; 2004-376184/35.

XX DR N-PSDB; ADO43457.

XX PT Novel salivary Lutzomyia longipalpis polypeptide, useful for inhibiting
XX symptom of Leishmania infection or preventing Leishmania infection in
XX subjects.

XX PS Claim 2; SEQ ID NO 63; 145pp; English.

XX The present sequence is the protein sequence of LJM11, a Lutzomyia
XX longipalpis (New World sand fly) salivary polypeptide. The invention
XX provides substantially purified L. longipalpis polypeptides and the
XX polynucleotides encoding them, as well as vectors, host cells, antibodies
XX and pharmaceutical compositions comprising the polypeptides or
XX polynucleotides. A claimed method for inducing an immune response to L
XX longipalpis in a subject involves administering a L. longipalpis salivary
XX polypeptide (or its variant or immunogenic fragment) or a polynucleotide
XX encoding it. The immune response is a T-cell or B-cell response, and the
XX subject is preferably a dog or a human. A claimed method for inhibiting a
XX symptom of a Leishmania infection or preventing a Leishmania infection in
XX a subject comprises administering a L. longipalpis salivary protein or
XX polynucleotide. A claimed method of diagnosing Leishmania infection
XX comprises contacting a solid substrate comprising at least 3, 6 or 10 L.

CC longipalpis salivary polypeptides with a sample from the subject and
CC detecting binding of a component of the sample to at least one of the
CC polypeptides.

XX SQ Sequence 399 AA;

Query Match 96.6%; Score 28; DB 8; Length 399;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||:||||
Db 305 KVIFFA 310

RESULT 67

ABB61977

ID ABB61977 standard; protein; 564 AA.

XX AC ABB61977;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 12723.

XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX DR N-PSDB; ABL06080.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.

XX PS Disclosure; SEQ ID NO 12723; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at fcp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 564 AA;

Query Match 93.1%; Score 27; DB 4; Length 564;
Best Local Similarity 66.7%; Pred. No. 9.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
|||:||||
Db 53 KIIFFA 58

RESULT 68
 ABB68472
 ID ABB68472 standard; protein; 1443 AA.
 XX
 AC ABB68472;
 XX
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 32208.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR
 PR 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL12575.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 PT
 XX
 PS Disclosure; SEQ ID NO 32208; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1443 AA;
 Query Match 93.1%; Score 27; DB 4; Length 1443;
 Best Local Similarity 66.7%; Pred. No. 2.5e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 1204 KLIFFA 1209
 ||:||||
 RESULT 69
 AAW02314
 ID AAW02314 standard; peptide; 6 AA.
 XX
 AC AAW02314;
 XX
 XX
 DT 02-MAY-1997 (first entry)
 XX
 DE Beta-amyloid modulator peptide #5.
 XX
 KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
 KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
 KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
 XX

KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
 KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
 KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
 KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
 XX
 OS Synthetic.
 XX
 PN WO9628471-A1.
 XX
 PD 19-SEP-1996.
 XX
 PF 14-MAR-1996; 96WO-US003492.
 XX
 PR 14-MAR-1995; 95US-00404831.
 PR 07-JUN-1995; 95US-00475579.
 PR 27-OCT-1995; 95US-00548998.
 XX
 XX (PHAR-) PHARM PEPTIDES INC.
 XX
 XX Findeis MA, Benjamin H, Garnick MB, Geffter ML, Hundal A;
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ, Molineaux S;
 PI Kubasek W, Chin J, Lee J, Kelley M;
 XX
 DR WPI; 1996-433762/43.
 XX
 XX Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
 PT protein coupled (in)directly to at least 1 modifying gp., useful in
 PT treatment of Alzheimer's disease.
 PT
 XX
 PS Claim 16; Page 91; 106pp; English.
 XX
 CC AAW02310-W02332 represent the peptide portions of the beta-amyloid
 CC modulator compounds of the invention. Beta-amyloid peptide is a 4
 CC kilodalton peptide that is the major protein component of amyloid
 CC plaques. Amyloid plaques are present both in the brain lesions, and in
 CC the walls of cerebral blood vessels in Alzheimer's disease patients. The
 CC amyloid modulators of the invention comprise an amyloidogenic protein or
 CC peptide (such as this sequence) coupled directly or indirectly to at
 CC least one modifying group. The modifying group is preferably a cyclic,
 CC heterocyclic, or polycyclic group, such as decalin, a cholanyl group, a
 CC biotin containing group, or a fluorescein containing group. These
 CC compounds then modulate the aggregation of these sequences to natural
 CC amyloid proteins or peptides when contacted with the natural
 CC amyloidogenic proteins or peptides. The modulator compounds can be used
 CC in the treatment of disorders associated with amyloidosis, such as
 CC familial amyloid polyneuropathy, familial amyloid cardiomyopathy,
 CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
 CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
 CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
 CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
 CC and other types of amyloidosis. The modulators are also useful for the
 CC treatment of disorders associated with beta-amyloidosis, especially
 CC Alzheimer's disease
 XX
 SQ Sequence 6 AA;
 Query Match 89.7%; Score 26; DB 2; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 1 KLVFFA 6
 ||:||||
 RESULT 70
 AAW89378
 ID AAW89378 standard; peptide; 6 AA.
 XX
 AC AAW89378;
 XX
 XX
 DT 02-MAR-1999 (first entry)
 XX

DE Beta-amyloid peptide derivative A-beta-16-21.
 XX Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
 KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
 KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;
 KW Creutzfeldt-Jakob disease; bAP.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX US5854204-A.
 XX
 XX 29-DEC-1998.
 XX
 XX 14-MAR-1996; 96US-00612785.
 XX
 XX 14-MAR-1995; 95US-00404831.
 XX 07-JUN-1995; 95US-00475579.
 XX 27-OCT-1995; 95US-00548998.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX
 XX Hundal A, Geffer ML, Kasman L, Musso G, Molineaux S, Benjamin H;
 PI Findeis MA, Chin J, Lee J, Kelley M, Reed M, Wakefield J;
 PI Garnick MB, Kubasek W, Signer ER;
 XX
 XX WPI; 1999-094964/08.
 XX
 XX New peptide(s) derived from beta-amyloid peptide that inhibit amyloid
 PT aggregation - and neurotoxicity, specifically for treatment and
 PT prevention of Alzheimer's disease.
 XX
 XX Example 12; Col 64; 52pp; English.
 XX
 XX The present invention describes beta-amyloid peptide (bAP) derivatives.
 CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
 CC peptides, specifically bAP, and their neurotoxicity, so are useful for
 CC treating and preventing any disease involving amyloidosis, specifically
 CC Alzheimer's disease but also Down's syndrome, familial amyloid
 CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and
 CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
 CC these diseases, in vitro or in vivo, by detecting binding of bAP to
 CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
 CC even when bAP is present in molar excess. The present sequence represents
 CC a bAP derivative
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 89.7%; Score 26; DB 2; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 1 KLVFFA 6
 RESULT 71
 AAB48484
 ID AAB48484 standard; peptide; 6 AA.
 XX
 XX AAB48484;
 XX
 XX 02-MAR-2001 (first entry)
 XX
 XX Antifibrillogenic peptide #11.
 DE
 XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX
 XX Homo sapiens.
 OS
 XX

FH Key Location/Qualifiers
 FT Modified-site 6 /note= "C-terminal amide"
 XX
 XX WO200068263-A2.
 XX
 XX 16-NOV-2000.
 XX
 XX 04-MAY-2000; 2000WO-CA000515.
 XX
 XX 05-MAY-1999; 99US-0132592P.
 XX
 XX (NEUR-) NEUROCHEM INC.
 XX
 XX Chalifour R, Gervais F, Gupta A;
 XX
 XX WPI; 2001-031852/04.
 XX
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 XX
 XX Claim 7; Page 25; 46pp; English.
 XX
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 89.7%; Score 26; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFFA 6
 Db 1 KLVFFA 6
 RESULT 72
 AAB48476
 ID AAB48476 standard; peptide; 6 AA.
 XX
 XX AAB48476;
 XX
 XX 02-MAR-2001 (first entry)
 XX
 XX Antifibrillogenic peptide #3.
 DE
 XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX
 XX Homo sapiens.
 OS
 XX WO200068263-A2.
 XX
 XX 16-NOV-2000.
 XX
 XX 04-MAY-2000; 2000WO-CA000515.
 XX
 XX 05-MAY-1999; 99US-0132592P.
 XX
 XX (NEUR-) NEUROCHEM INC.
 XX
 XX Chalifour R, Gervais F, Gupta A;
 XX
 XX WPI; 2001-031852/04.
 XX

PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
PT its isomer or peptidomimetic.
XX
XX
PS Claim 7; Page 25; 46pp; English.
XX
CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
CC useful for treating amyloidosis disorders such as Alzheimer's disease.
CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
CC binding region and the prot-prot interaction region of the human amyloid
CC protein
XX
XX Sequence 6 AA;
Query Match 89.7%; Score 26; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
Db 1 KLVFFA 6
|:|||||
|:|||||

RESULT 73
AAB82632
ID AAB82632 standard; peptide; 6 AA.
XX
AC AAB82632;
XX
DT 02-OCT-2001 (first entry)
XX
DE All-D peptide used in Alzheimer's disease vaccine.
XX
KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
KW therapy; antigen.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..6 /note= "all D-form residues"
FT Modified-site 6 /note= "C-terminal amide"
FT
XX WO200139796-A2.
XX
PD 07-JUN-2001.
XX
XX 29-NOV-2000; 2000WO-CA001413.
XX
XX 29-NOV-1999; 99US-0168594P.
XX
XX 28-NOV-2000; 2000US-00724842.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Chalfour R, Hebert L, Kong X, Gervais F;
XX
XX WPI; 2001-441458/47.
XX
XX Preventing/treating amyloid-related disease, especially Alzheimer's
PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
PT which elicits production of antibodies to prevent fibrillogenesis and
PT associated cellular toxicity.
XX
XX Disclosure; Page 11; 31pp; English.
XX
CC The present sequence is that of an all-D peptide suitable for use for
CC preparing vaccines for preventing or treating Alzheimer's disease and
CC other amyloid related disorders in humans. It is based on a portion of
CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
CC inserting 1 or more amino acid residues, or by substituting 1 or more

CC amino acid residues with other amino acid residues or non-amino acid
CC fragments. Vaccines of the invention are produced using 'non-self'
CC peptides synthesised from the unnatural D-configuration amino acids to
CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
CC aggregated to be operative or immunogenic. They preferably interact with
CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
CC fragments, protein conjugates, immunogenic derivative peptides and
CC immunogenic peptidomimetics. Examples include all-D peptides
CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
CC related diseases may be localised amyloidosis, e.g. diabetes type II,
CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
CC prion protein related disorders, or systemic amyloidosis associated with
CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
CC amyloidosis found in long-term haemodialysis patients. The present all-D
CC peptide was demonstrated to elicit antibody production in rabbits, and
CC provided greater anti-fibrillogenic activity than its all-L equivalent
XX
XX Sequence 6 AA;
Query Match 89.7%; Score 26; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVVFFA 6
Db 1 KLVFFA 6
|:|||||
|:|||||

RESULT 74
ABG71009
ID ABG71009 standard; peptide; 6 AA.
XX
XX AC ABG71009;
XX
DT 05-DEC-2002 (first entry)
XX
DE Long form beta-amyloid protein fragment #6.
XX
KW Beta-amyloid; amyloid modulator; amyloidogenic protein; amyloidosis;
KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
KW isolated cardiac amyloid; systemic senile amyloidosis; scrapie; myeloma;
KW bovine spongiform encephalopathy; BSE; Creutzfeldt-Jakob disease;
KW adult onset diabetes; Gerstmann-Strausler-Scheinker syndrome;
KW insulinoma; atrial amyloidosis; idiopathic amyloidosis; haemodialysis;
KW macroglobulinaemia-associated amyloidosis; reactive amyloidosis;
KW primary localised cutaneous nodular amyloidosis; Sjogren's syndrome;
KW hereditary cerebral haemorrhage with amyloidosis; Muckle-Wells syndrome;
KW hereditary non-neuropathic systemic amyloidosis;
KW familial Mediterranean Fever.
XX
XX Homo sapiens.
XX
XX US2002098173-A1.
XX
XX 25-JUL-2002.
XX
XX 04-OCT-2001; 2001US-00972475.
XX
XX 14-MAR-1995; 95US-00404831.
XX
XX 07-JUN-1995; 95US-00475579.
XX
XX 27-OCT-1995; 95US-00548998.
XX
XX 14-MAR-1996; 96US-00617267.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX
XX Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
PI Kasman L, Musso G, Signer ER, Wakefield J, Reed WJ;

XX WPI; 2002-697709/75.
 XX
 XX Amyloid modulator useful for treating a disorder associated with
 PT amyloidosis, comprises an amyloidogenic protein and/or a peptide fragment
 PT coupled to a modifying group.
 XX
 XX Example 12; Page 35; 41pp; English.
 XX
 CC The invention describes an amyloid modulator comprising an amyloidogenic
 CC protein and/or peptide fragment coupled to a modifying group so that the
 CC compound modulates the aggregation of natural amyloid proteins or
 CC peptides. The modulator is used for treating a disorder associated with
 CC amyloidosis e.g. familial amyloid polynuropathy (Portuguese, Japanese
 CC and Swedish types), familial amyloid cardiomyopathy (Danish type),
 CC isolated cardiac amyloid, systemic senile amyloidosis, scrapie, bovine
 CC spongiform encephalopathy, Creutzfeldt-Jakob disease, adult onset
 CC diabetes, Gerstmann-Strausler-Scheinker syndrome, insulinoma, isolated
 CC atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or
 CC macroglobulinaemia-associated amyloidosis, primary localised cutaneous
 CC nodular amyloidosis associated with Sjogren's syndrome, reactive
 CC (secondary) amyloidosis, familial Mediterranean Fever and familial
 CC amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome),
 CC hereditary cerebral haemorrhage with amyloidosis of Icelandic type,
 CC amyloidosis associated with long term haemodialysis, hereditary non-
 CC neuropathic systemic amyloidosis (familial amyloid polynuropathy III),
 CC familial amyloidosis of Finnish type, amyloidosis associated with
 CC medullary carcinoma of the thyroid, fibrinogen-associated hereditary
 CC renal amyloidosis and lysosome-associated hereditary systemic
 CC amyloidosis. The compound is capable of altering and inhibiting beta-
 CC amyloid protein (beta-AP) aggregation of natural amyloidogenic proteins
 CC or peptides when contacted with a molar excess amount of natural beta-APs
 CC relative to the modulator. This sequence represents a fragment of the
 CC long form of beta-amyloid used in the creation of an amyloid modulator
 XX
 SQ Sequence 6 AA;
 Query Match 89.7%; Score 26; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFEFA 6
 DB |:|:|:|
 1 KLVFEFA 6
 RESULT 75
 ABB05157
 ID ABB05157 standard; peptide; 6 AA.
 XX
 XX ABB05157;
 AC
 DT 02-APR-2002 (first entry)
 XX
 DE Beta amyloid peptide (16-21) SEQ ID NO:9.
 XX
 KW Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta;
 KW APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease;
 KW neurotropic; neuroprotective; immunosuppressive; antimicrobial; auditory;
 KW antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic;
 KW amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;
 KW amyloidogenic disease; beta amyloid deposition; amyloidosis;
 KW hereditary cerebral haemorrhage; familial amyloid polynuropathy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX US6319498-B1.
 PN
 XX 20-NOV-2001.
 PD
 XX 14-MAR-1996; 96US-00617267.
 PF
 XX

PR 14-MAR-1995; 95US-00404831.
 PR 07-JUN-1995; 95US-00475579.
 PR 27-OCT-1995; 95US-00548998.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX
 XX Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A;
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;
 XX
 XX WPI; 2002-146668/19.
 XX
 CC Amyloid modulator compound useful for treatment of an amyloidogenic
 CC disease such as Alzheimer's disease comprises an aggregation core domain
 CC and a modifying group attached to it.
 XX
 PS Disclosure; Col 18; 54pp; English.
 XX
 CC The present invention describes an amyloid modulator compound (I)
 CC comprising an aggregation core domain and a modifying group attached to
 CC it. (I) has neurotropic, neuroprotective, immunosuppressive, antimicrobial,
 CC antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic
 CC and auditory activities, and can be used as a natural amyloid aggregation
 CC inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide
 CC (beta-AP). (I) are used in the manufacture of a medicament for the
 CC diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's
 CC disease and other clinical occurrences of beta amyloid deposition such as
 CC Down's syndrome individuals and in patients with hereditary cerebral
 CC haemorrhage with amyloidosis, and for treating a disorder associated with
 CC amyloidosis such as familial amyloid polynuropathy. (I) reduces the
 CC toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)
 CC not only reduces the formation of neurotoxic aggregates but also have the
 CC ability to reduce the neurotoxicity of performed A-beta fibrils. The
 CC present sequence represents a beta-AP peptide, which is used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 6 AA;

Query Match 89.7%; Score 26; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVVFEFA 6
 DB |:|:|:|
 1 KLVFEFA 6

Search completed; December 29, 2005, 17:33:37
 Job time : 82.7742 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78.1936 Seconds
(without alignments)
54.137 Million cell updates/sec

Title: US-10-009-122-7
Perfect score: 29
Sequence: 1 KAVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	143	2	Q91Y69 MESAU
2	29	100.0	162	2	Q9N284 BOVIN
3	29	100.0	248	2	Q9BGL4 SHEEP
4	29	100.0	261	1	Y1086 HAEIN
5	29	100.0	261	2	Q4QLX2 HAE18
6	29	100.0	277	2	Q73KK6 TREDE
7	29	100.0	314	2	Q9M7Y6 ARATH
8	29	100.0	381	2	Q5LIA8 GEOKA
9	29	100.0	389	2	Q8KHB6 CLOSTRIDIUM
10	29	100.0	469	2	Q8S807 ARATH
11	29	100.0	632	2	Q9N1P6 CANFA
12	29	100.0	654	2	Q6U7G9 MELGA
13	29	100.0	660	1	MMP2 HUMAN
14	29	100.0	660	2	Q5IY21 TUPGB
15	29	100.0	661	2	Q95JAA PIG
16	29	100.0	661	2	Q9GLE5 BOVIN
17	29	100.0	662	1	MMP2 MOUSE
18	29	100.0	662	1	MMP2 RABIT
19	29	100.0	662	1	MMP2 RAT
20	29	100.0	662	2	Q6GMM9 RAT
21	29	100.0	663	1	MMP2 CHICK
22	29	100.0	767	2	Q8KTW1 CLOSTRIDIUM
23	29	100.0	770	2	Q7XXG3 ORYSA
24	29	100.0	840	2	Q66QH3 ORYSA
25	29	100.0	842	2	Q60HB5 ORYSA
26	29	100.0	842	2	Q69DS7 ORYSA
27	29	100.0	945	2	Q9N175 SHEEP
28	29	100.0	1147	1	NOS2 RAT
29	29	100.0	1147	2	Q8X576 RAT
30	29	100.0	1147	2	Q9QW28 SP.
31	29	100.0	1147	2	Q9R0W4 RAT

32	28	96.6	118	2	Q8YLS2 RALSO
33	28	96.6	169	2	Q8UI59 AGR75
34	28	96.6	283	2	Q19334 CAEL
35	28	96.6	305	2	Q8EM92 OCEIH
36	28	96.6	355	2	Q6LJY6 PHOPR
37	28	96.6	1044	2	Q8XIN5 CLOPE
38	26	89.7	85	2	Q19641 CAEL
39	26	89.7	99	2	Q731J0 WOLPM
40	26	89.7	109	2	Q8XQ19 RALSO
41	26	89.7	126	2	Q6G347 BARHE
42	26	89.7	131	2	Q6C1M8 YARLI
43	26	89.7	137	2	Q6G346 BARHE
44	26	89.7	137	2	Q5SKK3 THE8
45	26	89.7	142	2	Q4JC95 SULAC
46	26	89.7	149	2	Q5WU01 LEGPL
47	26	89.7	149	2	Q5X274 LEGPA
48	26	89.7	149	2	Q5ZSR4 LEGPH
49	26	89.7	150	2	Q51314 GNOSO
50	26	89.7	156	1	GUAD BACSU
51	26	89.7	156	2	Q5WB80 BACSK
52	26	89.7	166	2	Q59317 PYRHO
53	26	89.7	185	2	Q67590 AQUAE
54	26	89.7	191	1	CSRPI CHICK
55	26	89.7	191	1	CSRPI COTUA
56	26	89.7	229	2	Q9RR88 DEIRA
57	26	89.7	232	2	Q67QU1 SYMTH
58	26	89.7	233	2	Q527F8 MAGGR
59	26	89.7	233	2	Q30760 RHOSH
60	26	89.7	235	2	Q9N2Y5 CAEL
61	26	89.7	266	2	Q5UEW2 9PROT
62	26	89.7	268	2	Q5GU79 XANOR
63	26	89.7	276	2	Q7QS35 GIALA
64	26	89.7	285	2	Q48777 ARATH
65	26	89.7	290	2	Q5A5P9 CANAL
66	26	89.7	296	2	Q751V7 ORYSA
67	26	89.7	319	1	VG12 IGHV1
68	26	89.7	318	2	Q8GX90 ARATH
69	26	89.7	321	2	Q6ASCI DESPS
70	26	89.7	340	2	Q9EZ99 ZYMWO
71	26	89.7	348	1	CYSA METCA
72	26	89.7	352	2	Q83MJ3 SHIFL
73	26	89.7	352	2	Q72FT5 DESVH
74	26	89.7	383	2	Q6M190 DBEBA
75	26	89.7	390	2	Q4HML6 CAMLA
76	26	89.7	403	2	Q4WJL6 ASFPU
77	26	89.7	421	1	YIHN ECOLI
78	26	89.7	421	2	Q8FEG3 ECOLI6
79	26	89.7	421	2	Q8X8P3 ECOS7
80	26	89.7	425	2	Q895U4 CLOTE
81	26	89.7	426	2	Q84QAB ORYSA
82	26	89.7	428	2	Q4KEQ1 PSBP5
83	26	89.7	432	2	Q6L6X3 9VIRU
84	26	89.7	432	2	Q6L6X4 9VIRU
85	26	89.7	432	2	Q6L6X5 9VIRU
86	26	89.7	432	2	Q75PQ4 9VIRU
87	26	89.7	433	2	Q5YF80 9VIRU
88	26	89.7	453	2	Q68Y86 9VIRU
89	26	89.7	453	2	Q6GVF2 9VIRU
90	26	89.7	453	2	Q6GVF3 9VIRU
91	26	89.7	453	2	Q6GVF4 9VIRU
92	26	89.7	453	2	Q6GVF6 9VIRU
93	26	89.7	453	2	Q6GVF7 9VIRU
94	26	89.7	453	2	Q6GVF8 9VIRU
95	26	89.7	453	2	Q6GVF9 9VIRU
96	26	89.7	453	2	Q6GVG0 9VIRU
97	26	89.7	453	2	Q6GVG1 9VIRU
98	26	89.7	453	2	Q6GVG2 9VIRU
99	26	89.7	453	2	Q6GVG3 9VIRU
100	26	89.7	453	2	Q6PNE1 9VIRU
101	26	89.7	453	2	Q6QNG1 9VIRU
102	26	89.7	453	2	Q6QNG4 9VIRU
103	26	89.7	453	2	Q6QNG5 9VIRU
104	26	89.7	453	2	Q6QNG6 9VIRU

Q8YLS2	ralstonia s
Q8UI59	agrobacteri
Q19334	caenorhabdi
Q8EM92	oceanobacil
Q6LJY6	photobacter
Q8XIN5	clostridium
Q19641	caenorhabdi
Q731J0	wolbachia p
Q8XQ19	ralstonia s
Q6G347	bartonella
Q6C1M8	yarowella li
Q6G346	bartonella
Q5SKK3	thermus the
Q4JC95	sulfolobus
Q5WU01	legionella
Q5X274	legionella
Q5ZSR4	legionella
Q51314	nostoc sp.
Q34598	bacillus su
Q5WB80	bacillus cl
Q59317	pyrococcus
Q67590	aquifex aeo
P67966	gallus gall
P67967	coturnix co
Q9RR88	deinococcus
Q67QU1	syntrophobacte
Q527F8	magnaporthe
Q30760	rhodospirillum rubrum
Q9N2Y5	caenorhabdi
Q5UEW2	uncultured
Q5GU79	xanthomonas
Q7Q835	giardia lam
Q48777	arabidopsis
Q5A5P9	candida alb
Q751V7	oryza sativ
Q00165	ictaluriid h
Q8GX90	arabidopsis
Q6ASCI	desulfotale
Q9EZ99	zymomonas m
Q609Q1	methylococc
Q83MJ3	shigella fl
Q72FT5	desulfovibr
Q6M190	bdellovibri
Q4HML6	campylobact
Q4WJL6	aspergillus
P32135	escherichia
Q8FEG3	escherichia
Q8X8P3	escherichia
Q895U4	clostridium
Q84QAB	oryza sativ
Q4KEQ1	pseudomonas
Q6L6X3	red sea bre
Q6L6X4	rock break
Q6L6X5	sea bass ir
Q75PQ4	turbot irid
Q5YF80	rock bream
Q68Y86	olive floun
Q6GVF2	korean flou
Q6GVF3	korean flou
Q6GVF4	korean flou
Q6GVF6	korean flou
Q6GVF7	korean flou
Q6GVF8	korean flou
Q6GVF9	korean flou
Q6GVG0	korean flou
Q6GVG1	korean flou
Q6GVG2	korean flou
Q6GVG3	korean flou
Q6PNE1	turbot redd
Q6QNG1	rock bream
Q6QNG4	rock bream
Q6QNG5	rock bream
Q6QNG6	rock bream

105	26	89.7	453	2	Q6QNG7_9VIRU	Q6qng7	rock bream	178	25	86.2	46	2	Q81W20_BACAN	Q81w20	bacillus an
106	26	89.7	453	2	Q6QNG8_9VIRU	Q6qng8	rock bream	179	25	86.2	54	2	Q4z1B9_PLABE	Q4z1b9	plasmidium
107	26	89.7	453	2	Q6QNH0_9VIRU	Q6qnh0	rock bream	180	25	86.2	61	2	Q72A11_DESVH	Q72a11	desulfovibr
108	26	89.7	453	2	Q6QNH1_9VIRU	Q6qnh1	rock bream	181	25	86.2	72	2	Q7Y541_BPR69	Q7y541	bacterioph
109	26	89.7	453	2	Q7T3Y6_9VIRU	Q7t3y6	dwarf goura	182	25	86.2	75	2	Q4KA43_PSEF5	Q4ka43	pseudomonas
110	26	89.7	453	2	Q7T3Y7_9VIRU	Q7t3y7	african lam	183	25	86.2	76	2	Q6MKJ3_BDEBA	Q6mkj3	bdellovibr1
111	26	89.7	453	2	Q7T3Z1_RSIV	Q7t3z1	red sea bre	184	25	86.2	76	2	Q72DT7_DESVH	Q72dt7	desulfovibr
112	26	89.7	453	2	Q8M445_RSIV	Q8m445	red sea bre	185	25	86.2	95	2	Q5LDJ7_BACFR	Q5ldj7	bacterioides
113	26	89.7	453	2	Q8V5D9_9VIRU	Q8v5d9	infectious	186	25	86.2	95	2	Q64UL9_BACFN	Q64ul9	bacterioides
114	26	89.7	453	2	Q516L1_9VIRU	Q516l1	rock bream	187	25	86.2	100	2	Q8YM06_ANASP	Q8ym06	anabaena sp
115	26	89.7	453	2	Q516L2_9VIRU	Q516l2	rock bream	188	25	86.2	107	2	Q4U9W4_THEAN	Q4u9w4	theileria a
116	26	89.7	453	2	Q77ZP6_9VIRU	Q77zpz6	sea baas ir	189	25	86.2	109	2	Q650T2_ORISA	Q650t2	oryza sativ
117	26	89.7	453	2	Q7T3Y4_9VIRU	Q7t3y4	grouper sle	190	25	86.2	119	2	Q6UVP6_9CHLO	Q6uvp6	pseudendocl
118	26	89.7	453	2	Q4KSF0_9VIRU	Q4ksf0	orange-spot	191	25	86.2	120	1	COP1_STAAR	P03861	staphylococ
119	26	89.7	457	1	TRME_LISIN	Q926u7	listeria in	192	25	86.2	122	2	Q7QD79_ANOBA	Q7qd79	anopheles g
120	26	89.7	458	2	Q4TRD0_9SPHN	Q4trd0	erythroba	193	25	86.2	122	2	Q4YZC4_PLABE	Q4yzc4	plasmidium
121	26	89.7	464	1	COAT_IRV1	P18162	tipula irid	194	25	86.2	128	2	Q4RIS1_TETNG	Q4ris1	tetraodon n
122	26	89.7	465	2	Q4U3U9_9VIRU	Q4u3u9	trichoplusi	195	25	86.2	129	2	Q4M0F9_9BURK	Q4m0f9	burkholderi
123	26	89.7	467	1	COAT_IRV6	Q05815	chilo iride	196	25	86.2	132	2	Q45455_BACSU	Q45455	bacillus su
124	26	89.7	468	2	Q83LY5_SHIFL	Q83ly5	shigella fl	197	25	86.2	134	1	ACPS_ZYMMO	Q5nl87	zymomonas m
125	26	89.7	472	1	COAT_IRV22	P22166	simulium ir	198	25	86.2	141	2	Q96YD6_SULTO	Q96yde6	sulfolobus
126	26	89.7	479	2	Q9RFD8_RHOSH	Q9rfd8	rhodobacter	199	25	86.2	141	2	Q5ERC9_CARAU	Q5erc9	carassius a
127	26	89.7	479	2	Q9Z5E2_RHOSH	Q9z5e2	rhodobacter	200	25	86.2	141	2	Q4SJV9_TETNG	Q4sjv9	tetraodon n
128	26	89.7	483	2	Q5FQ43_GLUOX	Q5fq43	gluonobact	201	25	86.2	144	2	Q61G33_CAEHR	Q61g33	caenorhabdi
129	26	89.7	487	2	Q8BTV9_MOUSE	Q8btv9	mus musculu	202	25	86.2	144	2	Q9LA12_PASMU	Q9la12	pasteurella
130	26	89.7	494	2	Q6NT77_HUMAN	Q6nt77	homo sapien	203	25	86.2	144	2	Q9CPF9_PASMU	Q9cpf9	pasteurella
131	26	89.7	496	2	Q6C9A3_YARLI	Q6c9a3	yarrowia li	204	25	86.2	152	2	Q7W079_BORPE	Q7w079	bordelella
132	26	89.7	496	2	Q8D2N2_WIGHR	Q8d2n2	wiggleswort	205	25	86.2	160	2	Q84L47_MIRJA	Q84l47	mirabilis j
133	26	89.7	498	2	Q5YZV4_NOCFA	Q5yzv4	nocardia fa	206	25	86.2	167	2	Q4UDQ7_THEAN	Q4udq7	theileria a
134	26	89.7	504	2	Q4H3G7_CIOIN	Q4h3g7	ciona intes	207	25	86.2	167	2	Q965S0_CAEPEL	Q965s0	caenorhabdi
135	26	89.7	525	2	Q5FVY8_XENTR	Q5fvy8	aspergillu	208	25	86.2	167	2	Q4N5T6_THEPA	Q4n5t6	theileria p
136	26	89.7	539	2	Q5B5V3_EMENI	Q5b5v3	aspergillu	209	25	86.2	172	2	Q92K27_RHIME	Q92k27	rhizobium m
137	26	89.7	547	2	Q4TC12_TETNG	Q4tc12	tetraodon n	210	25	86.2	174	2	Q680L9_ARATH	Q680l9	arabidopsis
138	26	89.7	555	2	Q9P103_HUMAN	Q9p103	homo sapien	211	25	86.2	174	2	Q8L9P8_ARATH	Q8l9p8	arabidopsis
139	26	89.7	555	2	Q8NCA4_HUMAN	Q8nc44	homo sapien	212	25	86.2	186	1	GLI19_ORISA	P23835	oryza sativ
140	26	89.7	555	2	Q8BXN9_MOUSE	Q8bxn9	mus musculu	213	25	86.2	186	2	P93414_ORISA	P93414	oryza sativ
141	26	89.7	556	2	Q8R2P9_MOUSE	Q8r2p9	mus musculu	214	25	86.2	190	2	Q6MJF8_BDEBA	Q6mjf8	bdellovibr1
142	26	89.7	558	2	Q8BU98_MOUSE	Q8bu98	mus musculu	215	25	86.2	191	1	Y1137_METJA	Q58537	methanococ
143	26	89.7	559	2	Q7NSY8_CHRVO	Q7nsy8	chromobacte	216	25	86.2	192	2	Q4PMI1_9RICK	Q4pmi1	candidatus
144	26	89.7	564	2	Q8NBN3_HUMAN	Q8nb33	homo sapien	217	25	86.2	199	2	Q4UMD0_RICFE	Q4umd0	ricketsia
145	26	89.7	634	2	Q7RYI1_NEUCR	Q7ryi1	neurospora	218	25	86.2	202	2	Q7SE50_NEUCR	Q7se50	neurospora
146	26	89.7	646	2	Q5FS65_GLUOX	Q5fs65	gluonobact	219	25	86.2	202	2	Q25Y98_HELPS	Q25y98	helicobacte
147	26	89.7	647	2	Q8WU27_HUMAN	Q8wu27	homo sapien	220	25	86.2	206	2	Q67T36_SYMTH	Q67t36	symbiobacte
148	26	89.7	679	2	Q5YY78_NOCFA	Q5yy78	nocardia fa	221	25	86.2	209	2	Q4FV94_9GAMM	Q4fv94	psychrobact
149	26	89.7	715	2	Q5PCX6_SALPA	Q5pcx6	salmonella	222	25	86.2	209	2	Q8YMX5_ANASP	Q8ymx5	anabaena sp
150	26	89.7	715	2	Q824Z0_SALTI	Q824z0	salmonella	223	25	86.2	210	2	Q5F654_NEIG1	Q5f654	neisseria g
151	26	89.7	728	2	Q7NBR7_MYCGA	Q7nbr7	mycoplasma	224	25	86.2	210	2	Q5JSP2_NEIMA	Q5jsp2	neisseria m
152	26	89.7	733	2	Q8KTI9_MYCSY	Q8kti9	mycoplasma	225	25	86.2	210	2	Q9K184_NEIMA	Q9k184	neisseria m
153	26	89.7	742	2	Q8KTJ1_MYCSY	Q8ktj1	mycoplasma	226	25	86.2	212	2	Q57AX8_BRUBU	Q57ax8	brucella ab
154	26	89.7	743	2	Q8XTJ0_MYCSY	Q8xtj0	mycoplasma	227	25	86.2	212	2	Q8FYG0_BRUSU	Q8fyg0	brucella su
155	26	89.7	844	2	Q6JEB32_9BURK	Q6je32	burkholderi	228	25	86.2	212	2	Q9L6H7_BRUME	Q9l6h7	brucella me
156	26	89.7	939	2	Q6AK45_DESPS	Q6ak45	desulfotale	229	25	86.2	214	2	Q92LJ7_RHIME	Q92lj7	rhizobium m
157	26	89.7	960	2	Q418E7_GIBZE	Q418e7	gibberella	230	25	86.2	215	2	Q521S9_MAGRR	Q521s9	magnaporthe
158	26	89.7	1041	2	Q5LD76_BACFR	Q5ld76	bacterioides	231	25	86.2	220	2	Q8T3Z2_DROME	Q8t3z2	drosophila
159	26	89.7	1041	2	Q64U98_BACFR	Q64u98	bacterioides	232	25	86.2	226	1	Y209_METTH	Q82311	methanobact
160	26	89.7	1041	2	Q8A9Y5_BACTN	Q8a9y5	bacterioides	233	25	86.2	228	2	Q5AXR0_EMENI	Q5axr0	aspergillus
161	26	89.7	1055	2	Q94887_HUMAN	Q94887	homo sapien	234	25	86.2	229	2	Q4WVZ8_ASPFU	Q4wvz8	aspergillus
162	26	89.7	1065	2	Q91V88_MOUSE	Q91v88	mus musculu	235	25	86.2	231	2	Q8C6Y8_MOUSE	Q8c6y8	mus musculu
163	26	89.7	1139	1	SRBP2_CRIGR	Q60429	cricetulus	236	25	86.2	234	2	Q5JEG7_PYRKO	Q5jeg7	pyrococcus
164	26	89.7	1411	2	Q73Y53_MYCPA	Q73y53	mycobacteri	237	25	86.2	234	2	Q8U3K3_PYRFO	Q8u3k3	pyrococcus
165	26	89.7	1701	2	Q61164_PLAYO	Q61164	plasmidium	238	25	86.2	240	2	Q6NUA9_XENLA	Q6nu9a	xenopus lae
166	26	89.7	1701	2	Q7RC08_PLAYO	Q7rc08	plasmidium	239	25	86.2	246	2	Q9V9U6_DROME	Q9v9u6	drosophila
167	26	89.7	1723	2	Q8WRD0_PLABE	Q8wrd0	plasmidium	240	25	86.2	246	2	Q6SEF21_9BACT	Q6sef21	uncultured
168	26	89.7	1769	2	Q4YQU3_PLABE	Q4yqu3	plasmidium	241	25	86.2	246	2	Q73NMG_TREDE	Q73nm6	treponema d
169	26	89.7	1869	2	Q997D0_9COMO	Q997d0	broad bean	242	25	86.2	247	2	Q92K30_HELPS	Q92k30	helicobacte
170	26	89.7	2397	1	MOX11_SCHPO	Q09854	schizosacch	243	25	86.2	249	2	Q4NHD7_9MICC	Q4nhd7	arthrobact
171	26	89.7	2601	2	Q4YQB7_PLABE	Q4yqb7	plasmidium	244	25	86.2	251	2	Q7N2P7_PHOLL	Q7n2p7	photothabd
172	26	89.7	3888	2	Q51X35_MAGGR	Q51x35	magnaporthe	245	25	86.2	252	2	Q7NUJ0_CHRVO	Q7nuj0	chromobacte
173	26	89.7	4212	2	Q4V2I8_BURMA	Q4v2i8	burkholderi	246	25	86.2	253	2	Q9Z1I1_ACICA	Q9z1i1	acinetobact
174	26	89.7	5835	2	Q63LK8_BURPS	Q63lk8	burkholderi	247	25	86.2	255	2	Q5TU56_ANOGA	Q5tu56	anopheles g
175	25	86.2	22	2	Q4Y666_PLABE	Q4y666	plasmidium	248	25	86.2	255	2	Q9VHU5_DROME	Q9vhu5	drosophila
176	25	86.2	42	2	Q7UKA9_RHODPI	Q7uka9	rhodopirell	249	25	86.2	258	2	Q6G411_BARHE	Q6g411	bartonella
177	25	86.2	46	2	Q73F18_BACC1	Q73f18	bacillus ce	250	25	86.2	260	2	Q50SI4_ENTHI	Q50si4	entamoeba h

251 25 86.2 260 2 P94512_BACSU
 252 25 86.2 263 2 Q92VA5_RHIME
 253 25 86.2 268 1 TRUA_TREDE
 254 25 86.2 268 2 Q84148_MIRJA
 255 25 86.2 268 2 Q52JP4_CHICK
 256 25 86.2 270 2 Q4WEP8_ASPPU
 257 25 86.2 271 2 Q65GA6_BACLD
 258 25 86.2 276 2 Q6BFP3_PARTE
 259 25 86.2 276 2 Q940Q3_ARATH
 260 25 86.2 276 2 Q62RR1_BACLD
 261 25 86.2 282 1 PNMT_HUMAN
 262 25 86.2 282 2 Q6FHD9_HUMAN
 263 25 86.2 285 2 Q9KMB5_VIBCH
 264 25 86.2 291 2 Q87JU8_VIBPA
 265 25 86.2 293 2 Q9ZAF0_9ZZZZ
 266 25 86.2 293 2 Q9KY30_STRCO
 267 25 86.2 295 2 Q8D6E6_VIBVY
 268 25 86.2 295 2 Q7MD99_VIBVY
 269 25 86.2 297 2 Q8PID6_XANAC
 270 25 86.2 298 2 Q97VK7_SULSO
 271 25 86.2 299 2 Q5NTR3_9BACT
 272 25 86.2 300 2 Q4ZTF5_PSESY
 273 25 86.2 300 2 Q80B08_9POXV
 274 25 86.2 302 2 Q7AGM6_ECO57
 275 25 86.2 303 2 Q9CLP3_PASMU
 276 25 86.2 303 2 Q6TVN6_9POXV
 277 25 86.2 303 2 Q6TW16_9POXV
 278 25 86.2 307 2 Q6TVA4_9POXV
 279 25 86.2 313 2 Q71KR8_KLEFL
 280 25 86.2 317 2 Q4QEH6_LEIMA
 281 25 86.2 321 2 Q9WZ88_THEMA
 282 25 86.2 322 1 OR1J1_HUMAN
 283 25 86.2 323 2 Q8X9H6_ECO57
 284 25 86.2 324 2 Q41FV0_GIBZE
 285 25 86.2 325 2 Q4TJG6_9SPHN
 286 25 86.2 326 1 PELA_EMENI
 287 25 86.2 326 2 Q5BFP9_EMENI
 288 25 86.2 327 2 Q6FKK4_CANGA
 289 25 86.2 327 2 Q7WS58_BORPA
 290 25 86.2 327 2 Q7WDB5_BORBP
 291 25 86.2 327 2 Q7VZ12_BORPE
 292 25 86.2 331 2 Q4HS16_CAMUP
 293 25 86.2 331 2 Q821X4_CHLCV
 294 25 86.2 331 2 Q9Z6V0_CHLPN
 295 25 86.2 332 2 Q9YCL2_AERPE
 296 25 86.2 332 2 Q5L571_CHLAB
 297 25 86.2 334 2 Q6LH05_PHOPR
 298 25 86.2 337 2 Q4M1D9_BURK
 299 25 86.2 340 1 YR03_CABEL
 300 25 86.2 340 2 Q63KW3_BURPS

ALIGNMENTS

RESULT 1
 Q91Y69_MESAU
 ID Q91Y69_MESAU PRELIMINARY; PRT; 143 AA.
 AC Q91Y69_1
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Matrix metalloproteinase-2 (Fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Cricetinae; Mesocricetus.
 RN NCBI_TaxID=10036;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Tracheal surface;
 RA Ko K.H., Shin C.Y., Lee W.J., Yoo B.K., Ryu J.R., Park K.H.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF260254; RAKS1635.1; -; mRNA.
 DR HSSP; P08253; 1CK7.
 DR INTEROPS; M10.004; -.
 DR InterPro; IPR000585; Hemopexin.
 DR Pfam; PF00045; Hemopexin; 3.
 DR SMART; SM00120; HX; 3.
 DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
 FT NON_TER 1 143 143
 SQ SEQUENCE 143 AA; 16316 MW; 1B4310F9E6A023EF CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFPA 6
 |||||
 Db 21 KAVFFPA 26
 RESULT 2
 Q9N284_BOVIN
 ID Q9N284_BOVIN PRELIMINARY; PRT; 162 AA.
 AC Q9N284_1
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DE MMP-2 (Fragment).
 DE MMP-2 (Fragment).
 GN Name=bmmp-2;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Rutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 RN NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sato T., Hirata M., Ito A., Hashizume K.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB043994; BAA96387.1; -; mRNA.
 DR HSSP; P08253; 1CK7.
 DR INTEROPS; M10.003; -.
 DR InterPro; IPR000585; Hemopexin.
 DR Pfam; PF00045; Hemopexin; 3.
 DR SMART; SM00120; HX; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 162 AA; 18351 MW; B8898B49E5E5326A CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 162;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFPA 6
 |||||
 Db 33 KAVFFPA 38
 RESULT 3
 Q9BGL4_SHEEP
 ID Q9BGL4_SHEEP PRELIMINARY; PRT; 248 AA.
 AC Q9BGL4_1
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Gelatinase A (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Caprinae; Ovis.
 RN NCBI_TaxID=9940;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Ovary;

```

RX MEDLINE=21859324; PubMed=11870075;
RA Rieke W.A., Smith G.W., Smith M.F.;
RT "Matrix metalloproteinase expression and activity following
RT prostaglandin F(2 alpha)-induced luteolysis.";
RL Biol. Reprod. 66:685-691(2002).
DR EMBL; AF267159; AAGS9847.1; -; mRNA.
DR HSSP; P08253; IGMD.
DR MEROPS; M10.003; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; P:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00045; Hemopexin; 3.
DR Pfam; PF00413; Peptidase M10; 1.
DR PRINTS; PR00138; MATRIXIN.
DR ProDom; PD000995; FN_Type_II; 1.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00120; HX; 3.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 248
SQ SEQUENCE 248 AA; 28034 MW; 56F421C2D6DC133E CRC64;

Query Match 100.0%; Score 29; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 184 KAVFFA 189

RESULT 4
Y1086_HAEIN
ID Y1086_HAEIN STANDARD; PRT; 261 AA.
AC P45030;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical protein H11086.
GN OrderedLocusNames=H11086;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kierlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Spruyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
RL Science 269:496-512(1995).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: Belongs to the DUF140 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration

```

```

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U32788; AAC22742.1; -; Genomic_DNA.
DR PIR; D64166; D64166.
DR TIGR; H11086; -.
DR InterPro; IPR003453; DUF140.
DR Pfam; PF02405; DUF140; 1.
DR TIGRFAMs; TIGR00056; DUF140; 1.
KW Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 13
FT TRANSMEM 50 70 Potential.
FT TRANSMEM 90 110 Potential.
FT TRANSMEM 148 168 Potential.
FT TRANSMEM 199 219 Potential.
FT TRANSMEM 239 259 Potential.
SQ SEQUENCE 261 AA; 28015 MW; 4BC3695F247A6BF6 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 205 KAVFFA 210

RESULT 5
Q4QLK2_HAB18
ID Q4QLK2_HAB18 PRELIMINARY; PRT; 261 AA.
AC Q4QLK2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Conserved ABC-type transport system protein, permease component.
GN OrderedLocusNames=NT11249;
OS Haemophilus influenzae (strain 86-028NP).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=281310;
RN [1]
NUCLEOTIDE SEQUENCE.
RX PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
RA Harrison A., Dyer D.W., Gillaspay A., Ray W.C., Mungur R., Carson M.B.,
RA Zhong H., Gipson J., Gipson M., Johnson L.S., Lewis L., Bakaletz L.O.,
RA Munson R.S. Jr.;
RT "Genomic sequence of an otitis media isolate of nontypeable
RT Haemophilus influenzae: comparative study with H. influenzae serotype
RT d, strain KW20.";
RL J. Bacteriol. 187:4627-4636(2005).
DR EMBL; CF000057; AAX88095.1; -; Genomic_DNA.
DR InterPro; IPR003453; DUF140.
DR Pfam; PF02405; DUF140; 1.
DR TIGRFAMs; TIGR00056; DUF140; 1.
KW Complete proteome.
SQ SEQUENCE 261 AA; 28075 MW; 0EB1BEEDD2FA133A CRC64;

Query Match 100.0%; Score 29; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 205 KAVFFA 210

RESULT 6
Q73KX6_TREDE
ID Q73KX6_TREDE PRELIMINARY; PRT; 277 AA.
AC Q73KX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

```


DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Amino acid ABC transporter, amino acid-binding protein, putative.
 GN OrderedLocusNames=TDE2091;
 OS Treponema denticola.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=158;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 35405 / DSM 14222;
 RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
 RA Sehadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.P.,
 RA Dodeon R.J., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.P.,
 RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
 RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
 RA Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
 RA Shatman S., McLeod M.P., Smajs J.K., Pal S., Amin A.,
 RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
 RA Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.,
 RT "Comparison of the genome of the oral pathogen Treponema denticola
 RT with other spirochete genomes."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).
 RL EMBL; AE017253; AAS12611.1; -; Genomic_DNA.
 DR TIGR; TDE2091; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:003288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001311; SBP_glu_receptor.
 DR InterPro; IPR001638; SBP_bac_3.
 DR Pfam; PF00497; SBP_bac_3; 1.
 DR SMART; SM00062; PBPB; 1.
 DR PROSITE; PS01039; SBP_BACTERIAL_3; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 277 AA; 31013 MW; AC9F1BC5DB10A16E CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 277;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 DB 8 KAVFFA 13
 RESULT 7
 ID Q9WY6_ARATH PRELIMINARY; PRT; 314 AA.
 AC Q9WY6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE F3222.6 protein.
 GN Name=F3222.6;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B., Wu D.,
 RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Uterback T.R.,
 RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC023912; AAF63818.1; -; Genomic_DNA.
 DR InterPro; IPR000575; APH-trans.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; UNKNOWN_1.
 DR PROSITE; PS01636; APH; 1.
 SQ SEQUENCE 314 AA; 34938 MW; B531A6DFA610A5DB CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 314;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 DB 282 KAVFFA 287
 RESULT 8
 ID Q5LIA8_GEOKA PRELIMINARY; PRT; 381 AA.
 AC Q5LIA8;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Proton/sodium antiporter.
 GN OrderedLocusNames=GK0987;
 OS Geobacillus kaustophilus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 OX NCBI_TaxID=1462;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HTA426;
 RX PubMed=15576355; DOI=10.1093/nar/gkh970;
 RA Takami H., Takaki Y., Chee G.-J., Nishi S., Shimamura S., Suzuki H.,
 RA Matsui S., Uchiyama I.;
 RT "Thermoadaptation trait revealed by the genome sequence of
 RT thermophilic Geobacillus kaustophilus."
 RL Nucleic Acids Res. 32:6292-6303 (2004).
 DR EMBL; BA000043; BAD75272.1; -; Genomic_DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
 DR GO; GO:0006885; P:regulation of pH; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR006153; Na_H_exchanger; 1.
 DR Pfam; PF00999; Na_H_exchanger; 1.
 KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 381 AA; 39481 MW; AE3EA4252A7E367B CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 381;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 DB 179 KAVFFA 184
 RESULT 9
 ID Q8KHB6_CLODI PRELIMINARY; PRT; 389 AA.
 AC Q8KHB6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE S-layer protein variable domain SlpA (Fragment).
 GN Name=slpA;
 OS Clostridium difficile.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OX NCBI_TaxID=1496;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 43597, 90-111, and 93-136;
 RX MEDLINE=22083941; PubMed=12089261;
 RX DOI=10.1128/JCM.40.7.2452-2458.2002;
 RA Karjalainen T., Saumier N., Barc M.C., Delmege M., Collignon A.;
 RT "Clostridium difficile genotyping based on slpA variable region in S-
 RT layer gene sequence: an alternative to serotyping."
 RL J. Clin. Microbiol. 40:2452-2458 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 43597, 90-111, and 93-136;

```

RA Karjalainen T.K., Saunier N.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458880; AAM75944.1; -; Genomic DNA.
DR EMBL; AF458881; AAM75945.1; -; Genomic DNA.
DR EMBL; AF458882; AAM75946.1; -; Genomic DNA.
FT NON_TER 1
FT NON_TER 389
SQ SEQUENCE 389 AA; 41788 MW; C5ED8F4901C18F8C CRC64;

Query Match 100.0%; Score 29; DB 2; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 340 KAVFFA 345

RESULT 10
Q8S8Q7 ARATH PRELIMINARY; PRT; 469 AA.
AC Q8S8Q7_
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Putative selenium-binding protein (Pentatricopeptide repeat-containing protein).
DE ORFName=At2g34370;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]_
RP NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]_
RP NUCLEOTIDE SEQUENCE.
RA Underwood B.A., Xiao Y., Moskal W., Monaghan E., Wang W., Redman J.,
RA Wu H.C., Uterback T., Town C.D.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004481; AAM14949.1; -; Genomic DNA.
DR EMBL; DQ056566; AAY78716.1; -; mRNA.
DR PIR; T02325; T02325.
DR GO; GO:0005488; F.binding; IEA.
DR InterPro; IPR002885; PPR.
DR InterPro; IPR011990; TPR-like_helical.
DR Pfam; PF01535; PPR; 4.
DR TIGRFAMs; TIGR00756; PPR; 3.
KW Repeat.
SQ SEQUENCE 469 AA; 53856 MW; FB698FC0238437 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 213 KAVFFA 218

RESULT 11
Q9N1P6 CANFA
ID Q9N1P6_CANFA PRELIMINARY; PRT; 632 AA.
AC Q9N1P6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

```

```

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Matrix metalloproteinase-2 (Fragment).
GN Name=MMP-2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=fibrosarcoma;
RA Jalic H., Paria B., Balkin R., Baxendale V., Fang Y., Kitchell B.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177217; AAF67517.1; -; mRNA.
DR HSSP; P08253; 1GXD.
DR MEROPS; M10.003; -.
DR Ensembl; ENSCAFG0000009421; Canis familiaris.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRXIN.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HK; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 632 AA; 70991 MW; DBAE895497E129F3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 632;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 503 KAVFFA 508

RESULT 12
Q6U7G9 MELGA PRELIMINARY; PRT; 654 AA.
ID Q6U7G9_MELGA PRELIMINARY; PRT; 654 AA.
AC Q6U7G9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Gelatinase A.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Monsonego Ornan E., Tong A.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY376899; AAO98971.1; -; mRNA.
DR HSSP; P08254; 1B3D.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

```

"NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA [URL: <http://esg.gs.washington.edu>].", Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

[5]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

TISSUE=Brain;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J., Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[6]

NUCLEOTIDE SEQUENCE OF 1-51.

MEDLINE=90228972; PubMed=2158484;

Huntla P., Eddy R.L., Fan Y.S., Byers M.G., Shows T.B., Tryggvason K.;

"Completion of the primary structure of the human type IV collagenase proenzyme and assignment of the gene (CLG4) to the q21 region of chromosome 16."; Genomics 6:554-559(1990).

[7]

ENZYME REGULATION.

PubMed=11179305; DOI=10.1128/IAI.69.3.1402-1408.2001;

Gusman H., Travis J., Helmerhorst E.J., Potempa J., Troxler R.F., Oppenheim F.G.;

"Salivary histatin 5 is an inhibitor of both host and bacterial enzymes implicated in periodontal disease."; Infect. Immun. 69:1402-1408(2001).

[8]

PROCESSING OF KISS1.

MEDLINE=22761370; PubMed=12879005; DOI=10.1038/sj.onc.1206542;

Takino T., Koshikawa N., Miyamori H., Tanaka M., Sasaki T., Okada Y., Seki M., Sato H.;

"Cleavage of metastasis suppressor gene product KISS-1 protein/metastin by matrix metalloproteinases."; Oncogene 22:4617-4626(2003).

[9]

X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 443-660.

MEDLINE=96069777; PubMed=7593664;

Libeson A.M., Gittis A.G., Collier I.E., Marmer B.L., Goldberg G.I., Lattman E.E.;

"Crystal structure of the haemopexin-like C-terminal domain of gelatinase A."; Nat. Struct. Biol. 2:938-942(1995).

[10]

X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 459-660.

MEDLINE=96140723; PubMed=8549817; DOI=10.1016/0014-5793(95)01435-7;

Gohlke U., Gomis-Rueth F.-X., Crabbe T., Murphy G., Docherty A.J., Bode W.;

"The C-terminal (haemopexin-like) domain structure of human gelatinase A (MMP2): structural implications for its function."; FEBS Lett. 378:126-130(1996).

-1- FUNCTION: In addition to gelatin and collagens, it cleaves KISS1 at a Gly-|-Leu bond.

-1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-|-Ile-Ala-Gly-Gln.

CC -|- COFACTOR: Binds 4 calcium ions per subunit.
 CC -|- COFACTOR: Binds 2 zinc ions per subunit.
 CC -|- ENZYME REGULATION: Inhibited by histatin-3 1/24 (histatin-5).
 CC -|- SUBUNIT: Ligand for integrin alpha-V/beta-3.
 CC -|- TISSUE SPECIFICITY: Produced by normal skin fibroblasts.
 CC -|- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-MMP3).
 CC -|- SIMILARITY: Belongs to the peptidase M10A family.
 CC -|- SIMILARITY: Contains 3 fibronectin type-II domains.
 CC -|- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; J03210; AAA35701.1; -; mRNA.
 DR EMBL; M33789; AAA52027.1; -; Genomic_DNA.
 DR EMBL; M55593; AAA52028.1; -; Genomic_DNA.
 DR EMBL; M55592; AAA52028.1; JOINED; Genomic_DNA.
 DR EMBL; M55582; AAA52028.1; JOINED; Genomic_DNA.
 DR EMBL; M55583; AAA52028.1; JOINED; Genomic_DNA.
 DR EMBL; M55584; AAA52028.1; JOINED; Genomic_DNA.
 DR EMBL; M55585; AAA52028.1; JOINED; Genomic_DNA.
 DR EMBL; M55586; AAA52028.1; JOINED; Genomic_DNA.
 DR EMBL; M55587; AAA52028.1; JOINED; Genomic_DNA.
 DR EMBL; M55588; AAA52028.1; JOINED; Genomic_DNA.
 DR EMBL; M55589; AAA52028.1; JOINED; Genomic_DNA.
 DR EMBL; M55590; AAA52028.1; JOINED; Genomic_DNA.
 DR EMBL; M55591; AAA52028.1; JOINED; Genomic_DNA.
 DR EMBL; M55592; AAA52028.1; JOINED; Genomic_DNA.
 DR EMBL; AY738117; AAU10089.1; -; Genomic_DNA.
 DR EMBL; BC002576; AAH02576.1; -; mRNA.
 DR PIR; A28153; A28153.
 DR PDB; 1CK7; X-ray; A=30-660.
 DR PDB; 1CKW; NMR; A=278-336.
 DR PDB; 1EAK; X-ray; A/B/C/D=32-452.
 DR PDB; 1GEN; X-ray; @=443-660.
 DR PDB; 1GXD; X-ray; A/B=30-660.
 DR PDB; 1HOV; NMR; A=110-214.
 DR PDB; 1U7M; NMR; A=337-394.
 DR PDB; 1KS0; NMR; A=223-282.
 DR PDB; 1QIB; X-ray; A=115-216.
 DR PDB; 1RTG; X-ray; @=451-660.
 DR MEROPS; M10.003; -.
 DR Ensembl; ENSG0000087245; Homo sapiens.
 DR HGNC; HGNC:7166; MMP2.
 DR H-invDB; HIX0013041; -.
 DR MIM; 120360; -.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0004228; F:gelatinase A activity; TAS.
 DR GO; GO:0008270; F:zinc ion binding; TAS.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
 DR InterPro; IPR000562; FN_type2_col_bd.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR006026; Peptidase_M.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRXIN.
 DR ProDom; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRXIN.
 DR ProDom; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMG; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00023; FN2_1; 2.
 DR PROSITE; PS51092; FN2_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00059; FN2; 3.
 DR PROSITE; PS00023; FN2_1; 3.
 DR PROSITE; PS51092; FN2_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.

DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW 3D-structure; Calcium; Collagen degradation;
 KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
 KW Hydrolase; Metal-binding; Metalloprotease; Polymorphism; Protease;
 KW Repeat; Signal; Zinc; Zymogen.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 109 Activation peptide.
 FT CHAIN 110 660 72 kDa type IV collagenase.
 FT DOMAIN 228 276 Fibronectin type-II 1.
 FT DOMAIN 286 334 Fibronectin type-II 2.
 FT DOMAIN 344 392 Fibronectin type-II 3.
 FT DOMAIN 466 660 Hemopexin-like.
 FT REGION 110 221 Collagenase-like 1.
 Query Match 100.0%; Score 29; DB 1; Length 660;
 Best Local Similarity 100.0%; Pred. No. 3.le+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KAVFFA 6
 Db 531 KAVFFA 536
 RESULT 14
 ID Q51Y21_TUPGB PRELIMINARY; PRT; 660 AA.
 AC Q51Y21;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Matrix metalloproteinase 2.
 OS Tupaiia glis belangeri (Common tree shrew).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupaiia.
 OC NCBI_TaxID=37347;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15621657; DOI=10.1080/10425170400012925;
 RA Kenning M.S., Gentile A., McBrien N.A.;
 RT "Expression and cDNA sequence of matrix metalloproteinase-2 (MMP-2) in
 a mammalian model of human disease processes: Tupaiia belangeri.";
 RL DNA Seq. 15:332-337(2004).
 DR EMBL; AY600958; AAY44903.1; -; mRNA.
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000562; FN_type2_col_bd.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR006026; Peptidase_M.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRXIN.
 DR ProDom; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMG; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00023; FN2_1; 2.
 DR PROSITE; PS51092; FN2_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00059; FN2; 3.
 KW Calcium; Hydrolase; Metal-binding; Metalloprotease; Protease; Zinc.
 SQ SEQUENCE 660 AA; 73871 MW; FCTEB8481091C5ED CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 660;
 Best Local Similarity 100.0%; Pred. No. 3.le+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 KAVFFA 6
DB      531 KAVFFA 536

RESULT 15
Q95JAA4_PIG PRELIMINARY; PRT; 661 AA.
AC Q95JAA4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gelatinase A.
GN Name=MMP-2;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
NCBI_TaxID=9823;
RN [1]
NUCLEOTIDE SEQUENCE.
RC TISSUE=Tooth enamel organ;
RX MEDLINE=21480581; PubMed=11597028;
RA Caron C., Xue J., Sun X., Simmer J.P., Bartlett J.D.;
RT "Gelatinase A (MMP-2) in developing tooth tissues and amelogenin
RT hydrolysis.";
RL J. Dent. Res. 80:1660-1664(2001).
DR EMBL; AF295805; AAK97133.1; -; mRNA.
DR HSSP; P08253; IGXD.
DR MEROPS; M10.003; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase M10; 1.
DR PRINTS; PR00138; MATRINX.
DR PROSITE; PS000546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMC; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PRINTS; PR00138; MATRINX.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMC; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 661 AA; 73669 MW; 41CD448BD72D2CC2 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      532 KAVFFA 537

RESULT 16
Q9GLE5_BOVIN PRELIMINARY; PRT; 661 AA.
AC Q9GLE5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Matrix metalloproteinase 2.
OS Bos taurus (Bovine).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
NUCLEOTIDE SEQUENCE.
RA Yan L., Zhang B., Teang P., Fang J., Yu Y., Ingber D.E., Moses M.A.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF290428; AAG28169.1; -; mRNA.
DR HSSP; P08253; IGXD.
DR MEROPS; M10.003; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase M10; 1.
DR PRINTS; PR00138; FNTYPEII.
DR PRINTS; PR00138; MATRINX.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMC; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Metalloprotease; Protease.
SQ SEQUENCE 661 AA; 73776 MW; 90545F7645E5F84D CRC64;

Query Match 100.0%; Score 29; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      532 KAVFFA 537

RESULT 17
MMP2_MOUSE STANDARD; PRT; 662 AA.
ID MMP2_MOUSE
AC P33434;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
GN Name=Mmp2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
NUCLEOTIDE SEQUENCE.
RA Reponen P., Sahlberg C., Huhtala P., Hurskainen T., Thesleff I.,
RA Tryggvason K.;
RT "Molecular cloning of murine 72-kDa type IV collagenase and its
RT expression during mouse development.";
RL J. Biol. Chem. 267:7856-7862(1992).
RN [2]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

```

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan A.H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP DEVELOPMENTAL STAGE.
RC TISSUE=Embryo;
RX PubMed=274464;
RA Brenner C.A., Adler R.R., Rappolee D.A., Pedersen R.A., Werb Z.;
RT "Genes for extracellular-matrix-degrading metalloproteinases and their
RT inhibitor, TIMP, are expressed during early mammalian development.";
RL Genes Dev. 3:848-859 (1989).
CC -|- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types
CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-|-
CC Ile-Ala-Gly-Gln.
CC -|- COFACTOR: Binds 4 calcium ions per subunit (By similarity).
CC -|- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
CC -|- SUBUNIT: Ligand for integrin alpha-V/beta-3.
CC -|- DEVELOPMENTAL STAGE: Present in unfertilized eggs and at the
CC zygote and cleavage stages. Levels increase at the blastocyst
CC stage and with endoderm differentiation.
CC -|- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-
CC MMP3) (By similarity).
CC -|- SIMILARITY: Belongs to the peptidase M10A family.
CC -|- SIMILARITY: Contains 3 fibronectin type-II domains.
CC -|- SIMILARITY: Contains 1 hemopexin-like domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M84324; AAA39338.1; -; mRNA.
CC EMBL; BC070430; AAH70430.1; -; mRNA.
CC PIR; A42496; A42496.
CC HSP; P08253; LRTG.
CC MEROPS; M10.003; -.
CC Ensembl; ENSMUSG00000031740; Mus musculus.
CC MGI; MGI:97009; Mmp2.
CC GO; GO:0005615; C:extracellular space; TAS.
CC InterPro; IPR000562; FN type2 col_bd.
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR001818; Pept_M10A_M12B.
CC InterPro; IPR006025; Pept_M_Zn_BS.
CC InterPro; IPR006026; Peptidase_M.
CC Pfam; PF00040; fn2; 3.
CC Pfam; PF00045; Hemopexin; 4.
CC Pfam; PF00413; Peptidase_M10; 1.
CC Pfam; PF03933; Peptidase_M10_N; 1.
CC PRINTS; PR00013; FNTYPEII.
CC PRINTS; PR00138; MATRILIX.
CC ProDom; PD000995; FN Type_II; 3.
CC SMART; SM00059; FN2; 3.
CC SMART; SM00120; HK; 4.
CC SMART; SM00235; ZnMc; 1.
CC PROSITE; PS00546; CYSTEINE_SWITCH; 1.
CC PROSITE; PS00023; FN2_1; 3.

DR PROSITE; PS51092; FN2_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
KW Hydrolase; Metal-binding; Metalloprotease; Protease; Repeat; Signal;
KW Zinc; Zymogen.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 109 Activation peptide.
FT CHAIN 110 662 72 kDa type IV collagenase.
FT FIBRONECTIN 228 276 Fibronectin type-II 1.
FT FIBRONECTIN 286 334 Fibronectin type-II 2.
FT FIBRONECTIN 344 392 Fibronectin type-II 3.
FT DOMAIN 468 662 Hemopexin-like.
FT REGION 110 221 Collagenase-like 1.
FT REGION 222 396 Collagen-binding.
FT REGION 397 467 Collagenase-like 2.
FT ACT_SITE 404 404 By similarity.
FT METAL 134 134 Calcium 1 (By similarity).
FT METAL 168 168 Calcium 2 (By similarity).
FT METAL 178 178 Zinc 1 (By similarity).
FT METAL 180 180 Zinc 1 (By similarity).
FT METAL 185 185 Calcium 3 (By similarity).
FT METAL 186 186 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 193 193 Zinc 1 (By similarity).
FT METAL 200 200 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 202 202 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 204 204 Calcium 2 (By similarity).
FT METAL 206 206 Zinc 1 (By similarity).
FT METAL 208 208 Calcium 3 (By similarity).
FT METAL 209 209 Calcium 1 (By similarity).
FT METAL 211 211 Calcium 3 (By similarity).
FT METAL 403 403 Zinc 2 (catalytic) (By similarity).
FT METAL 407 407 Zinc 2 (catalytic) (By similarity).
FT METAL 413 413 Zinc 2 (catalytic) (By similarity).
FT METAL 478 478 Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL 523 523 Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL 571 571 Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL 620 620 Calcium 4 (via carbonyl oxygen) (By similarity).
FT SITE 102 102 Cysteine switch (Potential).
FT CARBOHYD 575 575 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 644 644 N-linked (GLCNAC. .) (Potential).
FT DISULFID 471 562 By similarity.
SQ SEQUENCE 662 AA; 74102 MW; C630A7DBDB272F02 CRC64;
Query Match 100.0%; Score 29; DB 1; Length 662;
Best Local Similarity 100.0%; Pred. No. 3.le+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
DB 533 KAVFFA 538
RESULT 18
MMP2_RABIT
ID MMP2_RABIT STANDARD; PRT; 662 AA.
AC P50757;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
GN Name=MMP2;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;

FT	METAL	193	Zinc 1 (By similarity).
FT	METAL	200	Calcium 2 (via carbonyl oxygen) (By similarity).
FT	FT		Calcium 2 (via carbonyl oxygen) (By similarity).
FT	METAL	202	Calcium 2 (via carbonyl oxygen) (By similarity).
FT	FT		Calcium 2 (By similarity).
FT	METAL	204	Zinc 1 (By similarity).
FT	METAL	206	Calcium 3 (By similarity).
FT	METAL	208	Calcium 1 (By similarity).
FT	METAL	209	Calcium 3 (By similarity).
FT	METAL	211	Zinc 2 (catalytic) (By similarity).
FT	METAL	403	Zinc 2 (catalytic) (By similarity).
FT	METAL	407	Zinc 2 (catalytic) (By similarity).
FT	METAL	433	Calcium 4 (via carbonyl oxygen) (By similarity).
FT	METAL	478	Calcium 4 (via carbonyl oxygen) (By similarity).
FT	METAL	523	Calcium 4 (via carbonyl oxygen) (By similarity).
FT	FT		Calcium 4 (via carbonyl oxygen) (By similarity).
FT	METAL	571	Calcium 4 (via carbonyl oxygen) (By similarity).
FT	FT		Calcium 4 (via carbonyl oxygen) (By similarity).
FT	METAL	620	Cysteine switch (Potential).
FT	FT	102	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	575	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	644	By similarity.
FT	DISULFID	471	By similarity.
FT	SEQUENCE	662 AA; 73803 MW; 1CC246B270E440C8 CRC64;	
SQ			

Query Match	100.0%;	Score 29;	DB 1;	Length 662;
Best Local Similarity	100.0%;	Pred. No. 3.1e-02;		
Matches 6;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1 KAVFFPA 6
Db	533 KAVFFPA 538

RESULT 19				
MMP2_RAT				
ID	MMP2_RAT	STANDARD;	PRT;	662 AA.
AC	P3436;	P97581;		
DT	01-FEB-1994	(Rel. 28, Created)		
DT	01-FEB-1994	(Rel. 28, Last sequence update)		
DT	13-SEP-2005	(Rel. 48, Last annotation update)		
DE	72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).			
DE	GN	Name=Mmp2;		
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muridea; Muridae; Murinae; Rattus.			
OC	NCBI_TaxID=10116;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=93249363; PubMed=7916617;			
RA	Marti H.P., McNeil L., Davies M., Martin J., Lovett D.H.;			
RT	"Homology cloning of rat 72 kDa type IV collagenase: cytokine and second-messenger inducibility in glomerular mesangial cells.";			
RL	Biochem. J. 291:441-446(1993).			
RL	[2]			
RN	NUCLEOTIDE SEQUENCE.			
RP	STRAIN=Wistar; TISSUE=Skin;			
RC	Okada A., Basset P.;			
RA	"The cloning of the cDNA encoding rat gelatinase A from a rat skin wound cDNA library.";			
RT				
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.			
CC	-I- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types			
CC	IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly- -			
CC	ile-Ala-Gly-Gln.			
CC	-I- COFACTOR: Binds 4 calcium ions per subunit (By similarity).			
CC	-I- COFACTOR: Binds 2 zinc ions per subunit (By similarity).			
CC	-I- SUBUNIT: Ligand for integrin alpha-V/beta-3.			
CC	-I- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-MMP3) (By similarity).			

CC -!- SIMILARITY: Belongs to the peptidase M10A family.
 CC -!- SIMILARITY: Contains 3 fibronectin type-II domains.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: X71466; CAA50583.1; -; mRNA.
 CC EMBL: U65656; AAB41692.1; -; mRNA.
 CC PIR: S34780; S34780.
 CC HSSP: P08253; 1RTG.
 CC MEROPS: M10.003; -.
 CC RGD: 621316; Mmp2.
 CC GO: GO:0004228; F.gelatinase A activity; IDA.
 CC GO: GO:0008237; F.metalloproteinase activity; TAS.
 CC InterPro: IPR000562; FN_type2_col_bd.
 CC InterPro: IPR000585; Hemopexin.
 CC InterPro: IPR001818; Pept_M10A_M12B.
 CC InterPro: IPR006025; Pept_M_Zn_BS.
 CC InterPro: IPR006026; Peptidase_M.
 CC Pfam: PF00040; fn2; 3.
 CC Pfam: PF00045; Hemopexin; 4.
 CC Pfam: PF00413; Peptidase M10; 1.
 CC Pfam: PF03933; Peptidase M10_N; 1.
 CC PRINTS: PR00013; FNTYPEII.
 CC PRINTS: PR00138; MATRXIN.
 CC ProDom: PD000995; FN_Type_II; 3.
 CC SMART: SM00059; FN2; 3.
 CC SMART: SM00120; HX; 4.
 CC SMART: SM00235; ZnMc; 1.
 CC PROSITE: PS00546; CYSTEINE_SWITCH; 1.
 CC PROSITE: PS00023; FN2_1; 3.
 CC PROSITE: PS10922; FN2_2; 3.
 CC PROSITE: PS00024; HEMOPEXIN; 1.
 CC PROSITE: PS00142; ZINC_PROTEASE; 1.
 CC KEGG: Collagen degradation; Extracellular matrix; Glycoprotein;
 KW Hydrolase; Metal-binding; Metalloprotease; Protease; Repeat; Signal;
 KW Zinc; Zymogen.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 109 Activation peptide.
 FT CHAIN 110 662 72 kDa type IV collagenase.
 FT DOMAIN 228 276 Fibronectin type-II 1.
 FT DOMAIN 286 334 Fibronectin type-II 2.
 FT DOMAIN 344 392 Fibronectin type-II 3.
 FT DOMAIN 468 662 Hemopexin-like.
 FT REGION 110 221 Collagenase-like 1.
 FT REGION 222 396 Collagen-binding.
 FT REGION 397 457 Collagenase-like 2.
 FT ACT_SITE 404 404 By similarity.
 FT METAL 134 134 Calcium 1 (By similarity).
 FT METAL 168 168 Calcium 2 (By similarity).
 FT METAL 178 178 Zinc 1 (By similarity).
 FT METAL 180 180 Zinc 1 (By similarity).
 FT METAL 185 185 Calcium 3 (By similarity).
 FT METAL 186 186 Calcium 3 (via carbonyl oxygen) (By similarity).
 FT METAL 193 193 Zinc 1 (By similarity).
 FT METAL 200 200 Calcium 2 (via carbonyl oxygen) (By similarity).
 FT METAL 202 202 Calcium 2 (via carbonyl oxygen) (By similarity).
 FT METAL 204 204 Calcium 2 (By similarity).
 FT METAL 206 206 Zinc 1 (By similarity).
 FT METAL 208 208 Calcium 3 (By similarity).
 FT METAL 209 209 Calcium 1 (By similarity).
 FT METAL 211 211 Calcium 3 (By similarity).
 FT METAL 403 403 Zinc 2 (catalytic) (By similarity).
 FT METAL 407 407 Zinc 2 (catalytic) (By similarity).
 FT METAL 413 413 Zinc 2 (catalytic) (By similarity).
 FT METAL 478 478 Calcium 4 (via carbonyl oxygen) (By similarity).

FT METAL 523 523 similarity).
 FT METAL 571 571 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT METAL 620 620 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT SITE 102 102 Cysteine switch (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 644 644 N-linked (GlcNAc...) (Potential).
 FT DISULFID 471 662 By similarity.
 FT CONFLICT 42 42 A -> S (in Ref. 2).
 FT CONFLICT 286 286 A -> G (in Ref. 2).
 FT CONFLICT 369 369 N -> S (in Ref. 2).
 FT CONFLICT 435 435 H -> N (in Ref. 2).
 FT CONFLICT 586 586 A -> S (in Ref. 2).
 SQ SEQUENCE 662 AA; 74182 MW; 7496B34B0A21884B CRC64;
 Query Match 100.0%; Score 29; DB 1; Length 662;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 DB 533 KAVFFA 538
 |||||
 |||||
 RESULT 20
 Q6GWM9 RAT PRELIMINARY; PRT; 662 AA.
 ID Q6GWM9 RAT PRELIMINARY;
 AC Q6GWM9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Mmp2 protein.
 GN Name=Mmp2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Roark S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RG NIH MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC074013; AAH74013.1; -; mRNA.
 DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO: GO:0004222; P:metalloendopeptidase activity; IEA.


```

DR GO: GO:0008270; P: zinc ion binding; IEA.
DR GO: GO:000508; P: proteolysis and peptidolysis; IEA.
DR InterPro: IPR000562; FN type2_col_bd.
DR InterPro: IPR000585; Hemopexin.
DR InterPro: IPR001818; Pept_M10A_M12B.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR InterPro: IPR006026; Peptidase_M.
DR Pfam: PF00040; fn2; 3.
DR Pfam: PF00045; Hemopexin; 4.
DR Pfam: PF00413; Peptidase_M10; 1.
DR Pfam: PF03933; Peptidase_M10_N; 1.
DR PRINTS: PR00013; FNTYPEII.
DR PRINTS: PR00138; MATRIKIN.
DR SMART: SM00120; HX; 4.
DR SMART: SM0059; FN2; 3.
DR SMART: SM00235; ZnMc; 1.
DR PROSITE: PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE: PS00023; FN2_1; 3.
DR PROSITE: PS1092; FN2_2; 3.
DR PROSITE: PS00024; HEMOPEXIN; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
KW Calcium; Hydrolase; Metal-binding; Metalloprotease; Protease; Zinc.
SQ SEQUENCE 662 AA; 74149 MW; C56BD787473FC03E CRC64;

Query March 100.0%; Score 29; DB 2; Length 662;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 533 KAVFFA 538

RESULT 21
MMP2 CHICK
ID _MMP2 CHICK STANDARD; PRT; 663 AA.
AC Q90611;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
GN Name=MMP2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=94280397; PubMed=8010954;
RA Aimes R.T., French D.L., Quigley J.P.;
RT "Cloning of a 72 kDa matrix metalloproteinase (gelatinase) from
RT chicken embryo fibroblasts using gene family PCR: expression of the
RT gelatinase increases upon malignant transformation.";
RL Biochem. J. 300:729-736(1994).
RN [2]
RP PROTEIN SEQUENCE OF 27-41 AND 107-122.
RX MEDLINE=91161603; PubMed=1848240;
RA Chen J.-M., Aimes R.T., Ward G.R., Youngleib G.L., Quigley J.P.;
RT "Isolation and characterization of a 70-kDa metalloprotease
RT (gelatinase) that is elevated in Rous sarcoma virus-transformed
RT chicken embryo fibroblasts.";
RL J. Biol. Chem. 266:5113-5121(1991).
CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types
CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-|-
CC Ile-Ala-Gly-Gln.
CC -1- COPACITOR: Binds 4 calcium ions per subunit (By similarity).
CC -1- COPACITOR: Binds 2 zinc ions per subunit (By similarity).
CC -1- SUBUNIT: Ligand for integrin alpha-V/beta-3.
CC -1- TISSUE SPECIFICITY: Produced by normal skin fibroblasts.
CC -1- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-

```

```

CC MMP3) (By similarity).
CC -1- SIMILARITY: Belongs to the peptidase M10A family.
CC -1- SIMILARITY: Contains 3 fibronectin type-II domains.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: U07775; AAA19596.1; -; mRNA.
CC PIR: S46492; S46492.
CC HSP: P08253; IQIB.
CC MEROPS: M10.003; -.
CC Ensembl: ENSGALG00000003580; Gallus gallus.
CC InterPro: IPR000562; FN_type2_col_bd.
CC InterPro: IPR000585; Hemopexin.
CC InterPro: IPR001818; Pept_M10A_M12B.
CC InterPro: IPR006025; Pept_M_Zn_BS.
CC InterPro: IPR006026; Peptidase_M.
CC Pfam: PF00040; fn2; 3.
CC Pfam: PF00045; Hemopexin; 4.
CC Pfam: PF00413; Peptidase_M10; 1.
CC Pfam: PF03933; Peptidase_M10_N; 1.
CC PRINTS: PR00013; FNTYPEII.
CC PRINTS: PR00138; MATRIKIN.
CC ProDom: PD000995; FN_Type_II; 3.
CC SMART: SM00059; FN2; 3.
CC SMART: SM00120; HX; 4.
CC SMART: SM00235; ZnMc; 1.
CC PROSITE: PS00546; CYSTEINE_SWITCH; 1.
CC PROSITE: PS00023; FN2_1; 3.
CC PROSITE: PS1092; FN2_2; 3.
CC PROSITE: PS00024; HEMOPEXIN; 1.
CC PROSITE: PS00142; ZINC_PROTEASE; 1.
KW Calcium; Collagen degradation; Direct protein sequencing;
KW Extracellular matrix; Hydrolase; Metal-binding; Metalloprotease;
KW Protease; Repeat; Signal; Zinc; Zymogen.
FT SIGNAL 1 26
FT PROPEP 27 106 Activation peptide.
FT CHAIN 107 663 72 kDa type IV collagenase.
FT DOMAIN 225 273 Fibronectin type-II 1.
FT DOMAIN 283 331 Fibronectin type-II 2.
FT DOMAIN 341 389 Fibronectin type-II 3.
FT DOMAIN 469 663 Hemopexin-like.
FT REGION 107 218 Collagenase-like 1.
FT REGION 219 393 Collagen-binding.
FT REGION 394 468 Collagenase-like 2.
FT ACT_SITE 401 401 By similarity.
FT METAL 131 131 Calcium 1 (By similarity).
FT METAL 165 165 Calcium 2 (By similarity).
FT METAL 175 175 Zinc 1 (By similarity).
FT METAL 177 177 Zinc 1 (By similarity).
FT METAL 182 182 Calcium 3 (By similarity).
FT METAL 183 183 Calcium 3 (via carbonyl oxygen) (By
FT METAL 190 190 similarity).
FT METAL 197 197 Zinc 1 (By similarity).
FT METAL 199 199 Calcium 2 (via carbonyl oxygen) (By
FT METAL 201 201 similarity).
FT METAL 203 203 Calcium 2 (By similarity).
FT METAL 205 205 Zinc 1 (By similarity).
FT METAL 206 206 Calcium 3 (By similarity).
FT METAL 208 208 Calcium 3 (By similarity).
FT METAL 400 400 Zinc 2 (catalytic) (By similarity).
FT METAL 404 404 Zinc 2 (catalytic) (By similarity).
FT METAL 410 410 Zinc 2 (catalytic) (By similarity).
FT METAL 479 479 Calcium 4 (via carbonyl oxygen) (By
FT METAL 524 524 similarity).
FT METAL 524 524 Calcium 4 (via carbonyl oxygen) (By

```

```

FT METAL 572 572 similarity).
FT Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT METAL 621 621 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT SITE 99 99 Cysteine switch (Potential).
FT DISULFID 472 663 By similarity.
FT CONFLICT 40 40 P -> Q (in Ref. 2).
FT CONFLICT 116 116 W -> T (in Ref. 2).
FT CONFLICT 122 122 T -> I (in Ref. 2).
SQ SEQUENCE 663 AA; 74941 MW; 8D6FDA4E67C3EBCA CRC64;

Query Match 100.0%; Score 29; DB 1; Length 663;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 534 KAVFFA 539

RESULT 22
Q8KTW1_CLODI PRELIMINARY; PRT; 767 AA.
AC Q8KTW1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Surface layer protein A.
OS Clostridium difficile.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1496;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkely;
RX MEDLINE=22077258; PubMed=12081960;
RX DOI=10.1128/JB.184.14.3886-3897.2002;
RA Calabi E., Fairweather N.;
RT "Patterns of sequence conservation in the S-layer proteins and related
sequences in Clostridium difficile."
RL J. Bacteriol. 184:3886-3897(2002).
DR EMBL; AF478571; AAM46790.1; -; Genomic_DNA.
DR InterPro; IPR007253; CW.binding_2.
DR Pfam; PF04122; CW.binding_2; 3.
SQ SEQUENCE 767 AA; 81461 MW; 7280626184495D70 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 767;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 358 KAVFFA 363

RESULT 23
Q7XX63_ORYSA PRELIMINARY; PRT; 770 AA.
AC Q7XX63;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE OSJNBa0052P16.14 protein.
GN Name=OSJNBa0052P16.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12447439; DOI=10.1038/nature01183;

```

```

RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4."
RL Nature 420:316-320(2002).
DR EMBL; AL662936; CAD39717.1; -; Genomic_DNA.
DR Gramene; Q7XX63; -;
DR GO; GO:0016829; P:lyase activity; IEA.
DR GO; GO:0000287; P:magnesium ion binding; IEA.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR001906; Terp synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth C; 2.
SQ SEQUENCE 770 AA; 86360 MW; 6CFAB6855D904EE1 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 555 KAVFFA 560

RESULT 24
Q66QH3_ORYSA PRELIMINARY; PRT; 840 AA.
AC Q66QH3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Syn-pinara-7.15-diene synthase.
OS Oryza sativa (indica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39946;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15299118; DOI=10.1104/pp.104.045971;
RX Wilderman P.R., Xu M., Jin Y., Coates R.M., Peters R.J.;
RT "Identification of syn-pinara-7,15-diene synthase reveals functional
clustering of terpene synthases involved in rice
phytoalexin/allelochemical biosynthesis."
RL Plant Physiol. 135:2098-2105(2004).
DR EMBL; AY616862; AAU05906.1; -; mRNA.
DR Gramene; Q66QH3; -;
DR GO; GO:0016829; P:lyase activity; IEA.
DR GO; GO:0000287; P:magnesium ion binding; IEA.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR001906; Terp synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth C; 1.
SQ SEQUENCE 840 AA; 94757 MW; B0ECC89323C86ASE CRC64;

Query Match 100.0%; Score 29; DB 2; Length 840;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 625 KAVFFA 630

```

```
RESULT 25
Q60HB5_ORYSA
ID Q60HB5_ORYSA PRELIMINARY; PRT; 842 AA.
AC Q60HB5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 9b-pimara-7,15-diene synthase.
GN Name=OsK54;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1538982; DOI=10.1271/bbb.68.2001;
RA Oikawa K., Kanno Y., Motegi A., Kenmoku H., Yamane H., Mitsuhashi W.,
RA Oikawa H., Toshima H., Itoh H., Matsuo M., Sassa T., Toyomae T.;
RT "Diterpene cyclases responsible for the biosynthesis of phytoalexins,
RT momilactones A, B, and oryzaalexins A-F in rice.";
RL Biosci. Biotechnol. Biochem. 68:2001-2006(2004).
DR EMBL; AB126934; BAD54751.1; -; mRNA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth C; 1.
SQ SEQUENCE 842 AA; 94868 MW; 928F88F8FCC35497 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 842;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 627 KAVFFA 632

RESULT 26
Q69DS7_ORYSA
ID Q69DS7_ORYSA PRELIMINARY; PRT; 842 AA.
AC Q69DS7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Ent-kaurene synthase like-4.
GN Name=OsK54;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15668792; DOI=10.1007/s00299-004-0896-6;
RA Margis-Pinheiro M., Zhou X.R., Zhu Q.H., Dennis E.S., Upadhyaya N.M.;
RA "Isolation and characterization of a Ds-tagged rice (Oryza sativa L.)
RT GA-responsive dwarf mutant defective in an early step of the
RT gibberellin biosynthesis pathway.";
RL Plant Cell Rep. 23:819-833(2005).
DR EMBL; AY347880; AAQ72563.1; -; mRNA.
DR Gramene; Q69DS7; -
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.

Query Match 100.0%; Score 29; DB 2; Length 842;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 627 KAVFFA 632

RESULT 27
Q9N175_SHEEP
ID Q9N175_SHEEP PRELIMINARY; PRT; 945 AA.
AC Q9N175;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inducible nitric oxide synthase (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22168784; PubMed=12181148;
RA Merhosh J.L., Baker R.S., Clark K.E.;
RT "Estrogen increases iNOS expression in the ovine coronary artery.";
RA Am. J. Physiol. Heart Circ. Physiol. 283:H1169-H1180(2002).
RL EMBL; AF223942; AAF34710.1; -; mRNA.
DR HSSP; P35228; INSI.
DR SNR; Q9N175; 1-326.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0045585; P:positive regulation of cytotoxic T-cell dif. .; ISS.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin-like.
DR InterPro; IPR008254; Flav_nitox synth.
DR InterPro; IPR001709; FPN_Cyt_reductase.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; OxRed_FAD/NAD(P).
DR Pfam; PF00667; FAD binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR Pfam; PF02898; NO synthase; 1.
DR PIRSF; PIRSF00033; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; PFNCR.
DR PROSITE; PS50902; FLAVODOXIN_LIKE; 1.
DR PROSITE; PS50001; NOS; UNKNOWN_1.
FT NON_TER 1 1
FT NON_TER 945 945
SQ SEQUENCE 945 AA; 108001 MW; 9A5ACFD40440A74F CRC64;

Query Match 100.0%; Score 29; DB 2; Length 945;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 344 KAVFFA 349

RESULT 28
NOS2_RAT
```

ID NOS2 RAT STANDARD; PRT; 1147 AA.
 AC Q06518; Q35765; Q35766; Q60591; Q60604; P97774; Q63267; Q64005;
 AC Q64558;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
 DE (Inducible NOS) (iNOS).
 GN Name=Nos2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Vascular smooth muscle;
 RX MEDLINE=931191721; PubMed=7680561;
 RA Nunokawa Y., Ishida N., Tanaka S.;
 RT "Cloning of inducible nitric oxide synthase in rat vascular smooth
 muscle cells.";
 RL Biochem. Biophys. Res. Commun. 191:89-94(1993).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Pancreatic islets;
 RX MEDLINE=95309542; PubMed=7540573;
 RA Karleen A.E., Andersen H.U., Vissing H., Larsen P.M., Fey S.J.,
 RA Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,
 RA Mandrup-Poulsen T., Boel E., Nerup J.;
 RT "Cloning and expression of cytokine-inducible nitric oxide synthase
 cDNA from rat islets of Langerhans.";
 RL Diabetes 44:753-758(1995).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Astrocyles;
 RX MEDLINE=942311594; PubMed=7513765;
 RA Galea E., Reis D.J., Feinstein D.L.;
 RT "Cloning and expression of inducible nitric oxide synthase from rat
 astrocytes.";
 RL J. Neurosci. Res. 37:406-414(1994).
 RN [4]
 RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94039059; PubMed=7693462;
 RA Adachi H., Iida S., Oguchi S., Ohehima H., Suzuki H., Nagasaki K.,
 RA Kawasaki H., Sugimura T., Esumi H.;
 RT "Molecular cloning of a cDNA encoding an inducible calmodulin-
 dependent nitric-oxide synthase from rat liver and its expression in
 COS 1 cells.";
 RL Eur. J. Biochem. 217:37-43(1993).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Hepatocyte;
 RX MEDLINE=93221515; PubMed=7682072;
 RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
 RT "Hepatocytes and macrophages express an identical cytokine inducible
 nitric oxide synthase gene.";
 RL Biochem. Biophys. Res. Commun. 191:767-774(1993).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Aorta;
 RX MEDLINE=94325351; PubMed=7519448; DOI=10.1016/0167-4781(94)90196-1;
 RA Geng Y.J., Almqvist M., Hansson G.K.;
 RT "cDNA cloning and expression of inducible nitric oxide synthase from
 rat vascular smooth muscle cells.";
 RL Biochim. Biophys. Acta 1218:421-424(1994).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RA Kosuga K., Yui Y., Hattori R., Sase K., Bizawa H., Aoyama T.,
 RA Inoue R., Sasayama S.;
 RT "Cloning of an inducible nitric oxide synthase from rat
 polymorphonuclear neutrophils.";
 RL Endothelium 2:217-221(1994).

RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97070590; PubMed=8913516;
 RA Tezumi-shita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,
 RA Fukaki S., Niwa M.;
 RT "Sequence analysis of inducible nitric oxide synthase in rat kidney,
 lung, and uterus.";
 RL Biol. Pharm. Bull. 19:1374-1376(1996).
 RN [9]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99066690; PubMed=9851365; DOI=10.1006/niox.1998.0184;
 RA Adams V., Krabbes S., Jiang H., Yu J., Rahmel A., Gielen S.,
 RA Schuler G., Hambrecht R.;
 RT "Complete coding sequence of inducible nitric oxide synthase from
 human heart and skeletal muscle of patients with chronic heart
 failure.";
 RL Nitric Oxide 2:242-249(1998).
 RN [10]
 RP NUCLEOTIDE SEQUENCE OF 426-788.
 RC STRAIN=Dahl/Rapp salt sensitive strain; TISSUE=Vascular smooth muscle;
 RX MEDLINE=98195092; PubMed=9535415;
 RA Chen P.Y., Gladish R.D., Sanders P.W.;
 RT "Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp
 salt-sensitive rats.";
 RL Hypertension 31:918-924(1998).
 RN [11]
 RP NUCLEOTIDE SEQUENCE OF 509-740.
 RC STRAIN=Wistar; TISSUE=Renal glomerulus;
 RA Saura M., Zaragoza C., Martinez-Balmar R., Perez-Sala D., Lamas S.;
 RT "Advances in the studies of NO synthesis regulation in mesangial
 cells.";
 RL Nephrologia 16:35-39(1996).
 RN [12]
 RP NUCLEOTIDE SEQUENCE OF 479-655.
 RC STRAIN=Sprague-Dawley; TISSUE=Renal glomerulus;
 RX MEDLINE=94276509; PubMed=7516453;
 RA Morrissey J.J., McCracken R., Kaneto H., Vehaskari M., Montani D.,
 RA Klahr S.;
 RT "Location of an inducible nitric oxide synthase mRNA in the normal
 kidney.";
 RL Kidney Int. 45:998-1005(1994).
 RN [13]
 RP NUCLEOTIDE SEQUENCE OF 420-479.
 RC TISSUE=Myocardium;
 RA Michel T., Balligand J.-L.;
 RT "Isolation and characterization of iNOS from rat cardiocytes.";
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule
 with diverse functions throughout the body.
 CC -!- CATALYTIC ACTIVITY: L-arginine + n NADPH + m O(2) = citrulline +
 nitric oxide + n NADP(+).
 CC -!- COFACTOR: Heme.
 CC -!- COFACTOR: FAD. Binds 1 mole of FAD.
 CC -!- COFACTOR: FMN. Binds 1 mole of FMN.
 CC -!- COFACTOR: Tetrahydrobiopterin (BH4). May stabilize the dimeric
 form of the enzyme.
 CC -!- ENZYME REGULATION: Not stimulated by calcium/calmodulin. Aspirin
 inhibits expression and function of this enzyme and effects may be
 exerted at the level of translational/posttranslational
 modification and directly on the catalytic activity (By
 similarity).
 CC -!- SUBUNIT: Homodimer. Binds SLC9A3R1 (By similarity).
 CC -!- TISSUE SPECIFICITY: In normal kidney, expressed primarily in the
 medullary thick ascending limb, with minor amounts in the
 medullary collecting duct and vasa recta bundle.
 CC -!- INDUCTION: By interferon gamma and lipopolysaccharides (LPS).
 CC -!- SIMILARITY: Belongs to the NOS family.
 CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.
 CC -!- CAUTION: Ref.9 sequence was originally thought to originate from
 human but appears to be from rat.

 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC -----
 DR EMBL; D14051; BAA03138.1; -; mRNA.
 DR EMBL; U26686; AAB5861.1; -; mRNA.
 DR EMBL; U03699; AAC13747.1; -; mRNA.
 DR EMBL; D12520; BAA02090.1; -; mRNA.
 DR EMBL; L12562; AAA41720.1; -; mRNA.
 DR EMBL; X76881; CAA54208.1; -; mRNA.
 DR EMBL; D44591; BAA07994.1; -; mRNA.
 DR EMBL; D83661; BAA12035.1; -; mRNA.
 DR EMBL; AF049656; AAC83553.1; -; mRNA.
 DR EMBL; AF051164; AAC83554.1; -; mRNA.
 DR EMBL; AF006619; AAC16401.1; -; mRNA.
 DR EMBL; AF006620; AAC16402.1; -; mRNA.
 DR EMBL; U48829; AAB18620.1; -; mRNA.
 DR EMBL; S71597; AAB31028.2; -; mRNA.
 DR EMBL; L36063; AAC02242.1; -; mRNA.
 DR PIR; I53165; I53165.
 DR PIR; I56575; I56575.
 DR PIR; JC5027; JC5027.
 DR PIR; S38253; S38253.
 DR PIR; S47647; S47647.
 DR HSP; P29477; INOS.
 DR SMR; Q6518; 80-499.
 DR Ensembl; ENSRNOG0000011023; Rattus norvegicus.
 DR RGD; 3185; Nos2.
 DR GO; GO:0005829; C:cytosol; ISS.
 DR GO; GO:0005516; F:calmodulin binding; ISS.
 DR GO; GO:0008603; F:cAMP-dependent protein kinase regulator act. .; IDA.
 DR GO; GO:0020037; F:heme binding; ISS.
 DR GO; GO:0004517; F:nitric-oxide synthase activity; IDA.
 DR GO; GO:0042742; P:defense response to bacteria; ISS.
 DR GO; GO:0007199; P:G-protein signaling, coupled to cGMP nucleo. .; IDA.
 DR GO; GO:0006954; P:inflammatory response; ISS.
 DR GO; GO:0006809; P:nitric oxide biosynthesis; TAS.
 DR GO; GO:0007165; P:signal transduction; IDA.
 DR GO; GO:0006801; P:superoxide metabolism; ISS.
 DR InterPro; IPR003097; FAD bd.
 DR InterPro; IPR008254; Flav nitox synth.
 DR InterPro; IPR001094; Flavodoxin like.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR004030; NO_synthase.
 DR InterPro; IPR012144; NOS.
 DR InterPro; IPR001433; Oxred FAD NAD bd.
 DR PANTHER; PTHR19386; NO_synthase; 1.
 DR Pfam; PF00667; FAD_binding_1; 1.
 DR Pfam; PF00258; Flavodoxin_1; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR PIRSF; PIRSF000333; NOS; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; PFNCR.

Query Match 100.0%; Score 29; DB 1; Length 1147;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||||
 Db 517 KAVFFA 522

RESULT 29

Q6XS76 RAT PRELIMINARY; PRT; 1147 AA.

AC Q6XS76;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Inducible nitric oxide synthase (Fragment).
 GN Name=Nos2;

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Wislar; TISSUE=Aortic smooth muscle;
 RA Cui Z., Tuladhar R., Hart S., Marber M., Pearson J., Baydoun A.R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY211532; AAP43670.1; -; mRNA.
 DR HSP; P29477; 1JWK.
 DR SMR; Q6XS76; 80-499.
 DR GO; GO:0005516; F:calmodulin binding; IEA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0010181; F:FMN binding; IEA.
 DR GO; GO:0004517; F:nitric-oxide synthase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006809; P:nitric oxide biosynthesis; IEA.
 DR InterPro; IPR003097; FAD_binding.
 DR InterPro; IPR001094; Flavodoxin like.
 DR InterPro; IPR008254; Flav nitox synth.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR012144; NOS.
 DR InterPro; IPR004030; NO_synthase.
 DR InterPro; IPR001433; Oxred FAD/NAD(P).
 DR Pfam; PF00667; FAD_binding_1; 1.
 DR Pfam; PF00258; Flavodoxin_1; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR Pfam; PF02898; NO_synthase; 1.
 DR PIRSF; PIRSF000333; NOS; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; PFNCR.
 DR PROSITE; PS50902; FLAVODOXIN LIKE; 1.
 DR PROSITE; PS60001; NOS; UNKNOWN_1.
 FT NON TER 1147 1147
 SQ SEQUENCE 1147 AA; 130673 MW; 204484F2231D9ECA CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1147;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||||
 Db 517 KAVFFA 522

RESULT 30

Q9QW28 9MURI PRELIMINARY; PRT; 1147 AA.

AC Q9QW28;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Cytokine inducible nitric oxide synthase, iNOS.

OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10118;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93221515; PubMed=7682072;
 RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
 RT "Hepatocytes and macrophages express an identical cytokine inducible
 RT nitric oxide synthase gene".
 RL Biochem. Biophys. Res. Commun. 191:767-774 (1993).
 DR HSP; P29477; INOS.
 DR SMR; Q9QW28; 80-499.
 DR GO; GO:0005829; C:cytosol; ISS.
 DR GO; GO:0005516; F:calmodulin binding; ISS.
 DR GO; GO:0020037; F:heme binding; ISS.

```

DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0045585; P:positive regulation of cytotoxic T-cell dif. . .; ISS.
DR GO; GO:0008601; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO_synthase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO_synthase; 1.
DR PIRSF; PIRSF00333; NOS; 1.
DR PRINTS; PRO0369; FLAVODOXIN.
DR PRINTS; PRO0371; FPNCR.
DR PROSITE; PS0902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN_1.
SQ SEQUENCE 1147 AA; 136625 MW; 2CAPB983E56F651A CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1147;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 517 KAVFFA 522

RESULT 31
Q9R0W4_RAT PRELIMINARY; PRT; 1147 AA.
ID Q9R0W4;
AC Q9R0W4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inducible nitric oxide synthase.
GN Name=iNOS;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wistar Kyoto;
RX MEDLINE=93326503; PubMed=10395902; DOI=10.1016/S0378-1119(99)00196-1;
RA Keinänen R.A., Vartiainen N., Koistinaho J.;
RT "Molecular cloning and characterization of the rat inducible nitric
oxide synthase (iNOS) gene.";
RL Gene 234:297-305(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=864711;
RA Iwashina M., Hirata Y., Imai T., Sato K., Marumo F.;
RT "Molecular cloning of endothelial, inducible nitric oxide synthase
gene from rat aortic endothelial cell.";
RL Eur. J. Biochem. 237:668-673(1996).
DR EMBL; AJ230462; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230463; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230465; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230464; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230467; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230469; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230471; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230473; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230475; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230484; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230483; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230482; CAB46089.1; JOINED; Genomic DNA.

```

```

DR EMBL; AJ230481; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230480; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230479; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230478; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230477; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230476; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230487; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230486; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230485; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230474; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230472; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230470; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230468; CAB46089.1; JOINED; Genomic DNA.
DR EMBL; AJ230466; CAB46089.1; JOINED; Genomic DNA.
DR PIR; JC5028; JC5028.
DR PIR; JC5029; JC5029.
DR PIR; S65440; S65440.
DR HSSP; P29477; INOS.
DR SMR; Q9R0W4; 80-499.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0004517; P:nitric-oxide synthase activity; ISS.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD bd.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR004030; NO_synthase.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR001433; Oxred_FAD_NAD_bd.
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO_synthase; 1.
DR PIRSF; PIRSF00333; NOS; 1.
DR PRINTS; PRO0369; FLAVODOXIN.
DR PRINTS; PRO0371; FPNCR.
DR PROSITE; PS0902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN_1.
SQ SEQUENCE 1147 AA; 130614 MW; E76B3F8407D54CF6 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1147;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 517 KAVFFA 522

RESULT 32
Q8Y1S2_RALSO PRELIMINARY; PRT; 118 AA.
ID Q8Y1S2;
AC Q8Y1S2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE PROBABLE SIGNAL PEPTIDE PROTEIN.
GN OrderedLocustNames=RSC0617; ORFNames=RS01518;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Attiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,

```

```

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646060; CAD14147.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 118 AA; 12054 MW; 9559DEA2C16CF42 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 118;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 8 KAIFFA 13

RESULT 33
Q8UI59 AGRT5
ID Q8UI59 AGRT5 PRELIMINARY; PRT; 169 AA.
AC Q8UI59;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Atu0441.
GN OrderedLocuNames=Atu0441.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Dupont;
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V.,
RA Neester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
C58.";
RL Science 294:2317-2323(2001).
DR EMBL; AB009014; AAL41460.1; -; Genomic_DNA.
DR PIR; AF2630; AF2630.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 169 AA; 19428 MW; FDBBB0BAC5D38EB CRC64;

Query Match 96.6%; Score 28; DB 2; Length 169;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 114 KAIFFA 119

RESULT 34
Q19334 CAEEL
ID Q19334 CAEEL PRELIMINARY; PRT; 283 AA.
AC Q19334; Q21599;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein M79.2.
GN ORFNames=M79.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

```

```

OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z50857; CAA90720.1; -; Genomic_DNA.
DR EMBL; Z50806; CAA90692.1; -; Genomic_DNA.
DR EMBL; Z50806; CAA90720.1; JOINED; Genomic_DNA.
DR EMBL; Z50857; CAA90692.1; JOINED; Genomic_DNA.
DR PIR; T20734; T20734.
DR Ensemble; M79.2; Caenorhabditis elegans.
DR WormBase; WBGene00010902; M79.2.
DR WormPep; M79.2; CR03507.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 283 AA; 32582 MW; 51638B43CB266860 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 283;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 157 KAIFFA 162

RESULT 35
Q8EM92 OCEIH
ID Q8EM92 OCEIH PRELIMINARY; PRT; 305 AA.
AC Q8EM92;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical conserved protein.
GN OrderedLocuNames=OB2966;
OS Oceanobacillus ihayensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus ihayensis isolated from the Iheya
Ridge and its unexpected adaptive capabilities to extreme
environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; BA000028; BAC14922.1; -; Genomic_DNA.
DR InterPro; IPR003507; Peptidase U61.
DR Pfam; PF02016; Peptidase U61.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 305 AA; 33528 MW; 6A7F3E282B2B5580 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 305;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   ||:||||
Db 75 KAIFFA 80

RESULT 36
Q6LJY6 PHOPR
ID Q6LJY6 PHOPR PRELIMINARY; PRT; 355 AA.
AC Q6LJY6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

```

```

DE Hypothetical protein.
GN OrderedLocusNames=PBPRB0521;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746425; DOI=10.1126/science.1103341;
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N.,
RA Lauro P.M., Cestaro A., Malacrida G., Simionati B., Camata N.,
RA Romualdi C., Bartlett D.H., Valle G.;
RT "Life at depth: Photobacterium profundum genome sequence and
RT expression analysis.";
RL Science 307:1459-1461(2005).
DR EMBL; CR378676; CAG22394.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 355 AA; 40056 MW; 6A3C866307079447 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 355;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 316 KAIFFA 321

RESULT 37
QBXINS CLOPE
ID QBXINS_CLOPE PRELIMINARY; PRT; 1044 AA.
AC QBXINS;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Alpha-mannosidase.
GN OrderedLocusNames=CPR2080;
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; BA000016; BAB81786.1; -; Genomic DNA.
DR GO; GO:0004559; F:alpha-mannosidase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006013; P:mannose metabolism; IEA.
DR InterPro; IPR000602; Glyco_hydro_38.
DR InterPro; IPR011682; Glyco_hydro_38C.
DR Pfam; PF01074; Glyco_hydro_38; 1.
DR Pfam; PF07748; Glyco_hydro_38C; 1.
KW Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 1044 AA; 121432 MW; 3CAB879447D42B6F CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1044;
Best Local Similarity 83.3%; Pred. No. 8.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 666 KAIFFA 671

RESULT 38
Q19641_CABE

```

```

ID Q19641 CABEEL PRELIMINARY; PRT; 85 AA.
AC Q19641;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Hypothetical protein F20D12.5.
GN ORFNames=F20D12.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- SIMILARITY: Contains 1 LIM zinc-binding domain.
DR EMBL; U40933; AAL27241.1; -; Genomic_DNA.
DR HSSP; P04006; LIML.
DR SMR; Q19641; 2-77.
DR Ensembl; F20D12.5; Caenorhabditis elegans.
DR WormBase; WBGene00017644; F20D12.5.
DR WormPep; F20D12.5; CE29767.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR001781; LIM_Zn_bd.
DR Pfam; PF00412; LIM; 1.
DR ProDom; PD000094; LIM; 1.
DR SMART; SM00132; LIM; 1.
DR PROSITE; PS00023; LIM DOMAIN 2; 1.
KW Complete proteome; Hypothetical protein; LIM domain; Metal-binding;
KW Zinc.
SQ SEQUENCE 85 AA; 9479 MW; 83B93440C82AE849 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 85;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 9 KAVYFA 14

RESULT 39
Q731J0_WOLPM
ID Q731J0_WOLPM PRELIMINARY; PRT; 99 AA.
AC Q731J0;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Oxidoreductase, putative.
GN OrderedLocusNames=WD0173;
OS Wolbachia pipientis wMel.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachieae; Wolbachia.
OX NCBI_TaxID=66077;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15024419; DOI=10.1371/journal.pbio.0020069;
RA Wu M., Sun L.V., Vamathevan J.J., Riegler M., DeBoy R.T.,
RA Brownlie J.C., McGraw E.A., Martin W., Esser C., Ahmadinejad N.,
RA Wigand C., Madupu R., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA Durkin A.S., Kolonay J.P., Nelson W.C., Mohamoud Y., Lee P.,
RA Berry K.J., Young M.B., Utterback T.R., Weidman J.F., Nierman W.C.,
RA Paulsen I.T., Nelson K.E., Tettelin H., O'Neill S.L., Eisen J.A.;
RT "Phylogenomics of the reproductive parasite Wolbachia pipientis wMel:
RT a streamlined genome overrun by mobile genetic elements.";
RL PLOS Biol. 2:327-341(2004).
DR EMBL; AE017256; AAS13922.1; -; Genomic_DNA.
DR TIGR; WD0173; -.

```


PubMed=15210978; DOI=10.1073/pnas.0305659101;
Alsmark U.C.B., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
RRA Candaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,
La Scola B., Holmberg M., Andersson S.G.E.;
"The louse-borne human pathogen Bartonella quintana is a genomic
derivative of the zoonotic agent Bartonella henselae.";
Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
RRL EMBL; EX897699; CAF22754.1; -; Genomic DNA.
DR Complete proteome; Hypothetical protein.
SKW SEQUENCE 126 AA; 14027 MW; 7A632D838151PFAE CRC64;

Query Match 89.7%; Score 26; DB 2; Length 126;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 KAVFFA 6
:|||||
Db 34 RAVFFA 39

RESULT 42
Q6C1M8 YARLI PRELIMINARY; PRT; 131 AA.
AC Q6C1M8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to w|NCU06209.1 Neurospora crassa NCU06209. 1 hypothetical
DE protein.
GN OrderedLocusNames=YALI0F14905g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
NCBI_TaxID=4952;
[1]
Nucleotide sequence [LARGE SCALE GENOMIC DNA].
RP PubMed=15229592; DOI=10.1038/nature02579;
RX Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neveglise C., Talia E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauntaux N., Joyet P., Kachouri R.,
RA Kerratt A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-P., Straub M.-L., Suleau A.,
RA Swennen D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zavanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RL "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
DR EMBL; CR382132; CAG78243.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SKW SEQUENCE 131 AA; 14843 MW; 5D7F9328DBC97E19 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 131;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 KAVFFA 6
:|||||
Db 126 KAVFFS 131

RESULT 43
Q6G346 BARHE PRELIMINARY; PRT; 131 AA.
AC Q6G346;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

```
DE Hypothetical protein.
GN OrderedLocusNames=BH09620;
OS Bartonella henselae (Rochalimaea henselae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bartonellaceae; Bartonella.
OX NCBI_TaxID=38323;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 49882 / Houston 1;
RX PubMed=15210978; DOI=10.1073/pnas.0305659101;
RA Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,
La Scola B., Holmberg M., Andersson S.G.E.;
RT "The louse-borne human pathogen Bartonella quintana is a genomic
RT derivative of the zoonotic agent Bartonella henselae.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
DR EMBL; BX897699; CAF27755.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 131 AA; 14730 MW; 48D91F115B67439 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 131;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   :|||||
DB 34 RAVFFA 39

RESULT 44
QSKK3 THET8
ID Q5SKK3_THET8 PRELIMINARY; PRT; 137 AA.
AC Q5SKK3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein THTA0640.
GN OrderedLocusNames=TTHA0640;
OS Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=300852;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HB8;
RA Masui R., Kurokawa K., Nakagawa N., Tokunaga F., Koyama Y.,
RA Shibata T., Oshima T., Yokoyama S., Yasunaga T., Kuramitsu S.;
RT "Complete genome sequence of Thermus thermophilus HB8.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP008226; BAD70463.1; -; Genomic_DNA.
DR InterPro; IPR007842; HEPN.
DR Pfam; PF05168; HEPN; 1.
DR PROSITE; PS50910; HEPN; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 137 AA; 15304 MW; 37D01C6D9C3287FA CRC64;

Query Match 89.7%; Score 26; DB 2; Length 137;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   :|||||
DB 43 KAVYFA 48

RESULT 45
QAJC95 SULAC
ID QAJC95_SULAC PRELIMINARY; PRT; 142 AA.
AC QAJC95;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Conserved membrane protein.
```

```
GN OrderedLocusNames=Saci_0164;
OS Sulfolobus acidocaldarius.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2285;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 33909 / NCIB 11770 / DSM 639;
RX PubMed=1595215; DOI=10.1128/JB.187.14.4992-4999.2005;
RA Chen L., Bruegger K., Skovgaard M., Redder P., She Q., Torarinsson E.,
RA Greve B., Aways M., Zibat A., Klenk H.-P., Garrett R.A.;
RT "The genome of Sulfolobus acidocaldarius, a model organism of the
RT Crenarchaeota.";
RL J. Bacteriol. 187:4992-4999(2005).
DR EMBL; CP000077; AAY79584.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 142 AA; 16221 MW; 5B92483FA7F864C4 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 142;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   :|||||
DB 82 KSVFFA 87

RESULT 46
QSWU01 LEGPL
ID Q5WU01_LEGPL PRELIMINARY; PRT; 149 AA.
AC Q5WU01;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=lpl2372;
OS Legionella pneumophila (strain Lens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297245;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch P., Kunst P.,
RA Etienne J., Glaser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
DR EMBL; CR628337; CAH16612.1; -; Genomic_DNA.
DR Legioli; lpl2372; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 149 AA; 16274 MW; F698CECF732B0837 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 149;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   :|||||
DB 37 KSVFFA 42

RESULT 47
Q5X274 LEGPA
ID Q5X274_LEGPA PRELIMINARY; PRT; 149 AA.
AC Q5X274;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=lpp2519;
OS Legionella pneumophila (strain Paris).
```

```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297246;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Czalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
DR EMBL; CR28336; CAH13672.1; -; Genomic_DNA.
DR Legionellist; lpp2519; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 149 AA; 16323 MW; 8489CE2861AD3D5A CRC64;

Query Match      89.7%; Score 26; DB 2; Length 149;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 37 KSVFFA 42

RESULT 48
Q5ZSR4 LEGPH
ID Q5ZSR4 LEGPH PRELIMINARY; PRT; 149 AA.
AC Q5ZSR4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN OrderedLocNames=lpq2453;
OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /
ATCC 33152).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=272624;
RN [1]
RP NUCLEOTIDE SEQUENCE
RX PubMed=15448271; DOI=10.1126/science.1099776;
RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA Asamani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,
RA Steshenko V., Park S.H., Zhao B., Teplitzskaya E., Edwards J.R.,
RA Pampou S., Georgiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
RA Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
RA Segal G., Qu X., Rzhetsky A., Zhang P., Cayanis E., De Jong P.J.,
RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
RT "The genomic sequence of the accidental pathogen Legionella
RT pneumophila.";
RL Science 305:1966-1968(2004).
DR EMBL; AB017354; ANU28513.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 149 AA; 16374 MW; 76C1CB2C5D08DF23 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 149;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 37 KSVFFA 42

RESULT 49
Q51314 9NOSO
ID Q51314 9NOSO PRELIMINARY; PRT; 150 AA.
AC Q51314;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24; Last annotation update)

```

```

DE SdNA replicating plasmid encoding a replication-associated protein
DE (repA) and three ORFs, complete cds.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=1180;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Walton D.K., Gendel S.M., Atherly A.G.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M81381; AAA25514.1; -; Genomic_DNA.
DR PIR; S27597; S27597.
SQ SEQUENCE 150 AA; 16660 MW; 7C34D00291E436A6 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 150;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 36 KALFFA 41

RESULT 50
GUAD_BACSU
ID GUAD_BACSU STANDARD; PRT; 156 AA.
AC Q34598;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Guanine deaminase (EC 3.5.4.3) (Guanase) (Guanine aminase) (Guanine
DE aminohydrolase) (GAH) (GDEase).
GN Names=guad; Synonyms=gde; OrderedLocNames=BSU13170;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=168;
RC Devine K.M.;
RA "Sequence of the Bacillus subtilis genome between xlyA and ykoR.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=168;
RC MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Duesterhoft A., Ehrlich S.D., Emerson P.T.,
RA Etian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.-Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert L., Holsappel S., Hosono S., Hulio M.-F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M.,
RA Kleim C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone P., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
RA Shin B.-S., Soldo B., Sorokin A., Taccioni E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzengraber T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,

```

```
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
RW [3]
RP FUNCTION.
RC STRAIN=168;
RX MEDLINE=20553169; PubMed=11101664;
RA Nygaard P., Bested S.M., Andersen K.A.K., Saxild H.H.;
RT "Bacillus subtilis guanine deaminase is encoded by the yknA gene and
RT is induced during growth with purines as the nitrogen source.";
RL Microbiology 146:3061-3069(2000).
CC -!- FUNCTION: Catalyzes the hydrolytic deamination of guanine,
CC producing xanthine and ammonia.
CC -!- CATALYTIC ACTIVITY: Guanine + H(2)O = xanthine + NH(3).
CC -!- COFACTOR: Zinc (By similarity).
CC -!- PATHWAY: Purine catabolism.
CC -!- INDUCTION: Expressed only during limited or partially limited
CC nitrogen conditions. Can be induced to high levels in the presence
CC of purines or intermediates of the purine catabolic pathway.
CC Expression seems indirectly controlled by tnrA and glnR.
CC -!- SIMILARITY: Belongs to the cytidine and deoxycytidylate deaminase
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AJ002571; CAA05596.1; -; Genomic DNA.
CC EMBL; Z99110; CAB13174.1; -; Genomic DNA.
CC PIR; F69857; F69857.
CC PDB; 1TIY; X-ray; A/B=1-156.
CC PDB; 1WKQ; X-ray; A/B=1-156.
CC Subtilist; BG13240; Guad.
CC InterPro; IPR002125; dCMP_cyt_deam; 1.
CC Pfam; PF00383; dCMP_cyt_deam; 1.
CC 3D-structure; Complete proteome; Hydrolase; Metal-binding;
KW Purine metabolism; Zinc.
FT METAL 53 53 Zinc (By similarity).
FT METAL 83 83 Zinc (By similarity).
FT METAL 86 86 Zinc (By similarity).
SQ SEQUENCE 156 AA; 17156 MW; B6498345A98BC214 CRC64;

Query Match 89.7%; Score 26; DB 1; Length 156;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 96 KAVFFA 101

RESULT 51
QSWB0 BACSK
ID QSWB0_BACSK PRELIMINARY; PRT; 156 AA.
AC QSWB0_
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Guanine deaminase (EC 3.5.4.3).
GN Name=gde; OrderedLocNames=ABC3819;
OS Bacillus clausii (strain KSM-K16).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=66692;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KSM-K16;
RA Takaki Y., Kageyama Y., Shinamura S., Suzuki H., Nishi S., Hatada Y.,
RA Kawai S., Ito S., Horikoshi K.;
RT "The complete genome sequence of the alkaliphilic Bacillus clausii
```

```
RT KSM-K16.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
EMBL; AP006627; BAD66350.1; -; Genomic DNA.
DR GO; GO:000892; F:guanine deaminase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR002125; dCMP_cyt_deam; 1.
DR Pfam; PF00383; dCMP_cyt_deam; 1.
DR PROSITE; PS00903; CYT dCMP DEAMINASES; UNKNOWN_1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 156 AA; 17287 MW; F2BFFFF2FB4B28A1 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 156;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 96 KAVFFA 101

RESULT 52
OS9317 PYRHO
ID OS9317 PYRHO PRELIMINARY; PRT; 166 AA.
AC OS9317;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 166aa long hypothetical L(+)-cartrate dehydratase.
GN OrderedLocNames=Phi684;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kavarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; BA000001; BAA30796.1; -; Genomic DNA.
DR PIR; D71049; D71049.
DR GO; GO:0016829; F:lyase activity; IEA.
DR InterPro; IPR004647; TtdB_fumA_fumB.
DR Pfam; PF05683; Fumerase_C7_1.
DR TIGRFAMs; TIGR00723; ttdB_fumA_fumB; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 166 AA; 18250 MW; A2A70CF533DD166 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 166;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 107 KAVFFA 112

RESULT 53
OS7590 AQUAE
ID OS7590 AQUAE PRELIMINARY; PRT; 185 AA.
AC OS7590;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-terminal fumarate hydratase, class I.
```

```

GN Name=fumX; OrderedLocusNames=AQ_1679;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
DR EMBL; AB000750; AAC07546.1; -; Genomic_DNA.
DR PIR; E70445; E70445.
DR GO; GO:0016829; F:lyase activity; IEA.
DR InterPro; IPR004647; TtDB_fumA_fumB.
DR Pfam; PF05683; Fumerase_C_1.
DR TIGRFAMs; TIGR00723; ttDB_fumA_fumB; 1.
KW Complete proteome.
SQ SEQUENCE 185 AA; 20441 MW; CBA8320A226E2558 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 185;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KAVFFA 6
|||:|
Db 117 KAVYFA 122

RESULT 54
CSRPI CHICK STANDARD; PRT; 191 AA.
AC P67966; P32965;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cysteine-rich protein 1 (CRP1) (CRP).
GN Name=CSRPI; Synonyms=CSRP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryonic fibroblast;
RX MEDLINE=94124603; PubMed=8294495; DOI=10.1083/jcb.124.1.117;
RA Crawford A.W., Pino J.D., Beckerle M.C.;
RT "Biochemical and molecular characterization of the chicken cysteine-
RT rich protein, a developmentally regulated LIM-domain protein that is
RT associated with the actin cytoskeleton.";
RL J. Cell Biol. 124:117-127(1994).
[2]
RN RP PROTEIN SEQUENCE OF 1-49; 69-83; 111-129 AND 177-188.
RX MEDLINE=93107157; PubMed=1469049; DOI=10.1083/jcb.119.6.1573;
RA Sadler I., Crawford A.W., Michelsen J.W., Beckerle M.C.;
RT "Zyxin and cCRP: two interactive LIM domain proteins associated with
RT the cytoskeleton.";
RL J. Cell Biol. 119:1573-1587(1992).
[3]
RN RP ZINC-BINDING.
RX MEDLINE=93281587; PubMed=8506279;
RA Michelsen J.W., Schmeichel K.L., Beckerle M.C., Winge D.R.;
RT "The LIM motif defines a specific zinc-binding protein domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:4404-4408(1993).
[4]
RN RP MUTAGENESIS.
RX MEDLINE=94209279; PubMed=8157637;
RA Michelsen J.W., Sewell A.K., Louis H.A., Olsen J.I., Davis D.R.,
RA Winge D.R., Beckerle M.C.;

```

```

RT "Mutational analysis of the metal sites in an LIM domain.";
RL J. Biol. Chem. 269:11108-11113(1994).
[5]
RN RP STRUCTURE BY NMR OF C-TERMINAL LIM DOMAIN.
RX MEDLINE=95393167; PubMed=7664053;
RA Perez-Alvarado G.C., Miles C., Michelsen J.W., Louis H.A., Winge D.R.;
RT "Structure of the carboxy-terminal LIM domain from the cysteine rich
RT protein CRP.";
RL Nat. Struct. Biol. 1:388-398(1994).
CC -1- FUNCTION: Heat stable protein, that interacts with zyxin. May be a
CC component of a signal transduction pathway that mediates adhesion-
CC stimulated changes in gene expression.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Associates with the actin cytoskeleton.
CC -1- TISSUE SPECIFICITY: Most prominent in tissues that are enriched in
CC smooth muscle cells, such as gizzard, stomach, and intestine.
CC Lower level in the heart, no expression in liver, skeletal muscle,
CC or brain.
CC -1- DEVELOPMENTAL STAGE: Expression levels increase dramatically
CC during smooth muscle maturation.
CC -1- DOMAIN: Glycine-rich repeats mediate the association with the
CC actin cytoskeleton (Probable).
CC -1- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X73831; CAAS2053.1; -; mRNA.
DR PIR; A49648; A49648.
DR PIR; B44358; B44358.
DR PIR; C44358; C44358.
DR PDB; 1B8T; NMR; A=1-191.
DR PDB; 1CTL; NMR; @=107-191.
DR InterPro; IPR001781; LIM_Zn_bd.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS50023; LIM_DOMAIN_2; 2.
KW 3D-structure; Direct protein sequencing; LIM domain; Metal-binding;
KW Nuclear protein; Repeat; Zinc.
FT INIT MET 0 0
FT DOMAIN 9 60 LIM zinc-binding 1.
FT DOMAIN 117 168 LIM zinc-binding 2.
FT MOTIF 63 68 Nuclear localization signal (Potential).
FT COMPBIAS 62 77 Gly-rich.
FT COMPBIAS 174 185 Gly-rich.
FT STRAND 7 8
FT TURN 10 12
FT STRAND 15 16
FT STRAND 22 24
FT TURN 25 26
FT STRAND 27 29
FT TURN 31 33
FT STRAND 35 35
FT TURN 37 39
FT STRAND 42 42
FT STRAND 48 51
FT TURN 52 53
FT STRAND 54 57
FT HELIX 58 65
FT STRAND 115 116
FT TURN 118 120
FT STRAND 123 124
FT STRAND 130 132
FT TURN 133 134
FT STRAND 135 137
FT TURN 139 141
FT STRAND 143 143
FT TURN 145 147

```

```

FT STRAND 150 150
FT STRAND 156 159
FT TURN 160 161
FT STRAND 162 165
FT HELIX 166 172
FT TURN 173 173
SQ SEQUENCE 191 AA; 20254 MW; BC1A45013C7BDA38 CRC64;

Query Match
Best Local Similarity 89.7%; Score 26; DB 1; Length 191;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 14 KAVYFA 19

RESULT 55
CSRPI_COTJA STANDARD; PRT; 191 AA.
ID CSRPI_COTJA
AC P67967; P32965;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cysteine-rich protein 1 (CRPI) (CRP).
GN Name=CSRPI; Synonyms=CSRP;
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OC NCBI_TaxID=93934;
RN [1]

RESULT 56
QRR88 DEIRA
ID QRR88_DEIRA PRELIMINARY; PRT; 229 AA.
AC QRR88_
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Molybdenum cofactor biosynthesis protein D/E.
GN OrderedLocNames=DR2607;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OC NCBI_TaxID=1299;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodeson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL; AE002090; AAP12145.1; -, Genomic_DNA.
DR PIR; E75252; E75252.
DR HSSP; P30748; INVI.
DR TIGR; DR2607; -.
DR GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
DR GO; GO:0006790; P:sulfur metabolism; IEA.
DR InterPro; IPR003448; Mo_biosynth_Moae.
DR InterPro; IPR010034; Moad.
DR InterPro; IPR003749; This.
DR PANTHER; PTHR10311; Mo_biosynth_Moae; 1.
DR Pfam; PF02391; Moae; 1.
DR Pfam; PF02597; This; 1.
DR TIGRFAMs; TIGR01682; moad; 1.
DR Complete proteome.
SQ SEQUENCE 229 AA; 25311 MW; CD0F8B7060118B38 CRC64;

Query Match
Best Local Similarity 89.7%; Score 26; DB 2; Length 229;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 4 RAVFFA 9

RESULT 57
Q67QUL SYNTH
ID Q67QUL_SYNTH PRELIMINARY; PRT; 232 AA.
AC Q67QUL_
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=SYTH967;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OC NCBI_TaxID=2734;
RN [1]

```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IAM14863; DOI=10.1093/nar/gkh830;
RX PubMed=15383646; Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Genome sequence of *Symbiobacterium thermophilum*, an uncultivable
bacterium that depends on microbial commensalism.";
RL Nucleic Acids Res. 32:4937-4944 (2004).
DR EMBL; AF006840; BAD39952.1; -; Genomic_DNA.
DR InterPro; IPR005834; Dehal like_hydro.
DR Pfam; PF00702; Hydrolase; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 232 AA; 24811 MW; D830F748F8D4D67E CRC64;

Query Match 89.7%; Score 26; DB 2; Length 232;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
||:||||
Db 3 KALFFA 8

RESULT 58
Q527F8 MAGGR PRELIMINARY; PRT; 233 AA.
AC Q527F8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG05732.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelheil A., Adekoya E.,
RA Alt-zahra M., Allen T., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collamore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe C., Jones C., Kamal M., Kanat A., Kamysaselis M., Karlsson E.,
RA Kells C., Kieu A., Kisher P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Legier J., Levine S., Lewis D., Lewis T.,
RA Lindblad-coh K., Liu X., Lokytisang T., Lokytisang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabellia R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Menes L.,
RA Mesirov J., Mihalav A., Minova T., Mikkelsen T., Mlenga V., Moru K.,
RA Moses J., Mullain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotoabo B.,
RA O'Neill K., Oaman S., Parker S., Perrin D., Phunthang P., Piquani B.,
RA Purcell S., Rachupka T., Ramaamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe P.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stenson K., Stone K., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Testaye S., Theodore J., Thoultsang Y., Topham K.,
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,

RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of *Magnaporthe grisea*.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACU01000565; EAA54941.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 25744 MW; C25C02486B8B34C CRC64;

Query Match 89.7%; Score 26; DB 2; Length 233;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
||:||||
Db 192 RAVFFA 197

RESULT 59
O30760 RHOSH PRELIMINARY; PRT; 233 AA.
AC O30760;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Autoinducer synthesis regulator.
GN Names=cerR;
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX MEDLINE=980533869; PubMed=9393720;
RA Puskas A., Greenberg E.P., Kaplan S., Schaefer A.L.;
RT "A quorum-sensing system in the free-living photosynthetic bacterium
RT Rhodobacter sphaeroides.";
RL J. Bacteriol. 179:7530-7537 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RX Cogez V., Puskas A., Gak E., Kaplan S., Bohin J.-P.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2.4.1T;
RA Puskas A., Cogez V., Gak E., Bohin J.-P., Kaplan S.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016298; AAC46021.1; -; Genomic_DNA.
DR HSP; P11470; 1PSE
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; C:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR005143; Autoind bd.
DR InterPro; IPR000792; HTH LuxR.
DR InterPro; IPR011991; Wing hlx DNA_bd.
DR Pfam; PF03472; Autoind_bind; 1.
DR Pfam; PF00196; GERE; 1.

```

DR PRINTS; PR00038; HTHLUXR.
DR ProDom; PD000307; HTH LUXR; 1.
DR SMART; SM00421; HTH LUXR; 1.
SQ SEQUENCE 233 AA; 26080 MW; 127DDE08E6DB8D48 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 233;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 92 RAVFFPA 97

RESULT 60
Q9N2Y5_CABEL PRELIMINARY; PRT; 235 AA.
AC Q9N2Y5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Y71G10AR.3.
GN ORFNames=Y71G10AR.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; AC024856; AAF60868.4; -; Genomic DNA.
DR Ensembl; Y71G10AR.3; Caenorhabditis elegans.
DR WormBase; WBGene00022137; Y71G10AR.3.
DR WormPep; Y71G10AR.3; CE36900.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 235 AA; 27638 MW; 206BEC3C9570D089 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 235;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 47 KAVFFS 52

RESULT 61
Q5UEW2_9PROT PRELIMINARY; PRT; 266 AA.
AC Q5UEW2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative sulfatase (Fragment).
GN ORFNames=Red2C11_75;
OS uncultured alpha proteobacterium BBAC2C11.
OC Bacteria; Proteobacteria; Alphaproteobacteria; SAR116 cluster;
OC environmental samples.
OX NCBI_TaxID=295349;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sabeni G., Beja O.;
RT "SAR116.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY744399; AAV31659.1; -; Genomic DNA.
DR GO; GO:0008484; P:sulfuric ester hydrolase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000917; Sulfatase.

DR PRINTS; PF00084; Sulfatase; 1.
DR NON TER 266 266
SQ SEQUENCE 266 AA; 29908 MW; 518924D95F9043A7 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 266;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 232 KALFFPA 237

RESULT 62
Q5GU79_XANOR PRELIMINARY; PRT; 268 AA.
AC Q5GU79;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=XOO4490;
OS Xanthomonas oryzae (pv. oryzae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=64187;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KACC10331 / KX085;
RX PubMed=15673718; DOI=10.1093/nar/gki206;
RA Lee B.-M., Park Y.-J., Park D.-S., Kang H.-W., Kim J.-G., Song B.-S.,
RA Park I.-C., Yoon U.-H., Hahn J.-H., Koo B.-S., Lee G.-B., Kim H.,
RA Park H.-S., Yoon K.-O., Kim J.-H., Jung C.-H., Koh N.-H., Seo J.-S.,
RA Go S.-J.;
RT "The genome sequence of Xanthomonas oryzae pathovar oryzae KACC10331,
RT the bacterial blight pathogen of rice."
RL Nucleic Acids Res. 33:577-586(2005).
DR EMBL; AE013598; AAW77744.1; -; Genomic DNA.
DR InterPro; IPR005184; DUF306_MetA_HslJ.
DR Pfam; PF01724; META; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 268 AA; 28691 MW; 7757E113FF1816S9 CRC64;

Query Match      89.7%; Score 26; DB 2; Length 268;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 2 RAVFFPA 7

RESULT 63
Q7QS35_GIALA PRELIMINARY; PRT; 276 AA.
AC Q7QS35;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP_661_5852.6682.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

```


DR EMBL; AACB01000125; ERA37819.1; -; Genomic_DNA.
 DR InterPro; IPR001498; UPF0029.
 DR Pfam; PF01205; UPF0029; 1.
 DR PROSITE; PS00910; UPF0029; UNKNOWN 1.
 SQ SEQUENCE 276 AA; 30612 MW; 09078636BA1D9667 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 276;
 Best Local Similarity 83.3%; Pred. No. 7.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||:
 Db 155 KSVFFA 160

RESULT 64

O48777 ARATH
 ID O48777 ARATH PRELIMINARY; PRT; 285 AA.
 AC O48777;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein At2g32880.
 GN Name=At2g32880;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.J.,
 RA Wu D., Maiti R., Roming C.M., Koo H., Fujii C.Y., Utterback T.R.,
 RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RA Town C.D., Kaul S.;
 RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AC003033; AAB91985.1; -; Genomic_DNA.
 DR PIR; T01119; T01119.
 DR InterPro; IPR002083; MATH.
 DR Pfam; PF00917; MATH; 1.
 DR SMART; SM00061; MATH; 2.
 DR PROSITE; PS00144; MATH; 2.
 DR PROSITE; PS00144; MATH; 2.
 KW Hypothetical protein.

SQ SEQUENCE 285 AA; 32882 MW; 192157DB0D30FE27 CRC64;
 Query Match 89.7%; Score 26; DB 2; Length 285;
 Best Local Similarity 83.3%; Pred. No. 7.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||:
 Db 137 KAVFFA 142

RESULT 65

O5A5P9 CANAL
 ID O5A5P9 CANAL PRELIMINARY; PRT; 290 AA.
 AC O5A5P9;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein CTK3.
 GN Name=CTK3; ORFNames=Ca019.12810, Ca019.5350;
 OS Candida albicans SC5314.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=237561;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SC5314;

RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
 RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S., P.T.,
 RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
 RA Davis R.W., Scherer S.;
 RT "The diploid genome sequence of Candida albicans.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SC5314;
 RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
 RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
 RA Jones T., Scherer S., Agabian N.;
 RT "Annotation of the Genome of Candida albicans.";
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AACQ01000059; EAK98097.1; -; Genomic_DNA.
 DR EMBL; AACQ01000059; EAK98178.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 290 AA; 34139 MW; 41D96D679D453249 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 290;
 Best Local Similarity 83.3%; Pred. No. 7.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||:
 Db 26 KAVFFA 31

RESULT 66

Q751V7 ORYSA
 ID Q751V7 ORYSA PRELIMINARY; PRT; 296 AA.
 AC Q751V7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative 6-phosphogluconolactonase (With alternative splicing).
 GN Name=OSUNB0059G13.23;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
 RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
 RA Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Heiao J., Blunt S.,
 RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
 RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
 RA White O., Salzberg S.L., Fraser C.M.;
 RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RA Buell R.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC120538; AAS07092.1; -; Genomic_DNA.
 DR Gramene; Q751V7; -;
 DR GO; GO:0017057; F:6-phosphogluconolactonase activity; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
 DR InterPro; IPR006148; GlucGalIsoM.
 DR InterPro; IPR005900; Phosphogluconolac.
 DR Pfam; PF01182; Glucosamine_iso; 1.
 DR TIGRFAMs; TIGR01198; pgl; 1.
 SQ SEQUENCE 296 AA; 33270 MW; 36B72EAB4C2FE65A CRC64;

Query Match 89.7%; Score 26; DB 2; Length 296;
 Best Local Similarity 83.3%; Pred. No. 7.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||:
 Db 137 KAVFFA 142

Db 240 KAVYFA 245

RESULT 67
VGI2_ICHV1
ID VGI2_ICHV1 STANDARD; PRT; 299 AA.
AC Q00165;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypothetical gene 12 zinc-binding protein.
GN Name=12;
OS Ictalurid herpesvirus 1 (ICHV-1) (Channel catfish herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Ictalurivirus.
OX NCBI_TaxID=10401;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Auburn 1;
RX MEDLINE=92087490; PubMed=1727613;
RA Davison A.J.;
RL "Channel catfish virus: a new type of herpesvirus.";
RL Virology 186:9-14(1992).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M75136; AAA08193.1; -; Genomic DNA.
DR EMBL; M75136; AAA08115.1; -; Genomic DNA.
DR PIR; D36787; ZBBE13.
DR InterPro; IPR001841; Znf_RING.
DR SMART; SM00184; RING; 1_RING.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 299 AA; 33108 MW; B78295A90A647EB CRC64;

Query Match 89.7%; Score 26; DB 1; Length 299;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVYFA 6
:|||||
Db 39 KAVYFA 44

RESULT 68
Q8GX90_ARATH
ID Q8GX90_ARATH PRELIMINARY; PRT; 318 AA.
AC Q8GX90;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein Atg32880.
GN Name=Atg32880;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK118361; BAC42975.1; -; mRNA.
DR InterPro; IPR002083; MATH.
DR Pfam; PF00917; MATH; 2.
DR SMART; SM00061; MATH; 2.
DR PROSITE; PS01444; MATH; 2.
KW Hypothetical protein.
SQ SEQUENCE 318 AA; 36701 MW; 14B0D9BF9EE0C7BD CRC64;

Query Match 89.7%; Score 26; DB 2; Length 318;
Best Local Similarity 83.3%; Pred. No. 8.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVYFA 6
:|||||
Db 137 KAVYFA 142

RESULT 69
Q6ASCI_DESPS
ID Q6ASCI_DESPS PRELIMINARY; PRT; 321 AA.
AC Q6ASCI;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Related to glycosyltransferase involved capsular polysaccharide
DE biosynthesis.
GN OrderedLocusNames=DP0013;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobulbaceae; Desulfotales.
OX NCBI_TaxID=84980;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LSv54 / DSM 12343;
RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
RA Rabus R., Ruepp A., Fricke T., Rattei T., Fartmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:887-902(2004).
DR EMBL; CR522870; CAG34742.1; -; Genomic DNA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR InterPro; IPR001173; Glyco trans 2.
DR Pfam; PF00535; Glycos transf 2; 1.
KW Complete proteome; Transferrase.
SQ SEQUENCE 321 AA; 37861 MW; B3DEC2F91FB040BD CRC64;

Query Match 89.7%; Score 26; DB 2; Length 321;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVYFA 6
:|||||
Db 190 KAVYFA 195

RESULT 70
Q9EZ99_ZYMOO
ID Q9EZ99_ZYMOO PRELIMINARY; PRT; 340 AA.
AC Q9EZ99; Q5NL26;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Tryptophanyl-tRNA synthase (EC 6.1.1.2).
GN Name=trpS; OrderedLocusNames=ZMO1640;
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
OX NCBI_TaxID=542;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ZM4;
RA Shin I.S., Kang H.S.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 31821 / ZM4 / CP4;
RX PubMed=15592456; DOI=10.1038/nbt1045;

```

RA Seo J.-S., Chong H., Park H.S., Yoon K.-O., Jung C., Kim J.J.,
RA Hong J.H., Kim H., Kim J.-H., Kil J.-I., Park C.J., Oh H.-M.,
RA Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.Y.,
RA Kang H.L., Lee S.Y., Lee K.J., Kang H.S.;
RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis
RL ZM4."
RL Nat. Biotechnol. 23:63-68(2005).
CC -1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
CC phosphate + L-tryptophyl-tRNA(Trp).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL: AF300471; AAG2413.1; -; Genomic_DNA.
DR EMBL: AE008692; AAV90264.1; -; Genomic_DNA.
DR HSP; P00953; 1MAU.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0016874; F:ligase activity; IEA.
DR GO: GO:0004830; F:tryptophan-tRNA ligase activity; IEA.
DR GO: GO:0006412; P:protein biosynthesis; IEA.
DR GO: GO:0006436; P:tryptophanyl-tRNA aminoacylation; IEA.
DR InterPro: IPR002305; tRNA-synt_1b.
DR InterPro: IPR001412; tRNA-synt_1.
DR InterPro: IPR002306; Trp tRNA-synt_1.
DR Pfam: PF00579; tRNA-synt_1b; 1.
DR PRINTS: PR01039; TRNASYNTHRP.
DR TIGRFAMs: TIGR00233; trps; 1.
DR PROSITE: PS00178; AA tRNA_LIGASE_I; 1.
DR ATP-binding; Aminoacyl-tRNA synthetase; Complete proteome; Ligase;
KW Nucleotide-binding; Protein biosynthesis.
SQ SEQUENCE 340 AA; 37475 MW; 383EACB86ABEB883 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 340;
Best Local Similarity 83.3%; Pred. No. 8.e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 81 RAVFFA 86
:|||||

RESULT 71
CYSA_METCA
ID CYSA_METCA STANDARD; PRT; 348 AA.
AC Q609Q1;
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Sulfate/thiosulfate import ATP-binding protein cysA (EC 3.6.3.25)
DE (Sulfate-transporting ATPase).
GN Name=cysA; OrderedLocNames=MCA1181;
OS Methylococcus capsulatus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
OC Methylococcaceae; Methylococcus.
OX NCBI_TaxID=414;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bath / NCIMB 11132;
RX PubMed=15383840; DOI=10.1371/journal.pbio.0020303;
RA Ward N.L., Larsen O., Sakva J., Bruseeth L., Khouri H.M., Durkin A.S.,
RA Dinitrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E.,
RA Meche B.A., Wu M., Heidelberg J.F., Paulsen I.T., Pouts D.E.,
RA Ravel J., Tettelin H., Ren Q., Read T.D., DeBoy R.T., Seshadri R.,
RA Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J.,
RA Grindhaug S.H., Holt I.E., Eidhammer I., Jonassen I., Vanaken S.,
RA Utterback T.R., Feldblyum T.V., Fraser C.M., Lillehaug J.R.,
RA Eisen J.A.;
RT "Genomic insights into methanotrophy: the complete genome sequence of
RT Methylococcus capsulatus (Bath).";
RL PLOS Biol. 2:1616-1628(2004).
CC -1- FUNCTION: Part of the ABC transporter complex cysAWTP involved in
CC sulfate/chiosulfate import. Responsible for energy coupling to the
CC transport system (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + sulfate(Out) = ADP + phosphate +
CC sulfate(In).

CC -1- SUBUNIT: The complex is composed of two ATP-binding proteins
CC (cysA), two transmembrane proteins (cysT and cysW) and a solute-
CC binding protein (cysP) (Probable).
CC -1- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC Sulfate/tungstate importer (TC 3.A.1.6) subfamily.
CC -1- SIMILARITY: Contains 1 ABC transporter domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AE017282; AAU92758.1; -; Genomic_DNA.
CC TIGR: MCA1181; -.
CC InterPro: IPR003593; AAA ATPase.
CC InterPro: IPR003439; ABC transp like.
CC InterPro: IPR005666; Sulph_transp1.
CC Pfam: PF00005; ABC_tran; 1.
CC ProDom: PD000006; ABC_transporter; 1.
CC SMART: SM00382; AAA; 1.
CC TIGRFAMs: TIGR00968; 3a0106s01; 1.
CC PROSITE: PS00211; ABC_TRANSPORTER_1; 1.
CC PROSITE: PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome; Hydrolase; Inner membrane; Membrane;
KW Nucleotide-binding; Sulfate transport; Transport.
KT DOMAIN 3 237
FT NP_BIND 35 42 ATP (By similarity).
SQ SEQUENCE 348 AA; 38768 MW; 05F3EEF976A11885 CRC64;

Query Match 89.7%; Score 26; DB 1; Length 348;
Best Local Similarity 83.3%; Pred. No. 9.e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 271 KALFFA 276
:|||||

RESULT 72
Q83MJ3 SHIFL
ID Q83MJ3 SHIFL PRELIMINARY; PRT; 352 AA.
AC Q83MJ3; Q7UB67;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Putative resistance protein.
DE Name=yjN; OrderedLocNames=S3802, SF3944;
GN Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157."
RL Nucleic Acids Res. 30:4432-4441(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/JIAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.P., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

```

RA Schwartz D.C., Blattner F.R.;
 RT "Complete genome sequence and comparative genomics of Shigella
 flexneri serotype 2a strain 2457T.";
 RL Infect. Immun. 71:2775-2786(2003).
 DR EMBL; AE005674; AAN45379.2; -; Genomic_DNA.
 DR EMBL; AB016990; AAP18819.1; -; Genomic_DNA.
 DR InterPro; IPR011701; MFS_1.
 DR Pfam; PF07690; MFS_1; 1.
 KW Complete proteome.
 SQ SEQUENCE 352 AA; 38913 MW; 2CEA79CE6252270B CRC64;

Query Match 89.7%; Score 26; DB 2; Length 352;
 Best Local Similarity 83.3%; Pred. No. 9.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 :|||||
 Db 332 RAVFFA 337

RESULT 73
 Q72FT5 DESVH
 ID Q72FT5_DESVH PRELIMINARY; PRT; 352 AA.
 AC Q72FT5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Membrane protein, putative.
 GN OrderedLocusNames=DVU0128;
 OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303).

OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 OX NCBI_TaxID=882;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15077118; DOI=10.1038/nbt959;
 RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
 RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
 RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
 RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
 RA Peterson J.D., Davidson T.M., Zafar N., Zhou L., Radune D.,
 RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
 RA Felblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
 RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
 Desulfovibrio vulgaris Hildenborough.";
 RL Nat. Biotechnol. 22:554-559(2004).

DR EMBL; AB017309; AAS94612.1; -; Genomic_DNA.
 DR TIGR; DVU0128; -;
 DR InterPro; IPR002549; UPF0118.
 DR Pfam; PF01594; UPF0118; 1.

KW Complete proteome.
 SQ SEQUENCE 352 AA; 36026 MW; 787856A87410B493 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 352;
 Best Local Similarity 83.3%; Pred. No. 9.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 :|||||
 Db 23 KALFFA 28

RESULT 74
 Q6MI90 DBEBA
 ID Q6MI90_DBEBA PRELIMINARY; PRT; 383 AA.
 AC Q6MI90;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative polysaccharide deacetylase precursor (EC 3.5.1.-).
 GN OrderedLocusNames=Bd3279;
 OS Bdellovibrio bacteriovorus.

OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
 OC Bdellovibrionaceae; Bdellovibrio.
 OX NCBI_TaxID=959;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
 RC PubMed=14752164; DOI=10.1126/science.1093027;
 RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
 RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
 RA Sockett R.E., Schuster S.C.;
 RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
 genomic perspective.";
 RL Science 303:689-692(2004).
 DR EMBL; BX842655; CAB78090.1; -; Genomic_DNA.
 DR GO; GO:0016810; F:hydrolase activity, acting on carbon-nitrog. . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR002509; Polysac-deacet.
 DR Pfam; PF01522; Polysacc deac_1; 1.
 KW Complete proteome; Hydrolase; Signal.
 FT SIGNAL 11 Potential.
 SQ SEQUENCE 383 AA; 42819 MW; 7A1A4EF645C565BC CRC64;

Query Match 89.7%; Score 26; DB 2; Length 383;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 :|||||
 Db 197 KAMFFA 202

RESULT 75
 Q4HML6 CAMLA
 ID Q4HML6_CAMLA PRELIMINARY; PRT; 390 AA.
 AC Q4HML6;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Cyanate MFS transporter, putative.
 GN ORFNames=CLA1389;
 OS Campylobacter lari RM2100.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Campylobacteraceae; Campylobacter.

OX NCBI_TaxID=306263;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RM2100;
 RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Raeko D.A.,
 RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
 RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
 RA Ayodeji M.A., Shvartebeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
 RA Nelson K.E.;
 RT "Major structural and novel potential virulence mechanisms from the
 genomes of multiple Campylobacter species.";
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

DR EMBL; AAFK01000001; EAL55536.1; -; Genomic_DNA.
 SQ SEQUENCE 390 AA; 42990 MW; 29E9CF925C147383 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 390;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 :|||||
 Db 75 KALFFA 80

Search completed: December 29, 2005, 17:47:22
 Job time : 90.1936 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.29032 Seconds
(without alignments)
13.656 Million cell updates/sec

Title: US-10-009-122-7

Perfect score: 29

Sequence: 1 KAVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- 1: /cgm2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgm2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgm2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgm2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 5: /cgm2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 6: /cgm2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgm2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgm2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	660	7	US-11-186-284-125
2	29	100.0	708	6	US-10-821-234-917
3	25	86.2	210	6	US-10-467-657-6318
4	25	86.2	560	6	US-10-623-155-225
5	25	86.2	563	6	US-10-821-234-1067
6	24	82.8	19	6	US-10-923-605-5
7	24	82.8	19	6	US-10-934-818-5
8	24	82.8	40	7	US-11-016-706-36
9	24	82.8	40	7	US-11-098-674-12
10	24	82.8	42	6	US-10-923-605-1
11	24	82.8	42	6	US-10-934-818-1
12	24	82.8	42	7	US-11-016-706-37
13	24	82.8	43	6	US-10-934-818-6
14	24	82.8	43	6	US-10-250-581-1
15	24	82.8	43	6	US-10-250-581-1
16	24	82.8	288	6	US-10-467-657-1272
17	24	82.8	423	6	US-10-525-710-44
18	24	82.8	489	6	US-10-467-657-7846
19	24	82.8	770	6	US-10-982-545-15
20	24	82.8	770	6	US-10-789-273-38
21	23	79.3	9	6	US-10-982-891-44
22	23	79.3	114	6	US-10-467-657-5012
23	23	79.3	283	7	US-11-082-389-252
24	23	79.3	283	7	US-11-082-389-254
25	23	79.3	310	6	US-10-454-437-328
26	23	79.3	23	6	US-10-467-657-2080
27	23	79.3	23	6	US-10-467-657-5540
28	23	79.3	23	6	US-10-995-561-895
29	23	79.3	23	6	US-10-995-561-896
30	22	75.9	210	6	US-10-467-657-3436
31	22	75.9	211	6	US-10-821-234-1372
32	22	75.9	216	6	US-10-467-657-5976
33	22	75.9	269	7	US-11-179-977-11
34	22	75.9	335	7	US-11-092-353-2
35	22	75.9	341	6	US-10-131-826A-256
36	22	75.9	341	7	US-11-099-691-6
37	22	75.9	397	7	US-10-467-657-2684
38	22	75.9	478	7	US-11-092-353-4
39	22	75.9	550	6	US-10-467-657-234
40	22	75.9	550	6	US-10-467-657-924
41	22	75.9	645	6	US-10-510-386-32
42	22	75.9	989	6	US-10-821-234-975
43	22	75.9	1070	7	US/11/062
44	22	75.9	1095	7	US/11/062
45	22	75.9	1169	7	US-11-077-550-20
46	21	72.4	28	6	US-10-250-581-14
47	21	72.4	28	6	US-10-250-581-17
48	21	72.4	28	6	US-10-250-581-14
49	21	72.4	28	6	US-10-250-581-17
50	21	72.4	40	6	US-10-250-581-15
51	21	72.4	40	6	US-10-250-581-18
52	21	72.4	40	6	US-10-250-581-18
53	21	72.4	40	6	US-10-250-581-16
54	21	72.4	42	6	US-10-250-581-19
55	21	72.4	42	6	US-10-250-581-16
56	21	72.4	42	6	US-10-250-581-19
57	21	72.4	42	6	US-10-467-657-4978
58	21	72.4	54	6	US-11-123-896-344
59	21	72.4	71	7	US-11-123-896-335
60	21	72.4	73	7	US-10-467-657-9209
61	21	72.4	105	6	US-10-000-463-759
62	21	72.4	105	7	US-11-000-463-759
63	21	72.4	115	6	US-10-793-626-1554
64	21	72.4	127	6	US-10-467-657-3152
65	21	72.4	134	6	US-10-467-657-6860
66	21	72.4	153	6	US-10-467-657-4112
67	21	72.4	162	6	US-10-467-657-9046
68	21	72.4	167	6	US-10-467-657-5306
69	21	72.4	189	6	US-10-467-657-6854
70	21	72.4	189	6	US-10-467-657-7856
71	21	72.4	191	6	US-10-467-657-818
72	21	72.4	213	6	US-10-981-873-40
73	21	72.4	227	6	US-10-980-388-86
74	21	72.4	230	6	US-10-510-386-198
75	21	72.4	244	6	US-10-454-437-238
76	21	72.4	244	6	US-10-454-437-240
77	21	72.4	264	6	US-10-873-528-70
78	21	72.4	299	6	US-10-467-657-4424
79	21	72.4	355	6	US-10-467-657-7996
80	21	72.4	358	6	US-10-467-657-7030
81	21	72.4	366	6	US-10-467-657-7024
82	21	72.4	372	6	US-10-467-657-7964
83	21	72.4	372	6	US-10-467-657-590
84	21	72.4	406	6	US-10-467-657-7420
85	21	72.4	418	6	US-10-467-657-5788
86	21	72.4	422	6	US-10-525-710-40
87	21	72.4	429	6	US-10-588-730-79
88	21	72.4	439	6	US-10-793-626-2408
89	21	72.4	481	6	US-10-995-561-959
90	21	72.4	483	6	US-10-793-626-3132
91	21	72.4	495	6	US-10-613-744-5
92	21	72.4	500	6	US-10-957-569-18
93	21	72.4	550	7	US-11-055-822-866
94	21	72.4	613	6	US-10-467-657-5796
95	21	72.4	616	6	US-10-613-744-4
96	21	72.4	716	6	US-10-131-826A-512
97	21	72.4	716	7	US-11-147-047-52
98	21	72.4	801	6	US-10-467-657-6470

99	21	72.4	897	6	US-10-821-234-1523	Sequence 1523, Ap	172	20	69.0	338	6	US-10-467-657-6798	Sequence 6798, Ap
100	21	72.4	898	7	US-11-099-691-7	Sequence 7, Appli	173	20	69.0	347	6	US-10-467-657-2014	Sequence 2014, Ap
101	21	72.4	1141	6	US-10-995-561-1009	Sequence 1009, Ap	174	20	69.0	355	7	US-10-454-437-102	Sequence 102, App
102	21	72.4	1141	6	US-10-995-561-1010	Sequence 1010, Ap	175	20	69.0	355	7	US-11-068-686-4	Sequence 4, Appli
103	20	69.0	5	7	US-11-098-674-1	Sequence 1, Appli	176	20	69.0	356	7	US-11-075-185-16	Sequence 16, Appli
104	20	69.0	9	7	US-11-032-498-28	Sequence 28, Appli	177	20	69.0	357	6	US-10-467-657-2500	Sequence 2500, Ap
105	20	69.0	28	6	US-10-250-581-2	Sequence 2, Appli	178	20	69.0	357	6	US-10-467-657-6648	Sequence 6648, Ap
106	20	69.0	28	6	US-10-250-581-2	Sequence 2, Appli	179	20	69.0	363	6	US-10-995-561-602	Sequence 602, App
107	20	69.0	38	6	US-10-467-657-2058	Sequence 2058, Ap	180	20	69.0	365	6	US-10-624-932-24	Sequence 24, Appli
108	20	69.0	40	6	US-10-250-581-3	Sequence 3, Appli	181	20	69.0	376	6	US-10-995-561-844	Sequence 844, App
109	20	69.0	40	6	US-10-250-581-3	Sequence 3, Appli	182	20	69.0	376	6	US-10-995-561-848	Sequence 848, App
110	20	69.0	42	6	US-10-250-581-4	Sequence 4, Appli	183	20	69.0	380	6	US-10-624-932-20	Sequence 20, Appli
111	20	69.0	42	6	US-10-250-581-4	Sequence 4, Appli	184	20	69.0	380	6	US-10-624-932-22	Sequence 22, Appli
112	20	69.0	47	6	US-10-467-657-5436	Sequence 5436, Ap	185	20	69.0	380	6	US-10-995-561-846	Sequence 846, App
113	20	69.0	48	6	US-10-467-657-4322	Sequence 4322, Ap	186	20	69.0	380	7	US-11-108-528-28	Sequence 28, Appli
114	20	69.0	56	6	US-10-467-657-1050	Sequence 1050, Ap	187	20	69.0	387	6	US-10-467-657-5522	Sequence 5522, Ap
115	20	69.0	75	6	US-10-467-657-1496	Sequence 1496, Ap	188	20	69.0	390	6	US-10-995-561-847	Sequence 847, App
116	20	69.0	92	6	US-10-467-657-2378	Sequence 2378, Ap	189	20	69.0	395	6	US-10-467-657-1950	Sequence 1950, Ap
117	20	69.0	95	6	US-10-467-657-8785	Sequence 8785, Ap	190	20	69.0	396	6	US-10-510-386-238	Sequence 238, App
118	20	69.0	100	7	US-11-123-896-137	Sequence 137, App	191	20	69.0	399	6	US-10-510-386-30	Sequence 30, Appli
119	20	69.0	104	6	US-10-821-234-1227	Sequence 1227, Ap	192	20	69.0	400	6	US-10-793-626-1056	Sequence 1056, Ap
120	20	69.0	107	6	US-10-793-626-1586	Sequence 1586, Ap	193	20	69.0	401	7	US-11-055-823-336	Sequence 336, App
121	20	69.0	126	6	US-10-793-626-2766	Sequence 2766, Ap	194	20	69.0	402	6	US-10-467-657-9070	Sequence 9070, Ap
122	20	69.0	127	7	US-11-106-796-10	Sequence 10, Appli	195	20	69.0	402	7	US-11-000-463-449	Sequence 449, App
123	20	69.0	129	6	US-10-501-039-8	Sequence 8, Appli	196	20	69.0	413	6	US-10-467-657-11858	Sequence 11858, Ap
124	20	69.0	131	6	US-10-467-657-9073	Sequence 9073, Ap	197	20	69.0	426	6	US-10-467-657-2120	Sequence 2120, Ap
125	20	69.0	133	6	US-10-467-657-9195	Sequence 9195, Ap	198	20	69.0	428	7	US-11-000-463-448	Sequence 448, App
126	20	69.0	137	6	US-10-793-626-530	Sequence 530, App	199	20	69.0	436	6	US-10-467-657-7694	Sequence 7694, App
127	20	69.0	137	6	US-10-467-657-6584	Sequence 6584, App	200	20	69.0	444	6	US-10-467-657-362	Sequence 362, App
128	20	69.0	135	6	US-10-467-657-2420	Sequence 2420, Ap	201	20	69.0	450	6	US-10-467-657-7094	Sequence 7094, Ap
129	20	69.0	156	6	US-10-793-626-2452	Sequence 2452, Ap	202	20	69.0	450	6	US-10-467-657-8028	Sequence 8028, Ap
130	20	69.0	168	7	US-11-000-463-824	Sequence 824, App	203	20	69.0	451	7	US-10-467-657-7104	Sequence 7104, Ap
131	20	69.0	175	6	US-10-467-657-7504	Sequence 7504, Ap	204	20	69.0	453	7	US-11-082-389-198	Sequence 198, App
132	20	69.0	183	6	US-10-467-657-6906	Sequence 6906, Ap	205	20	69.0	456	6	US-10-467-657-4350	Sequence 4350, Ap
133	20	69.0	196	6	US-10-793-626-630	Sequence 630, App	206	20	69.0	472	6	US-10-467-657-2268	Sequence 2268, Ap
134	20	69.0	196	6	US-10-967-527A-26	Sequence 26, Appli	207	20	69.0	485	6	US-10-821-234-934	Sequence 934, App
135	20	69.0	201	6	US-10-467-657-458	Sequence 458, App	208	20	69.0	485	6	US-10-204-029-7	Sequence 7, Appli
136	20	69.0	202	7	US-11-082-389-364	Sequence 364, App	209	20	69.0	490	7	US-11-074-176-316	Sequence 316, App
137	20	69.0	207	6	US-10-467-657-1816	Sequence 1816, Ap	210	20	69.0	494	6	US-10-467-657-4376	Sequence 4376, Ap
138	20	69.0	211	6	US-10-467-657-6932	Sequence 6932, Ap	211	20	69.0	495	7	US-11-074-176-60	Sequence 60, Appli
139	20	69.0	215	6	US-10-131-826A-4	Sequence 4, Appli	212	20	69.0	507	6	US-10-467-657-1612	Sequence 1612, Ap
140	20	69.0	220	6	US-10-467-657-3154	Sequence 3154, Ap	213	20	69.0	513	6	US-10-467-657-5464	Sequence 5464, Ap
141	20	69.0	227	6	US-10-467-657-1514	Sequence 1514, Ap	214	20	69.0	514	7	US-11-186-284-228	Sequence 228, App
142	20	69.0	228	6	US-10-793-626-1862	Sequence 1862, Ap	215	20	69.0	523	6	US-10-131-826A-246	Sequence 246, App
143	20	69.0	228	6	US-10-467-657-568	Sequence 568, App	216	20	69.0	524	6	US-10-689-743-13	Sequence 13, Appli
144	20	69.0	228	6	US-10-467-657-4838	Sequence 4838, Ap	217	20	69.0	525	7	US-11-082-389-350	Sequence 350, App
145	20	69.0	229	6	US-10-131-826A-410	Sequence 410, App	218	20	69.0	528	6	US-10-793-626-1930	Sequence 1930, Ap
146	20	69.0	233	6	US-10-821-234-1322	Sequence 1322, Ap	219	20	69.0	540	6	US-10-858-730-293	Sequence 293, App
147	20	69.0	239	6	US-10-980-388-78	Sequence 78, Appli	220	20	69.0	554	6	US-11-000-463-240	Sequence 240, App
148	20	69.0	240	6	US-10-467-657-6276	Sequence 6276, Ap	221	20	69.0	555	6	US-10-454-437-100	Sequence 100, App
149	20	69.0	242	6	US-10-821-234-1073	Sequence 1073, Ap	222	20	69.0	558	6	US-10-467-657-4258	Sequence 4258, Ap
150	20	69.0	254	7	US-11-103-957-27	Sequence 27, Appli	223	20	69.0	560	7	US-11-080-991-62	Sequence 62, Appli
151	20	69.0	255	7	US-11-185-111-36	Sequence 36, Appli	224	20	69.0	572	6	US-10-467-657-1022	Sequence 1022, Ap
152	20	69.0	257	7	US-11-102-240-94	Sequence 94, Appli	225	20	69.0	578	6	US-10-858-730-103	Sequence 103, App
153	20	69.0	269	6	US-10-467-657-330	Sequence 330, App	226	20	69.0	582	7	US-11-090-439-58	Sequence 58, Appli
154	20	69.0	272	6	US-10-467-657-2520	Sequence 2520, Ap	227	20	69.0	592	6	US-10-467-962B-95	Sequence 95, Appli
155	20	69.0	288	6	US-10-873-528-18	Sequence 18, Appli	228	20	69.0	592	6	US-10-524-647-112	Sequence 112, App
156	20	69.0	291	7	US-10-432-483-12	Sequence 12, Appli	229	20	69.0	599	6	US-10-467-657-3972	Sequence 3972, Ap
157	20	69.0	291	7	US-11-102-883-22	Sequence 22, Appli	230	20	69.0	614	7	US-11-126-841A-2	Sequence 2, Appli
158	20	69.0	292	7	US-11-102-883-22	Sequence 22, Appli	231	20	69.0	614	7	US-11-126-841A-13	Sequence 13, Appli
159	20	69.0	294	6	US-10-467-657-7686	Sequence 7686, Ap	232	20	69.0	626	6	US-10-467-657-1196	Sequence 1196, Ap
160	20	69.0	311	6	US-10-793-626-2450	Sequence 2450, Ap	233	20	69.0	677	6	US-10-131-826A-230	Sequence 230, App
161	20	69.0	316	7	US-10-467-657-2334	Sequence 2334, Ap	234	20	69.0	693	6	US-10-467-657-6176	Sequence 6176, Ap
162	20	69.0	316	7	US-11-082-389-62	Sequence 62, Appli	235	20	69.0	721	6	US-10-467-962B-49	Sequence 49, Appli
163	20	69.0	318	6	US-10-131-826A-374	Sequence 374, App	236	20	69.0	724	7	US-11-184-380-4	Sequence 4, Appli
164	20	69.0	324	6	US-10-467-657-2504	Sequence 2504, Ap	237	20	69.0	741	6	US-10-467-657-6266	Sequence 6266, Ap
165	20	69.0	331	6	US-10-467-657-7692	Sequence 7692, Ap	238	20	69.0	835	7	US-11-186-283-2	Sequence 2, Appli
166	20	69.0	334	6	US-10-467-657-8440	Sequence 8440, Ap	239	20	69.0	835	7	US-11-186-283-8	Sequence 8, Appli
167	20	69.0	325	6	US-10-454-437-142	Sequence 142, App	240	20	69.0	852	6	US-10-467-657-5004	Sequence 5004, Ap
168	20	69.0	330	6	US-10-510-386-82	Sequence 82, Appli	241	20	69.0	858	6	US-10-613-744-6	Sequence 6, Appli
169	20	69.0	333	7	US-11-082-389-202	Sequence 202, App	242	20	69.0	907	7	US-11-103-957-82	Sequence 82, Appli
170	20	69.0	335	6	US-10-467-657-3818	Sequence 3818, Ap	243	20	69.0	916	6	US-10-467-657-4242	Sequence 4242, Ap
171	20	69.0	338	6	US-10-467-657-136	Sequence 136, App	244	20	69.0	964	7	US-11-103-957-13	Sequence 13, Appli

245 20 69.0 1027 6 US-10-793-626-3106
 246 20 69.0 1076 6 US-10-467-657-3708
 247 20 69.0 1144 6 US-10-467-962B-89
 248 20 69.0 1259 6 US-10-467-657-5510
 249 20 69.0 1274 6 US-10-454-437-360
 250 20 69.0 1362 7 US-11-043-633-33
 251 20 69.0 1363 7 US-11-043-693-32
 252 20 69.0 1368 7 US-11-043-693-34
 253 20 69.0 1531 7 US-11-103-957-15
 254 20 69.0 2004 6 US-10-467-657-84
 255 20 69.0 2004 6 US-10-467-657-6322
 256 20 69.0 3433 6 US-10-714-781A-67
 257 20 69.0 3623 6 US-10-995-561-593
 258 20 69.0 4128 6 US-10-770-726-77
 259 19 65.5 28 6 US-10-250-581-5
 260 19 65.5 28 6 US-10-250-581-8
 261 19 65.5 28 6 US-10-250-581-11
 262 19 65.5 28 6 US-10-250-581-5
 263 19 65.5 28 6 US-10-250-581-8
 264 19 65.5 28 6 US-10-250-581-11
 265 19 65.5 39 6 US-10-467-657-2174
 266 19 65.5 40 6 US-10-250-581-6
 267 19 65.5 40 6 US-10-250-581-9
 268 19 65.5 40 6 US-10-250-581-12
 269 19 65.5 40 6 US-10-250-581-6
 270 19 65.5 40 6 US-10-250-581-9
 271 19 65.5 42 6 US-10-250-581-12
 272 19 65.5 42 6 US-10-250-581-7
 273 19 65.5 42 6 US-10-250-581-10
 274 19 65.5 42 6 US-10-250-581-13
 275 19 65.5 42 6 US-10-250-581-7
 276 19 65.5 42 6 US-10-250-581-10
 277 19 65.5 42 6 US-10-250-581-13
 278 19 65.5 50 6 US-10-467-657-7892
 279 19 65.5 52 6 US-10-467-657-3656
 280 19 65.5 83 6 US-10-467-657-5366
 281 19 65.5 95 7 US-11-055-822-238
 282 19 65.5 95 7 US-11-055-822-632
 283 19 65.5 95 7 US-11-055-822-1102
 284 19 65.5 96 6 US-10-467-657-3380
 285 19 65.5 97 6 US-10-650-326B-2
 286 19 65.5 97 6 US-10-995-561-900
 287 19 65.5 98 6 US-10-467-657-3490
 288 19 65.5 102 6 US-10-667-295-43
 289 19 65.5 102 6 US-10-793-626-2592
 290 19 65.5 107 6 US-10-467-657-1018
 291 19 65.5 113 7 US-11-073-605-10
 292 19 65.5 124 6 US-10-467-657-8548
 293 19 65.5 128 6 US-10-793-626-1208
 294 19 65.5 138 6 US-10-467-657-2052
 295 19 65.5 141 6 US-10-667-295-42
 296 19 65.5 141 6 US-10-467-657-5544
 297 19 65.5 150 7 US-11-109-156-32
 298 19 65.5 153 6 US-10-467-657-7674
 299 19 65.5 153 6 US-10-467-657-6432
 300 19 65.5 157 7 US-11-116-144-167

ALIGNMENTS

RESULT 1
 US-11-186-284-125
 ; Sequence 125, Application US/11186284
 ; Publication No. US20050266493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Berger, Allison
 ; APPLICANT: Guillemette, Tracy L.
 ; APPLICANT: Kamatkar, Shubhangi
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Monahan, John E.
 ; APPLICANT: Thibodeau, Stephen N.

Sequence 3106, Ap
 Sequence 5708, Ap
 Sequence 89, Appl
 Sequence 5510, Ap
 Sequence 360, Appl
 Sequence 33, Appl
 Sequence 32, Appl
 Sequence 34, Appl
 Sequence 15, Appl
 Sequence 84, Appl
 Sequence 6322, Ap
 Sequence 67, Appl
 Sequence 53, Appl
 Sequence 77, Appl
 Sequence 5, Appl
 Sequence 11, Appl
 Sequence 5, Appl
 Sequence 8, Appl
 Sequence 11, Appl
 Sequence 9, Appl
 Sequence 12, Appl
 Sequence 12, Appl
 Sequence 10, Appl
 Sequence 13, Appl
 Sequence 7, Appl
 Sequence 10, Appl
 Sequence 13, Appl
 Sequence 7892, Ap
 Sequence 3656, Ap
 Sequence 5366, Ap
 Sequence 238, App
 Sequence 632, App
 Sequence 1102, Ap
 Sequence 3380, Ap
 Sequence 2, Appli
 Sequence 900, App
 Sequence 3490, Ap
 Sequence 43, Appl
 Sequence 2592, Ap
 Sequence 1018, Ap
 Sequence 10, Appl
 Sequence 8548, Ap
 Sequence 1208, Ap
 Sequence 2052, Ap
 Sequence 42, Appl
 Sequence 5544, Ap
 Sequence 32, Appl
 Sequence 7674, Ap
 Sequence 8432, Ap
 Sequence 167, App

APPLICANT: BURGART, Lawrence J.
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
 ; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; TITLE OF INVENTION: THERAPY OF COLON CANCER
 ; FILE REFERENCE: MPM01-029P2RNM
 ; CURRENT APPLICATION NUMBER: US/11/186,284
 ; CURRENT FILING DATE: 2005-07-21
 ; PRIOR APPLICATION NUMBER: US/10/301,822
 ; PRIOR FILING DATE: 2002-11-21
 ; PRIOR APPLICATION NUMBER: US 60/339,971
 ; PRIOR FILING DATE: 2001-12-10
 ; PRIOR APPLICATION NUMBER: US 60/361,978
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: US 60/381,988
 ; PRIOR FILING DATE: 2002-05-20
 ; NUMBER OF SEQ ID NOS: 228
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 125
 ; LENGTH: 660
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-186-284-125

Query Match 100.0%; Score 29; DB 7; Length 660;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFFA 6
 |||||
 Db 531 KAVFFFA 536

RESULT 2
 US-10-821-234-917
 ; Sequence 917, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pt_seq_genes Version 1.0
 ; SEQ ID NO 917
 ; LENGTH: 708
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-821-234-917

Query Match 100.0%; Score 29; DB 6; Length 708;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFFA 6
 |||||
 Db 579 KAVFFFA 584

RESULT 3
 US-10-467-657-6318
 ; Sequence 6318, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega

```
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6318
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6318

Query Match      86.2%; Score 25; DB 6; Length 210;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFF 5
Db      116 KAVFF 120

RESULT 4
US-10-623-155-225
; Sequence 225, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-225

Query Match      86.2%; Score 25; DB 6; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFF 5
Db      537 KAVFF 541

RESULT 5
US-10-821-234-1067
; Sequence 1067, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pt_SEQ_genes Version 1.0
; SEQ ID NO 1067

; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence

; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)_RES
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-923-605-5

Query Match      82.8%; Score 24; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 6.3;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFF 6
Db      4 KLVFF 9

RESULT 7
US-10-934-818-5
; Sequence 5, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
```



```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5

Query Match      82.8%; Score 24; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 6.3;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      4 KLVFFA 9

RESULT 8
US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; CURRENT APPLICATION NUMBER: US/11/016,706
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-36

Query Match      82.8%; Score 24; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      16 KLVFFA 21

RESULT 9
US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elmova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

Query Match      82.8%; Score 24; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      16 KLVFFA 21

RESULT 10
US-10-923-605-1
; Sequence 1, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-923-605-1

Query Match      82.8%; Score 24; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      16 KLVFFA 21

RESULT 11
US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1
```

```
Query Match      82.8%; Score 24; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      16 KLVFFA 21

RESULT 12
US-11-016-706-37
; Sequence 37, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-37

Query Match      82.8%; Score 24; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      16 KLVFFA 21

RESULT 13
US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match      82.8%; Score 24; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      16 KLVFFA 21

RESULT 14
US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match      82.8%; Score 24; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      16 KLVFFA 21

RESULT 15
US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match      82.8%; Score 24; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      16 KLVFFA 21

RESULT 16
US-10-467-657-1272
; Sequence 1272, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
```

; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1272
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1272

Query Match 82.8%; Score 24; DB 6; Length 288;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AVFFA 6
Db 44 AVFFA 48
|||||

RESULT 17

US-10-525-710-44
; Sequence 44, Application US/10525710
; Publication No. US20050260721A1
; GENERAL INFORMATION:
; APPLICANT: Kroger, Burkhard
; APPLICANT: Zelder, Oskar
; APPLICANT: Kolpprogge, Corinna
; APPLICANT: Schroder, Hartwig
; APPLICANT: Hahner, Stefan
; TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing
; TITLE OF INVENTION: Sulphur (mety)
; FILE REFERENCE: 13111-00006-US
; CURRENT APPLICATION NUMBER: US/10/525,710
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: PCT/EP 2003/009453
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: DE 102 39 082.7
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-10-525-710-44

Query Match 82.8%; Score 24; DB 6; Length 423;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 146 KAIPP 150
|||||

RESULT 18

US-10-467-657-7846
; Sequence 7846, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7846
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7846

Query Match 82.8%; Score 24; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AVFFA 6
Db 28 AVFFA 32
|||||

RESULT 19

US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Arja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease
; OTHER INFORMATION: nexin II (FN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; OTHER INFORMATION: Alzheimer's disease amyloid protein
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(40)
; OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-N1), A-beta 1-40
; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(687)
; OTHER INFORMATION: soluble APP-alpha
; FEATURE:
; NAME/KEY: PEPTIDE

/ LOCATION: (19)..(671)
/ OTHER INFORMATION: soluble APP-beta
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (672)..(770)
/ OTHER INFORMATION: C99
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (672)..(713)
/ OTHER INFORMATION: beta-amyloid protein 42
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (672)..(711)
/ OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
/ OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (688)..(770)
/ OTHER INFORMATION: C83
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (688)..(713)
/ OTHER INFORMATION: P3(42)
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (688)..(711)
/ OTHER INFORMATION: P3(40)
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (712)..(770)
/ OTHER INFORMATION: gamma-CTF(59)
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (714)..(770)
/ OTHER INFORMATION: gamma-CTF(57)
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (721)..(770)
/ OTHER INFORMATION: gamma-CTF(50)
/ FEATURE:
/ NAME/KEY: PEPTIDE
/ LOCATION: (740)..(770)
/ OTHER INFORMATION: C31
/ OTHER INFORMATION: C31
US-10-982-545-15

Query Match 82.8%; Score 24; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 687 KLVFFA 692

RESULT 20
US-10-789-273-38
/ Sequence 38, Application US/10789273
/ Publication No. US20050249725A1
/ GENERAL INFORMATION:
/ APPLICANT: Basi, Guriq
/ APPLICANT: Saidanha, Jose
/ APPLICANT: Yednock, Ted
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
/ TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
/ FILE REFERENCE: ELN-002CP
/ CURRENT APPLICATION NUMBER: US/10/789,273
/ CURRENT FILING DATE: 2004-02-27
/ PRIOR APPLICATION NUMBER: US/10/388,389
/ PRIOR FILING DATE: 2003-03-12
/ PRIOR APPLICATION NUMBER: US 10/010,942
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: US 60/251,892
/ PRIOR FILING DATE: 2000-12-06

/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 38
/ LENGTH: 770
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-789-273-38

Query Match 82.8%; Score 24; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 687 KLVFFA 692

RESULT 21
US-10-982-891-44
/ Sequence 44, Application US/10982891
/ Publication No. US2005024484A1
/ GENERAL INFORMATION:
/ APPLICANT: GARCIA, ALPHONSE
/ APPLICANT: CAYLA, XAVIER
/ APPLICANT: REBOLLO, ANGELITA
/ TITLE OF INVENTION: METHODS OF SCREENING OF PPI-INTERACTING POLYPEPTIDES OR PROTEINS
/ TITLE OF INVENTION: PEPTIDES INHIBITING PPIC BINDING TO Bcl-2 PROTEINS, BCL-XL AND
/ TITLE OF INVENTION: BCL-W, AND USES THEREOF
/ FILE REFERENCE: 260990USOCONT
/ CURRENT APPLICATION NUMBER: US/10/982,891
/ CURRENT FILING DATE: 2004-11-08
/ PRIOR APPLICATION NUMBER: PCT/EP03/05453
/ PRIOR FILING DATE: 2003-05-06
/ PRIOR APPLICATION NUMBER: EP 02291170
/ PRIOR FILING DATE: 2002-05-07
/ NUMBER OF SEQ ID NOS: 83
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 44
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: MAMMALIAN
US-10-982-891-44

Query Match 79.3%; Score 23; DB 6; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.4e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 3 KAVMFA 8

RESULT 22
US-10-467-657-5012
/ Sequence 5012, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 5012
/ LENGTH: 114
/ TYPE: PRT

```
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5012

Query Match          79.3%; Score 23; DB 6; Length 114;
Best Local Similarity 66.7%; Pred. No. 61;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      34 RAVFFS 39

RESULT 23
US-11-082-389-252
; Sequence 252, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 252
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-254

Query Match          79.3%; Score 23; DB 7; Length 283;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 AVFFA 6
DB      264 AIFFA 268

RESULT 25
US-10-454-437-328
; Sequence 328, Application US/10454437
; Publication No. US2005027115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128CPCN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9

; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5012

Query Match          79.3%; Score 23; DB 6; Length 114;
Best Local Similarity 66.7%; Pred. No. 61;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      34 RAVFFS 39

RESULT 24
US-11-082-389-254
; Sequence 254, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
```

```
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 328
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-328

Query Match          79.3%; Score 23; DB 6; Length 310;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 AVFFA 6
      |:|||
Db      63 AIFFA 67

RESULT 26
US-10-793-626-2080
; Sequence 2080, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2080
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2080

Query Match          79.3%; Score 23; DB 6; Length 411;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 AVFFA 6
      |:|||
Db      304 AIFFA 308

RESULT 27
US-10-467-657-5540
; Sequence 5540, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
```

```
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5540
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5540

Query Match          79.3%; Score 23; DB 6; Length 557;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
Db      166 KAVMFA 171

RESULT 28
US-10-995-561-895
; Sequence 895, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 895
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-895

Query Match          79.3%; Score 23; DB 6; Length 974;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
Db      497 KAVLFA 502

RESULT 29
US-10-995-561-896
; Sequence 896, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 896
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-896

Query Match          79.3%; Score 23; DB 6; Length 997;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVEFA 6
      |||||
Db      520 KAVLFA 525
```

```
RESULT 30
US-10-467-657-3436
; Sequence 3436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3436
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3436
```

```
Query Match 75.9%; Score 22; DB 6; Length 190;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 KAVPPA 6
Db 46 KTVFYA 51
```

```
RESULT 31
US-10-821-234-1372
; Sequence 1372, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1372
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1372
```

```
Query Match 75.9%; Score 22; DB 6; Length 211;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 KAVPPA 6
Db 33 KTVFYA 38
```

```
RESULT 32
US-10-467-657-5976
; Sequence 5976, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
```

```
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5976
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5976
```

```
Query Match 75.9%; Score 22; DB 6; Length 216;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KAVFF 5
Db 8 KSVFF 12
```

```
RESULT 33
US-11-179-977-11
; Sequence 11, Application US/11179977
; Publication No. US20050249789A1
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
; FILE REFERENCE: GC511-PCT
; CURRENT APPLICATION NUMBER: US/11/179,977
; CURRENT FILING DATE: 2005-07-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Bacillus
US-11-179-977-11
```

```
Query Match 75.9%; Score 22; DB 7; Length 269;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 KAVFFA 6
Db 193 KAAFFS 198
```

```
RESULT 34
US-11-092-353-2
; Sequence 2, Application US/11092353
; Publication No. US20050272653A1
; GENERAL INFORMATION:
; APPLICANT: Knopf, John
; APPLICANT: Seehra, Jasbir
; TITLE OF INVENTION: BMP-3 PROPEPTIDES AND RELATED METHODS
; FILE REFERENCE: PHPP-P01-002
; CURRENT APPLICATION NUMBER: US/11/092,353
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: US 60/557,100
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-092-353-2
```

Query Match 75.9%; Score 22; DB 7; Length 335;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
DB 79 KAVFF 83

RESULT 35
US-10-131-826A-256
; Sequence 256, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 256
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-256

Query Match 75.9%; Score 22; DB 6; Length 341;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
DB 102 KALFF 106

RESULT 36
US-11-099-691-6
; Sequence 6, Application US/11099691
; Publication No. US2005026044A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: BANDMAN, Olga
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YANG, Junming
; TITLE OF INVENTION: CELL SIGNALING PROTEINS
; FILE REFERENCE: PF-0521 PCT
; CURRENT APPLICATION NUMBER: US/11/099,691
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US/09/700,444
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/085,343
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,010
; PRIOR FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc-feature
; FEATURE:
; OTHER INFORMATION: Incyte Clone 2472655
US-11-099-691-6

Query Match 75.9%; Score 22; DB 7; Length 341;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
DB 102 KALFF 106

RESULT 37
US-10-467-657-2684
; Sequence 2684, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2684
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2684

Query Match 75.9%; Score 22; DB 6; Length 397;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||||
 Db 309 KADFFA 314

RESULT 38

US-11-092-353-4
 ; Sequence 4, Application US/11092353
 ; Publication No. US20050272653A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Knopf, John
 ; APPLICANT: Seehra, Jasbir
 ; TITLE OF INVENTION: BMP-3 PROPEPTIDES AND RELATED METHODS
 ; FILE REFERENCE: PHFP-P01-002
 ; CURRENT APPLICATION NUMBER: US/11/092,353
 ; CURRENT FILING DATE: 2005-03-28
 ; PRIOR APPLICATION NUMBER: US 60/557,100
 ; PRIOR FILING DATE: 2004-03-26
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 478
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-092-353-4

Query Match 75.9%; Score 22; DB 7; Length 478;
 Best Local Similarity 80.0%; Pred. No. 4.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
 |||||
 Db 112 KAVFF 116

RESULT 39

US-10-467-657-234
 ; Sequence 234, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SPA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 234
 ; LENGTH: 550
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-234

Query Match 75.9%; Score 22; DB 6; Length 550;
 Best Local Similarity 80.0%; Pred. No. 4.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
 |||||
 Db 176 RAVFF 180

RESULT 40

US-10-467-657-924
 ; Sequence 924, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:

; APPLICANT: CHIRON SPA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 924
 ; LENGTH: 550
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-924

Query Match 75.9%; Score 22; DB 6; Length 550;
 Best Local Similarity 80.0%; Pred. No. 4.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
 |||||
 Db 176 RAVFF 180

RESULT 41

US-10-510-386-32
 ; Sequence 32, Application US/10510386
 ; Publication No. US20050244922A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andersen, Jens Tonne
 ; APPLICANT: Clausen, Ib Groth
 ; APPLICANT: Jorgensen, Steen Troels
 ; APPLICANT: Olsen, Peter Bjarke
 ; APPLICANT: Rasmussen, Michael Dolberg
 ; TITLE OF INVENTION: Improved Bacillus Host Cell
 ; FILE REFERENCE: 10294.204-US
 ; CURRENT APPLICATION NUMBER: US/10/510,386
 ; CURRENT FILING DATE: 2004-10-04
 ; NUMBER OF SEQ ID NOS: 248
 ; SOFTWARE: Patentin version 3.3
 ; SEQ ID NO 32
 ; LENGTH: 645
 ; TYPE: PRT
 ; ORGANISM: Bacillus licheniformis
 US-10-510-386-32

Query Match 75.9%; Score 22; DB 6; Length 645;
 Best Local Similarity 66.7%; Pred. No. 5.5e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||||
 Db 123 KGLFFA 128

RESULT 42

US-10-821-234-975
 ; Sequence 975, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047

; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 975_
; LENGTH: 989
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-975

Query Match 75.9%; Score 22; DB 6; Length 989;
Best Local Similarity 66.7%; Pred. No. 8.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
: : : : :
DB 312 ESVFFA 317

RESULT 43
US/11/062
; Sequence 4, Application US/11062471A
; Publication No. US2005025503A1
; GENERAL INFORMATION:
; APPLICANT: SHONE, Clifford Charles
; APPLICANT: SUTTON, John Mark
; APPLICANT: HALLIS, Basam
; APPLICANT: SILMAN, Nigel
; TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
; FILE REFERENCE: 1581.080001
; CURRENT APPLICATION NUMBER: US/11/062,471A
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: 09/831,050
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: PCT/GB99/03699
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: GB 9824282.9
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1070
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a linker,
US/11/062,471A-4

Query Match 75.9%; Score 22; DB 7; Length 1070;
Best Local Similarity 80.0%; Pred. No. 9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
: : : : :
DB 762 KSVFF 766

RESULT 44
US/11/062
; Sequence 7, Application US/11062471A
; Publication No. US2005025503A1
; GENERAL INFORMATION:
; APPLICANT: SHONE, Clifford Charles
; APPLICANT: SUTTON, John Mark
; APPLICANT: HALLIS, Basam
; APPLICANT: SILMAN, Nigel
; TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
; FILE REFERENCE: 1581.080001
; CURRENT APPLICATION NUMBER: US/11/062,471A
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: 09/831,050
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: PCT/GB99/03699
; PRIOR FILING DATE: 1999-11-05

; PRIOR APPLICATION NUMBER: GB 9824282.9
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human ;
US/11/062,471A-7

Query Match 75.9%; Score 22; DB 7; Length 1095;
Best Local Similarity 80.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
: : : : :
DB 787 KSVFF 791

RESULT 45
US-11-077-550-20
; Sequence 20, Application US/11077550
; Publication No. US2005024435A1
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford Charles
; APPLICANT: Quinn, Conrad Padraig
; APPLICANT: Foster, Keith Alan
; APPLICANT: Chaddock, John
; APPLICANT: Marks, Philip
; APPLICANT: Sutton, J. Mark
; APPLICANT: Stancombe, Patrick
; APPLICANT: Wayne, Jonathan
; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130004
; CURRENT APPLICATION NUMBER: US/11/077,550
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 10/241,596
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB9617671.4
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Clostridium botulinum
US-11-077-550-20

Query Match 75.9%; Score 22; DB 7; Length 1169;
Best Local Similarity 80.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
: : : : :
DB 983 KSVFF 987

RESULT 46
US-10-250-581-14
; Sequence 14, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...

;; TITLE OF INVENTION: Soluble cyclic analogs....
;; FILE REFERENCE: 16069
;; CURRENT APPLICATION NUMBER: US/10/250,581
;; CURRENT FILING DATE: 2004-01-14
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: Patent In Version 2.1
;; SEQ ID NO 14
;; LENGTH: 28
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (17)
;; OTHER INFORMATION: Xaa=Orn
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (17)..(21)
;; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
;; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-14

Query Match 72.4%; Score 21; DB 6; Length 28;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 KAVPF 5
|
|
|
Db 16 KKVFF 20

RESULT 47
US-10-250-581-17
;; Sequence 17, Application US/10250581
;; Publication No. US20040116337A1
;; GENERAL INFORMATION:
;; APPLICANT: Fraunhofer Society for Promotion of Applied ...
;; TITLE OF INVENTION: Soluble cyclic analogs....
;; FILE REFERENCE: 16069
;; CURRENT APPLICATION NUMBER: US/10/250,581
;; CURRENT FILING DATE: 2004-01-14
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: Patent In Version 2.1
;; SEQ ID NO 17
;; LENGTH: 28
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (17)
;; OTHER INFORMATION: Xaa=Dab
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (17)..(21)
;; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
;; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-17

Query Match 72.4%; Score 21; DB 6; Length 28;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 KAVPF 5
|
|
|
Db 16 KKVFF 20

RESULT 48
US-10-250-581-14
;; Sequence 14, Application US/10250581
;; Publication No. US20040116337A1
;; GENERAL INFORMATION:
;; APPLICANT: Fraunhofer Society for Promotion of Applied ...
;; TITLE OF INVENTION: Soluble cyclic analogs....

;; FILE REFERENCE: 16069
;; CURRENT APPLICATION NUMBER: US/10/250,581
;; CURRENT FILING DATE: 2004-01-14
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: Patent In Version 2.1
;; SEQ ID NO 14
;; LENGTH: 28
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (17)
;; OTHER INFORMATION: Xaa=Orn
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (17)..(21)
;; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
;; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-14

Query Match 72.4%; Score 21; DB 6; Length 28;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVPF 5
|
|
|
Db 16 KKVFF 20

RESULT 49
US-10-250-581-17
;; Sequence 17, Application US/10250581
;; Publication No. US20040116337A1
;; GENERAL INFORMATION:
;; APPLICANT: Fraunhofer Society for Promotion of Applied ...
;; TITLE OF INVENTION: Soluble cyclic analogs....
;; FILE REFERENCE: 16069
;; CURRENT APPLICATION NUMBER: US/10/250,581
;; CURRENT FILING DATE: 2004-01-14
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: Patent In Version 2.1
;; SEQ ID NO 17
;; LENGTH: 28
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (17)
;; OTHER INFORMATION: Xaa=Dab
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (17)..(21)
;; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
;; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-17

Query Match 72.4%; Score 21; DB 6; Length 28;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVPF 5
|
|
|
Db 16 KKVFF 20

RESULT 50
US-10-250-581-15
;; Sequence 15, Application US/10250581
;; Publication No. US20040116337A1
;; GENERAL INFORMATION:
;; APPLICANT: Fraunhofer Society for Promotion of Applied ...
;; TITLE OF INVENTION: Soluble cyclic analogs....
;; FILE REFERENCE: 16069

; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 15
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa-Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-15

Query Match 72.4%; Score 21; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 51
US-10-250-581-18
; Sequence 18, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 18
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa-Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-18

Query Match 72.4%; Score 21; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 52
US-10-250-581-15
; Sequence 15, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581

; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 15
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa-Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-15

Query Match 72.4%; Score 21; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 53
US-10-250-581-18
; Sequence 18, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 18
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa-Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-18

Query Match 72.4%; Score 21; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 54
US-10-250-581-16
; Sequence 16, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14

; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 16
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-16

Query Match 72.4%; Score 21; DB 6; Length 42;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 55
US-10-250-581-19
; Sequence 19, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 19
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-19

Query Match 72.4%; Score 21; DB 6; Length 42;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 56
US-10-250-581-16
; Sequence 16, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 16
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-16

Query Match 72.4%; Score 21; DB 6; Length 42;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 57
US-10-250-581-19
; Sequence 19, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 19
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-19

Query Match 72.4%; Score 21; DB 6; Length 42;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 58
US-10-467-657-4978
; Sequence 4978, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:

```
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4978
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4978
```

```
Query Match 72.4%; Score 21; DB 6; Length 54;
Best Local Similarity 80.0%; Pred. No. 81;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 AVFFA 6
Db 41 SVFFA 45
```

```
RESULT 59
US-11-123-896-344
; Sequence 344, Application US/11/123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 344
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Tulipa gesneriana
US-11-123-896-344
```

```
Query Match 72.4%; Score 21; DB 7; Length 71;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KAVFF 5
Db 3 RAIFF 7
```

```
RESULT 60
US-11-123-896-335
; Sequence 335, Application US/11/123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
```

```
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 335
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Tulipa gesneriana
US-11-123-896-335
```

```
Query Match 72.4%; Score 21; DB 7; Length 73;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KAVFF 5
Db 5 RAIFF 9
```

```
RESULT 61
US-10-467-657-9209
; Sequence 9209, Application US/10/467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9209
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9209
```

```
Query Match 72.4%; Score 21; DB 6; Length 105;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KAVFFA 6
Db 3 QTVFFA 8
```

```
RESULT 62
US-11-000-463-759
; Sequence 759, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
```

```

; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radjef T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785C1P4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 759
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-759

```

```

Query Match      72.4%; Score 21; DB 7; Length 105;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 AVFFA 6
Db      68 AVFYA 72

```

```

RESULT 63
US-10-793-626-1554
; Sequence 1554, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1554
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1554

```

```

Query Match      72.4%; Score 21; DB 6; Length 115;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 AVFFA 6
Db      23 SVFFA 27

```

```

RESULT 64
US-10-467-657-3152
; Sequence 3152, Application US/10467657
; Publication No. US20050260581A1

```

```

; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3152
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3152

```

```

Query Match      72.4%; Score 21; DB 6; Length 127;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 AVFFA 6
Db      52 ALFFA 56

```

```

RESULT 65
US-10-467-657-6860
; Sequence 6860, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6860
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6860

```

```

Query Match      72.4%; Score 21; DB 6; Length 134;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 AVFFA 6
Db      78 ALFFA 82

```

```

RESULT 66
US-10-467-657-4112
; Sequence 4112, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

```

```
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4112
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4112

Query Match          72.4%; Score 21; DB 6; Length 153;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 AVFFFA 6
DB      111 AVYFA 115

RESULT 67
US-10-467-657-9046
; Sequence 9046, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9046
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9046

Query Match          72.4%; Score 21; DB 6; Length 162;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFFA 6
DB      87 RAYFFFA 92

RESULT 68
US-10-467-657-5306
; Sequence 5306, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5306
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5306

Query Match          72.4%; Score 21; DB 6; Length 167;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFFA 6
DB      159 KAVAFPA 164

RESULT 69
US-10-467-657-6854
; Sequence 6854, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6854
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6854

Query Match          72.4%; Score 21; DB 6; Length 189;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 AVFFFA 6
DB      87 ALFFFA 91

RESULT 70
US-10-467-657-7856
; Sequence 7856, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7856
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7856

Query Match          72.4%; Score 21; DB 6; Length 189;
```


Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AVFFA 6
|:|:|
Db 87 ALFFA 91

RESULT 71

US-10-467-657-818
; Sequence 818, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: CONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 818
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-818

Query Match 72.4%; Score 21; DB 6; Length 191;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
|:|:|
Db 122 QAVFF 126

RESULT 72

US-10-981-873-40
; Sequence 40, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; PRIOR FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-981-873-40

Query Match 72.4%; Score 21; DB 6; Length 213;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFF 5
|:|:|
Db 203 KAAFF 207

RESULT 73

US-10-980-388-86
; Sequence 86, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Farodi, Luis A.
; APPLICANT: Hiesch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related App
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 86
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-86

Query Match 72.4%; Score 21; DB 6; Length 227;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
|:|:|
Db 81 KSIFP 85

RESULT 74

US-10-510-386-198
; Sequence 198, Application US/10510386
; Publication No. US2005024922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3

```

; SEQ ID NO 198
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-198

Query Match      72.4%; Score 21; DB 6; Length 230;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFF 5
Db      94 KAAFF 98

RESULT 75
US-10-454-437-238
; Sequence 238, Application US/10454437
; Publication No. US20050277115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habershauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; FILE REFERENCE: BGI-128PCPN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 238
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-238

Query Match      72.4%; Score 21; DB 6; Length 244;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      20 KAVFSA 25

```

Search completed: December 29, 2005, 18:50:17
Job time : 5.29032 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds
(without alignments)
37.818 Million cell updates/sec

Title: US-10-009-122-7

Perfect score: 29

Sequence: 1 KAVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA Main.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	3	US-09-867-847-16
2	29	100.0	6	3	US-09-867-847-24
3	29	100.0	6	3	US-09-915-092-6
4	29	100.0	6	3	US-09-915-092-14
5	29	100.0	6	3	US-09-747-408-7
6	29	100.0	6	3	US-09-747-408-15
7	29	100.0	6	5	US-10-728-028-6
8	29	100.0	6	5	US-10-728-028-14
9	29	100.0	6	5	US-10-825-958-14
10	29	100.0	6	5	US-10-825-958-22
11	29	100.0	37	4	US-10-641-924-6
12	29	100.0	37	4	US-10-642-255-6
13	29	100.0	74	4	US-10-115-223-19
14	29	100.0	74	4	US-10-115-223-25
15	29	100.0	74	4	US-10-402-212-19
16	29	100.0	74	4	US-10-402-212-25
17	29	100.0	108	4	US-10-115-223-20
18	29	100.0	108	4	US-10-115-223-26
19	29	100.0	108	4	US-10-402-212-20
20	29	100.0	108	4	US-10-402-212-26
21	29	100.0	193	4	US-10-115-223-18
22	29	100.0	193	4	US-10-115-223-24
23	29	100.0	193	4	US-10-402-212-18
24	29	100.0	193	4	US-10-402-212-24
25	29	100.0	222	4	US-10-115-223-17
26	29	100.0	222	4	US-10-402-212-17
27	29	100.0	228	4	US-10-115-223-23

28	29	100.0	228	4	US-10-402-212-23	Sequence 23, Appl
29	29	100.0	261	5	US-10-795-159-697	Sequence 97, App
30	29	100.0	429	4	US-10-115-223-45	Sequence 45, Appl
31	29	100.0	429	4	US-10-402-212-45	Sequence 45, Appl
32	29	100.0	468	5	US-10-450-763-54360	Sequence 54360, A
33	29	100.0	660	3	US-09-391-104-19	Sequence 19, Appl
34	29	100.0	660	3	US-09-801-196-35	Sequence 35, Appl
35	29	100.0	660	3	US-09-918-715-208	Sequence 208, App
36	29	100.0	660	4	US-10-219-329-14	Sequence 14, Appl
37	29	100.0	660	4	US-10-301-822-125	Sequence 125, App
38	29	100.0	660	4	US-10-153-185-14	Sequence 14, Appl
39	29	100.0	660	4	US-10-219-561-14	Sequence 14, Appl
40	29	100.0	660	4	US-10-131-985-25	Sequence 25, Appl
41	29	100.0	660	4	US-10-447-315-3	Sequence 3, Appli
42	29	100.0	660	4	US-10-032-376A-14	Sequence 14, Appl
43	29	100.0	660	4	US-10-335-207-14	Sequence 14, Appl
44	29	100.0	660	4	US-10-480-621-1	Sequence 1, Appli
45	29	100.0	660	4	US-10-474-794-208	Sequence 208, App
46	29	100.0	660	5	US-10-601-059-14	Sequence 14, Appl
47	29	100.0	660	5	US-10-872-198-131	Sequence 131, App
48	29	100.0	660	5	US-10-901-417-25	Sequence 25, Appl
49	29	100.0	660	5	US-10-979-159-208	Sequence 208, App
50	29	100.0	660	5	US-10-287-436A-489	Sequence 489, App
51	29	100.0	660	5	US-10-287-436A-1185	Sequence 1185, Ap
52	29	100.0	660	6	US-11-021-951-131	Sequence 131, App
53	29	100.0	660	6	US-11-031-488-14	Sequence 14, Appl
54	29	100.0	663	4	US-10-115-223-30	Sequence 30, Appl
55	29	100.0	663	4	US-10-402-212-30	Sequence 30, Appl
56	29	100.0	718	4	US-10-369-493-4873	Sequence 4873, Ap
57	29	100.0	737	4	US-10-369-493-7633	Sequence 7633, Ap
58	29	100.0	770	4	US-10-437-963-138526	Sequence 138526, A
59	29	100.0	1330	5	US-10-450-763-54358	Sequence 54358, A
60	28	96.6	383	4	US-10-369-493-4941	Sequence 4941, Ap
61	28	96.6	383	4	US-10-369-493-7699	Sequence 7699, Ap
62	26	89.7	49	4	US-10-424-599-278606	Sequence 278606,
63	26	89.7	61	4	US-10-424-599-150066	Sequence 150066,
64	26	89.7	65	5	US-10-926-683-1595	Sequence 1595, Ap
65	26	89.7	89	4	US-10-425-115-359391	Sequence 359391,
66	26	89.7	103	4	US-10-424-599-210814	Sequence 210814,
67	26	89.7	108	4	US-10-437-963-114838	Sequence 114838,
68	26	89.7	124	4	US-10-424-599-182643	Sequence 182643,
69	26	89.7	131	4	US-10-767-701-41102	Sequence 41102, A
70	26	89.7	138	5	US-10-450-763-39449	Sequence 39449, A
71	26	89.7	172	4	US-10-437-963-172959	Sequence 172959, A
72	26	89.7	206	4	US-10-767-701-31699	Sequence 31699, A
73	26	89.7	208	5	US-10-450-763-39451	Sequence 39451, A
74	26	89.7	210	4	US-10-282-122A-61639	Sequence 61639, A
75	26	89.7	258	4	US-10-425-115-286732	Sequence 286732,
76	26	89.7	270	4	US-10-437-963-176878	Sequence 176878,
77	26	89.7	308	4	US-10-425-115-332957	Sequence 332957,
78	26	89.7	314	4	US-10-425-115-286735	Sequence 286735,
79	26	89.7	320	4	US-10-425-114-43310	Sequence 43310, A
80	26	89.7	320	4	US-10-425-114-64659	Sequence 64659, A
81	26	89.7	323	4	US-10-437-963-117099	Sequence 117099,
82	26	89.7	334	3	US-09-933-767-348	Sequence 348, App
83	26	89.7	334	4	US-10-004-860-348	Sequence 348, App
84	26	89.7	334	4	US-10-023-282-348	Sequence 348, App
85	26	89.7	421	3	US-09-741-669-400	Sequence 400, App
86	26	89.7	421	4	US-10-282-122A-42751	Sequence 42751, A
87	26	89.7	441	5	US-10-821-273-34	Sequence 34, Appl
88	26	89.7	556	5	US-10-820-474A-119	Sequence 119, App
89	26	89.7	715	4	US-10-282-122A-75547	Sequence 75547, A
90	26	89.7	859	4	US-10-437-963-201533	Sequence 201533,
91	26	89.7	1042	4	US-10-282-122A-61918	Sequence 61918, A
92	26	89.7	1166	4	US-10-437-963-128203	Sequence 128203,
93	26	89.7	1172	5	US-10-450-763-36972	Sequence 36972, A
94	26	89.7	1749	4	US-10-437-963-142580	Sequence 142580,
95	25	86.2	5	3	US-09-850-061A-40	Sequence 40, Appl
96	25	86.2	5	4	US-10-721-774-40	Sequence 40, Appl
97	25	86.2	6	3	US-09-867-847-18	Sequence 18, Appl
98	25	86.2	6	3	US-09-867-847-26	Sequence 26, Appl
99	25	86.2	6	3	US-09-915-092-8	Sequence 8, Appli
100	25	86.2	6	3	US-09-915-092-16	Sequence 16, Appl

101	25	86.2	6	3	US-09-747-408-9	Sequence 9, Appli	174	25	86.2	256	5	US-10-733-923-20752	Sequence 20752, A
102	25	86.2	6	3	US-09-747-408-17	Sequence 17, Appli	175	25	86.2	268	4	US-10-369-493-20071	Sequence 20071, A
103	25	86.2	6	5	US-10-728-028-8	Sequence 8, Appli	176	25	86.2	268	4	US-10-425-115-308997	Sequence 308997, A
104	25	86.2	6	5	US-10-728-028-16	Sequence 16, Appli	177	25	86.2	282	3	US-09-845-713A-2	Sequence 2, Appli
105	25	86.2	6	5	US-10-825-958-16	Sequence 16, Appli	178	25	86.2	282	4	US-10-435-696-35	Sequence 35, Appli
106	25	86.2	6	5	US-10-825-958-24	Sequence 24, Appli	179	25	86.2	289	4	US-10-425-115-215163	Sequence 215163, A
107	25	86.2	22	4	US-10-425-115-347015	Sequence 347015, A	180	25	86.2	297	4	US-10-425-114-73046	Sequence 73046, A
108	25	86.2	25	3	US-09-764-877-1360	Sequence 1260, Ap	181	25	86.2	303	5	US-09-908-067A-16	Sequence 5, Appli
109	25	86.2	25	4	US-10-242-515-1360	Sequence 1260, Ap	182	25	86.2	314	3	US-09-908-067A-5	Sequence 16, Appli
110	25	86.2	34	5	US-10-499-352A-444	Sequence 444, App	183	25	86.2	317	4	US-10-425-115-225676	Sequence 225676, A
111	25	86.2	37	4	US-10-641-924-7	Sequence 7, Appli	184	25	86.2	322	3	US-09-816-028A-48	Sequence 48, Appli
112	25	86.2	37	4	US-10-642-255-7	Sequence 7, Appli	185	25	86.2	322	3	US-09-886-055-253	Sequence 253, App
113	25	86.2	39	4	US-10-424-599-220682	Sequence 220682, A	186	25	86.2	322	3	US-09-804-291-253	Sequence 253, App
114	25	86.2	55	4	US-10-424-599-171652	Sequence 171652, A	187	25	86.2	322	4	US-10-017-161-156	Sequence 156, App
115	25	86.2	60	4	US-10-437-963-173619	Sequence 173619, A	188	25	86.2	322	4	US-10-303-161-48	Sequence 48, Appli
116	25	86.2	62	4	US-10-424-599-197144	Sequence 197144, A	189	25	86.2	322	4	US-10-303-118-48	Sequence 48, Appli
117	25	86.2	62	4	US-10-424-599-212719	Sequence 212719, A	190	25	86.2	322	4	US-10-303-128-48	Sequence 48, Appli
118	25	86.2	63	4	US-10-424-599-217238	Sequence 217238, A	191	25	86.2	322	4	US-10-303-134-48	Sequence 48, Appli
119	25	86.2	65	4	US-10-029-386-28659	Sequence 28659, A	192	25	86.2	322	4	US-10-303-162-48	Sequence 48, Appli
120	25	86.2	65	4	US-10-425-115-367811	Sequence 367811, A	193	25	86.2	322	4	US-10-387-629-76	Sequence 76, Appli
121	25	86.2	66	4	US-10-424-599-201270	Sequence 201270, A	194	25	86.2	322	4	US-10-292-798-134	Sequence 134, App
122	25	86.2	70	4	US-10-425-115-292851	Sequence 292851, A	195	25	86.2	322	4	US-10-343-650A-582	Sequence 582, App
123	25	86.2	71	4	US-10-424-599-170927	Sequence 170927, A	196	25	86.2	322	4	US-10-473-518-2	Sequence 2, Appli
124	25	86.2	75	4	US-10-425-115-299056	Sequence 299056, A	197	25	86.2	322	4	US-10-820-536-48	Sequence 48, Appli
125	25	86.2	80	4	US-10-437-963-111335	Sequence 111335, A	198	25	86.2	322	4	US-10-845-408-48	Sequence 48, Appli
126	25	86.2	80	4	US-10-425-115-299931	Sequence 299931, A	199	25	86.2	322	4	US-10-845-412-48	Sequence 48, Appli
127	25	86.2	81	4	US-10-425-115-299931	Sequence 299931, A	200	25	86.2	322	5	US-10-846-219-48	Sequence 48, Appli
128	25	86.2	81	4	US-10-424-599-245453	Sequence 245453, A	201	25	86.2	322	5	US-10-821-604-48	Sequence 48, Appli
129	25	86.2	87	4	US-10-437-963-133986	Sequence 133986, A	202	25	86.2	322	5	US-10-847-993-48	Sequence 48, Appli
130	25	86.2	89	4	US-10-425-115-302836	Sequence 302836, A	203	25	86.2	322	5	US-10-821-573-48	Sequence 48, Appli
131	25	86.2	90	4	US-10-424-599-147666	Sequence 147666, A	204	25	86.2	322	5	US-10-850-807-48	Sequence 48, Appli
132	25	86.2	90	4	US-10-425-115-296215	Sequence 296215, A	205	25	86.2	322	5	US-10-850-125-48	Sequence 48, Appli
133	25	86.2	95	4	US-10-437-963-197590	Sequence 197590, A	206	25	86.2	322	5	US-10-830-825-48	Sequence 48, Appli
134	25	86.2	98	4	US-10-425-115-364147	Sequence 364147, A	207	25	86.2	322	5	US-10-962-334-48	Sequence 48, Appli
135	25	86.2	99	4	US-10-437-963-150181	Sequence 150181, A	208	25	86.2	322	5	US-10-830-937-48	Sequence 48, Appli
136	25	86.2	109	4	US-10-437-963-105773	Sequence 105773, A	209	25	86.2	322	5	US-10-962-235-48	Sequence 48, Appli
137	25	86.2	109	4	US-10-425-115-226514	Sequence 226514, A	210	25	86.2	322	5	US-10-961-882-48	Sequence 48, Appli
138	25	86.2	117	3	US-09-864-761-37128	Sequence 37128, A	211	25	86.2	322	5	US-10-819-316-253	Sequence 253, App
139	25	86.2	117	4	US-10-425-115-362628	Sequence 362628, A	212	25	86.2	322	5	US-10-819-316-531	Sequence 531, App
140	25	86.2	127	4	US-10-767-701-47243	Sequence 47243, A	213	25	86.2	327	4	US-10-437-963-109308	Sequence 109308, A
141	25	86.2	128	4	US-10-425-115-192450	Sequence 192450, A	214	25	86.2	332	4	US-10-274-694-2	Sequence 2, Appli
142	25	86.2	129	4	US-10-424-599-278483	Sequence 278483, A	215	25	86.2	332	4	US-10-369-493-11167	Sequence 11167, A
143	25	86.2	130	4	US-10-424-599-170319	Sequence 170319, A	216	25	86.2	332	4	US-10-369-493-22884	Sequence 22884, A
144	25	86.2	132	4	US-10-029-386-28941	Sequence 28941, A	217	25	86.2	332	5	US-10-332-448-2	Sequence 2, Appli
145	25	86.2	133	4	US-10-424-599-270652	Sequence 270652, A	218	25	86.2	347	3	US-09-939-484-6	Sequence 6, Appli
146	25	86.2	133	4	US-10-425-115-305393	Sequence 305393, A	219	25	86.2	347	3	US-09-939-483-6	Sequence 6, Appli
147	25	86.2	135	4	US-10-437-963-141578	Sequence 141578, A	220	25	86.2	354	6	US-11-097-143-6189	Sequence 6189, Ap
148	25	86.2	140	4	US-10-424-599-151465	Sequence 151465, A	221	25	86.2	366	4	US-10-424-599-278238	Sequence 278238, A
149	25	86.2	150	4	US-10-335-977-6540	Sequence 6540, Ap	222	25	86.2	373	4	US-10-437-963-167534	Sequence 167534, A
150	25	86.2	155	4	US-10-424-599-200083	Sequence 200083, A	223	25	86.2	380	4	US-10-369-493-7986	Sequence 7986, Ap
151	25	86.2	171	4	US-10-424-599-229782	Sequence 229782, A	224	25	86.2	382	4	US-10-369-493-11163	Sequence 11163, A
152	25	86.2	175	4	US-10-437-963-122124	Sequence 122124, A	225	25	86.2	411	4	US-10-282-122A-77801	Sequence 77801, A
153	25	86.2	180	4	US-10-424-599-252237	Sequence 252237, A	226	25	86.2	415	4	US-10-282-122A-68770	Sequence 68770, A
154	25	86.2	186	5	US-10-481-032A-214	Sequence 214, App	227	25	86.2	416	6	US-10-055-475-14	Sequence 14, Appli
155	25	86.2	186	5	US-10-481-032A-228	Sequence 228, App	228	25	86.2	416	6	US-11-042-922-14	Sequence 14, Appli
156	25	86.2	188	4	US-10-437-963-172476	Sequence 172476, A	229	25	86.2	430	4	US-10-058-636-2	Sequence 2, Appli
157	25	86.2	190	4	US-10-437-963-137998	Sequence 137998, A	230	25	86.2	430	4	US-10-799-016-2	Sequence 2, Appli
158	25	86.2	198	4	US-10-437-963-172452	Sequence 172452, A	231	25	86.2	454	3	US-09-993-811-12	Sequence 12, Appli
159	25	86.2	201	4	US-10-425-114-67850	Sequence 67850, A	232	25	86.2	473	5	US-10-472-928-4158	Sequence 4158, Ap
160	25	86.2	202	5	US-10-732-923-19034	Sequence 19034, A	233	25	86.2	473	5	US-10-617-320-3273	Sequence 3273, Ap
161	25	86.2	209	4	US-10-424-599-280085	Sequence 280085, A	234	25	86.2	481	6	US-11-097-143-3162	Sequence 3162, Ap
162	25	86.2	210	4	US-10-282-122A-65447	Sequence 65447, A	235	25	86.2	507	4	US-10-223-070-9	Sequence 9, Appli
163	25	86.2	210	4	US-10-282-122A-66099	Sequence 66099, A	236	25	86.2	514	6	US-10-055-475-13	Sequence 13, Appli
164	25	86.2	224	4	US-10-424-599-245461	Sequence 245461, A	237	25	86.2	514	6	US-11-042-922-13	Sequence 13, Appli
165	25	86.2	224	4	US-10-424-599-257424	Sequence 257424, A	238	25	86.2	530	3	US-09-804-014A-28	Sequence 28, Appli
166	25	86.2	246	6	US-11-097-143-2748	Sequence 2748, Ap	239	25	86.2	532	3	US-09-993-811-6	Sequence 6, Appli
167	25	86.2	247	4	US-10-335-977-6541	Sequence 6541, Ap	240	25	86.2	532	3	US-09-875-321-13	Sequence 13, Appli
168	25	86.2	247	4	US-10-335-977-6541	Sequence 6542, Ap	241	25	86.2	532	3	US-09-804-014A-31	Sequence 31, Appli
169	25	86.2	247	5	US-10-732-923-19035	Sequence 19035, A	242	25	86.2	532	4	US-10-162-012-13	Sequence 13, Appli
170	25	86.2	249	4	US-10-369-493-10584	Sequence 10584, A	243	25	86.2	532	4	US-10-254-010-2	Sequence 2, Appli
171	25	86.2	254	4	US-10-369-493-16714	Sequence 16714, A	244	25	86.2	532	4	US-10-162-102-13	Sequence 13, Appli
172	25	86.2	255	5	US-10-732-923-20940	Sequence 20940, A	245	25	86.2	532	5	US-10-916-061-13	Sequence 13, Appli
173	25	86.2	255	6	US-11-097-143-29655	Sequence 29655, A	246	25	86.2	539	4	US-10-282-122A-48163	Sequence 48163, A

247 25 86.2 552 4 US-10-282-122A-49134 Sequence 49134, A
248 25 86.2 558 4 US-10-282-122A-50632 Sequence 50632, A
249 25 86.2 560 3 US-09-735-705-225 Sequence 225, App
250 25 86.2 560 3 US-09-850-716A-225 Sequence 225, App
251 25 86.2 560 3 US-09-897-778-225 Sequence 225, App
252 25 86.2 560 3 US-09-943-075A-6 Sequence 6, Appl
253 25 86.2 560 3 US-09-738-626-5465 Sequence 5465, App
254 25 86.2 560 4 US-10-039-272-2 Sequence 2, Appl
255 25 86.2 560 4 US-10-007-700-225 Sequence 225, App
256 25 86.2 560 4 US-10-117-982-225 Sequence 225, App
257 25 86.2 560 4 US-10-463-106-2 Sequence 2, Appl
258 25 86.2 560 4 US-10-295-027-1258 Sequence 1258, App
259 25 86.2 560 4 US-10-313-986-225 Sequence 225, App
260 25 86.2 560 4 US-10-309-290-152 Sequence 152, App
261 25 86.2 560 4 US-10-408-765A-466 Sequence 466, App
262 25 86.2 560 5 US-10-775-972-225 Sequence 225, App
263 25 86.2 560 5 US-10-723-860-1128 Sequence 1128, App
264 25 86.2 560 5 US-10-922-124-225 Sequence 225, App
265 25 86.2 560 5 US-10-978-758-6 Sequence 6, Appl
266 25 86.2 560 5 US-10-631-467-821 Sequence 821, App
267 25 86.2 561 5 US-10-450-763-39378 Sequence 39378, A
268 25 86.2 563 4 US-10-282-122A-50907 Sequence 50907, A
269 25 86.2 572 4 US-10-227-884-42 Sequence 42, Appl
270 25 86.2 572 4 US-10-230-163-42 Sequence 42, Appl
271 25 86.2 572 4 US-10-230-338-42 Sequence 42, Appl
272 25 86.2 572 4 US-10-218-631-42 Sequence 42, Appl
273 25 86.2 572 4 US-10-230-414-42 Sequence 42, Appl
274 25 86.2 572 4 US-10-232-224-42 Sequence 42, Appl
275 25 86.2 572 4 US-10-216-159A-42 Sequence 42, Appl
276 25 86.2 572 4 US-10-218-849-42 Sequence 42, Appl
277 25 86.2 572 4 US-10-227-873-42 Sequence 42, Appl
278 25 86.2 572 4 US-10-227-883-42 Sequence 42, Appl
279 25 86.2 572 4 US-10-219-076-42 Sequence 42, Appl
280 25 86.2 572 4 US-10-230-434-42 Sequence 42, Appl
281 25 86.2 572 4 US-10-219-003-42 Sequence 42, Appl
282 25 86.2 572 4 US-10-219-075-42 Sequence 42, Appl
283 25 86.2 572 4 US-10-219-464-42 Sequence 42, Appl
284 25 86.2 572 4 US-10-219-466-42 Sequence 42, Appl
285 25 86.2 572 4 US-10-219-479-42 Sequence 42, Appl
286 25 86.2 572 4 US-10-219-481-42 Sequence 42, Appl
287 25 86.2 572 4 US-10-230-260-42 Sequence 42, Appl
288 25 86.2 572 4 US-10-232-231-42 Sequence 42, Appl
289 25 86.2 572 4 US-10-232-233-42 Sequence 42, Appl
290 25 86.2 572 4 US-10-216-165-42 Sequence 42, Appl
291 25 86.2 572 4 US-10-218-956-42 Sequence 42, Appl
292 25 86.2 572 4 US-10-219-468-42 Sequence 42, Appl
293 25 86.2 572 4 US-10-219-478-42 Sequence 42, Appl
294 25 86.2 572 4 US-10-219-536-42 Sequence 42, Appl
295 25 86.2 572 4 US-10-233-205-42 Sequence 42, Appl
296 25 86.2 572 4 US-10-219-072-42 Sequence 42, Appl
297 25 86.2 572 4 US-10-219-470-42 Sequence 42, Appl
298 25 86.2 572 4 US-10-219-474-42 Sequence 42, Appl
299 25 86.2 572 4 US-10-219-524-42 Sequence 42, Appl
300 25 86.2 572 4 US-10-219-528-42 Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-09-867-847-16
; Sequence 16, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-16

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 1 KAVFFPA 6

RESULT 2

US-09-867-847-24
; Sequence 24, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-24

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 1 KAVFFPA 6

RESULT 3

US-09-915-092-6
; Sequence 6, Application US/09915092
; Publication No. US2002011571A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert

```

; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-6

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 4
US-09-915-092-14
; Sequence 14, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-14

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 5
US-09-747-408-7
; Sequence 7, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24

```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-7

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 6
US-09-747-408-15
; Sequence 15, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-15

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 7
US-10-728-028-6
; Sequence 6, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

```
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-6

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 1 KAVFFA 6

RESULT 8
US-10-728-028-14
; Sequence 14, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-14

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 1 KAVFFA 6

RESULT 9
US-10-825-958-14
; Sequence 14, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-825-958-14

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 1 KAVFFA 6

RESULT 10
US-10-825-958-22
; Sequence 22, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-825-958-22

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 1 KAVFFA 6

RESULT 11
US-10-641-924-6
; Sequence 6, Application US/10641924
; Publication No. US20040096881A1
; GENERAL INFORMATION:
; APPLICANT: Blasko, Eric
; APPLICANT: Kauser, Katalin
; APPLICANT: Parkinson, John
; TITLE OF INVENTION: eNOS Mutants Useful for Gene Therapy
; FILE REFERENCE: 5303SAUSM1
; CURRENT APPLICATION NUMBER: US/10/641,924
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,638
; PRIOR FILING DATE: 2002-08-16
```

```
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-641-924-6

Query Match          100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 18 KAVFFA 23

RESULT 12
US-10-642-255-6
; Sequence 6, Application US/10642255
; Publication No. US20040120930A1
; GENERAL INFORMATION:
; APPLICANT: Dole, William P.
; APPLICANT: Kauser, Katalin
; APPLICANT: Qian, Hu Sheng
; APPLICANT: Rubanyi, Gabor
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant
; FILE REFERENCE: enOS
; CURRENT APPLICATION NUMBER: US/10/642,255
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,637
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-642-255-6

Query Match          100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 18 KAVFFA 23

RESULT 13
US-10-115-223-19
; Sequence 19, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
```

```
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-223-19

Query Match          100.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 14
US-10-115-223-25
; Sequence 25, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-25

Query Match          100.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 15
US-10-402-212-19
; Sequence 19, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
```


; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-19

Query Match 100.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 16

US-10-402-212-25
; Sequence 25, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-25

Query Match 100.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 17

US-10-115-223-20
; Sequence 20, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773

; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-223-20

Query Match 100.0%; Score 29; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 18

US-10-115-223-26
; Sequence 26, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-26

Query Match 100.0%; Score 29; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 19

US-10-402-212-20
; Sequence 20, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223

```
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-20

Query Match          100.0%; Score 29; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 20
US-10-402-212-26
; Sequence 26, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresh, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-26

Query Match          100.0%; Score 29; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 21
US-10-115-223-18
; Sequence 18, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresh, David A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MERO049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-223-18

Query Match          100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 22
US-10-115-223-24
; Sequence 24, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresh, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MERO049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-24

Query Match          100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 23
US-10-402-212-18
; Sequence 18, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
```

```
; APPLICANT: Chereah, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-18
```

```
Query Match      100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KAVFFA 6
        |||||
Db      64 KAVFFA 69
```

```
RESULT 24
US-10-402-212-24
; Sequence 24, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Chereah, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-24
```

```
Query Match      100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KAVFFA 6
        |||||
Db      64 KAVFFA 69
```

```
RESULT 25
US-10-115-223-17
; Sequence 17, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Chereah, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-223-17
```

```
Query Match      100.0%; Score 29; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KAVFFA 6
        |||||
Db      93 KAVFFA 98
```

```
RESULT 26
US-10-402-212-17
; Sequence 17, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Chereah, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-17
```

```
Query Match      100.0%; Score 29; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 KAVFFA 6
| | | | |
Db 93 KAVFFA 98

RESULT 27

US-10-115-223-23
; Sequence 23, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-23

Query Match 100.0%; Score 29; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| | | | |
Db 99 KAVFFA 104

RESULT 28

US-10-402-212-23
; Sequence 23, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-23

Query Match 100.0%; Score 29; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| | | | |
Db 99 KAVFFA 104

RESULT 29

US-10-795-159-697
; Sequence 697, Application US/10795159
; Publication No. US20050221439A1
; GENERAL INFORMATION:
; APPLICANT: BAKALETZ et al.
; TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE H. INFLUENZAE
; FILE REFERENCE: 28335/38815A
; CURRENT APPLICATION NUMBER: US/10/795,159
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 60/453,134
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 771
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 697
; LENGTH: 261
; TYPE: PRT
; ORGANISM: H. influenzae
US-10-795-159-697

Query Match 100.0%; Score 29; DB 5; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| | | | |
Db 205 KAVFFA 210

RESULT 30

US-10-115-223-45
; Sequence 45, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-223-45

Query Match 100.0%; Score 29; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| | | | |
Db 300 KAVFFA 305

; OTHER INFORMATION: Fibronectin type II domain identified by Pfam, accession name
; OTHER INFORMATION: fn2, E-value=4.4e-55, Pfam score of 147.1

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(468)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-54360

Query Match 100.0%; Score 29; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 361 KAVFFA 366

RESULT 33

US-09-391-104-19
; Sequence 19, Application US/09391104
; Publication No. US20020031817A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Palduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07/814,394
; PRIOR APPLICATION NUMBER: US 08/814,394
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-19

Query Match 100.0%; Score 29; DB 3; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 531 KAVFFA 536

RESULT 34

US-09-801-196-35
; Sequence 35, Application US/09801196
; Patent No. US20020037827A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Kai
; APPLICANT: Smith, Ryan
; APPLICANT: Fajardo, Mark
; APPLICANT: Moss, Patrick
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
; TITLE OF INVENTION: EXPRESSED IN SKIN CELLS
; FILE REFERENCE: 240083.509
; CURRENT APPLICATION NUMBER: US/09/801,196
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-196-35

RESULT 31

US-10-402-212-45
; Sequence 45, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; TITLE OF INVENTION: THE SCRIPPS RESEARCH INSTITUTE
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-45

Query Match 100.0%; Score 29; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 300 KAVFFA 305

RESULT 32

US-10-450-763-54360
; Sequence 54360, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-05-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 54360
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (221)..(258)
; OTHER INFORMATION: Type II fibronectin collagen-binding domain proteins domain
; OTHER INFORMATION: Identified by eMATRIX, accession number BL00023, p-value=4.682e-3
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (167)..(264)

```
Query Match      100.0%; Score 29; DB 3; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
DB      531 KAVFFA 536

RESULT 35
US-09-918-715-208
; Sequence 208, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 208
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-208

Query Match      100.0%; Score 29; DB 3; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
DB      531 KAVFFA 536

RESULT 36
US-10-219-329-14
; Sequence 14, Application US/10219329
; Publication No. US20030096757A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Weart, Ilona f.
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
; FILE REFERENCE: 1443.035W01
; CURRENT APPLICATION NUMBER: US/10/219,329
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-329-14

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
DB      531 KAVFFA 536

RESULT 37
US-10-301-822-125
; Sequence 125, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-301-822-125

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
DB      531 KAVFFA 536

RESULT 38
US-10-153-185-14
; Sequence 14, Application US/10153185
; Publication No. US20030148959A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-14

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
DB      531 KAVFFA 536

RESULT 39
US-10-153-185-14
; Sequence 14, Application US/10153185
; Publication No. US20030148959A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-14

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
DB      531 KAVFFA 536
```

Db 531 KAVFFA 536

|||||

RESULT 39
US-10-219-561-14
; Sequence 14, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-14

Query Match 100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

|||||

Db 531 KAVFFA 536

RESULT 40
US-10-131-985-25
; Sequence 25, Application US/10131985
; Publication No. US2003019940A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Occleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131,985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-25

Query Match 100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

|||||

Db 531 KAVFFA 536

RESULT 41
US-10-447-315-3
; Sequence 3, Application US/10447315
; Publication No. US20040071687A1
; GENERAL INFORMATION:
; APPLICANT: Rafii, Shahin
; APPLICANT: Heissig, Beate
; APPLICANT: Hattori, Koichi
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Adult Stem Cell Recruitment
; FILE REFERENCE: 1676.006US1
; CURRENT APPLICATION NUMBER: US/10/447,315
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US 60/383,658
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-315-3

Query Match 100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

|||||

Db 531 KAVFFA 536

RESULT 42
US-10-032-376A-14
; Sequence 14, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-376A-14

Query Match 100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

|||||

Db 531 KAVFFA 536

RESULT 43
US-10-335-207-14
; Sequence 14, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Sohail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207

```
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-207-14

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 44
US-10-480-621-1
; Sequence 1, Application US/10480621
; Publication No. US20040175817A1
; GENERAL INFORMATION:
; APPLICANT: Jepson, Holly
; APPLICANT: Minshull, Claire
; APPLICANT: Paupit, Richard
; APPLICANT: Rowsell, Sian
; TITLE OF INVENTION: A CRYSTALLISED CATALYTIC DOMAIN OF MATRIX
; TITLE OF INVENTION: METALLOPROTEINASE 9 (MMP9) AND THE USE OF
; TITLE OF INVENTION: ITS THREE DIMENSIONAL STRUCTURE TO DESIGN
; TITLE OF INVENTION: MMP9 MODULATORS
; FILE REFERENCE: 06275-377US1
; CURRENT APPLICATION NUMBER: US/10/480,621
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/SE02/01266
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: SE 0102298-7
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-480-621-1

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 45
US-10-474-794-208
; Sequence 208, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-208

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 46
US-10-601-059-14
; Sequence 14, Application US/10601059
; Publication No. US20040259802A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shu-Ping
; APPLICANT: Quirk, Stephen
; APPLICANT: Kimberly-Clark Worldwide, Inc.
; TITLE OF INVENTION: Anti-Chondrosarcoma Compounds
; FILE REFERENCE: 1443.064US1
; CURRENT APPLICATION NUMBER: US/10/601,059
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 10/335,207
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/219,329
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/US02/26319
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-601-059-14

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 47
US-10-872-198-131
; Sequence 131, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOETSMEIER
; APPLICANT: Ulrich Kettling
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.0002U4
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
```



```

; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-131

```

```

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KAVFFA 6
      |||||
Db      531 KAVFFA 536

```

```

RESULT 48
US-10-901-417-25
; Sequence 25, Application US/10901417
; Publication No. US20050026836A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: McClellan, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/901,417
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: US/10/131,985
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-901-417-25

```

```

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KAVFFA 6
      |||||
Db      531 KAVFFA 536

```

```

RESULT 49
US-10-979-159-208
; Sequence 208, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler

```

```

; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 208
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-979-159-208

```

```

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KAVFFA 6
      |||||
Db      531 KAVFFA 536

```

```

RESULT 50
US-10-287-436A-489
; Sequence 489, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 489
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-489

```

```

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KAVFFA 6
      |||||
Db      531 KAVFFA 536

```

```

RESULT 51
US-10-287-436A-1185
; Sequence 1185, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446

```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1185
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-1185

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 52
US-11-021-951-131
; Sequence 131, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
; APPLICANT: HAUPTS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHEIDIG, Andreas
; APPLICANT: VOTSMIEIER, Christian
; APPLICANT: Kettling, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 041156.000205
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-131

Query Match      100.0%; Score 29; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 53
US-11-031-488-14
; Sequence 14, Application US/11031488
; Publication No. US20050239710A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/11/031,488

; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: US/10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-031-488-14

Query Match      100.0%; Score 29; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 54
US-10-115-223-30
; Sequence 30, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-30

Query Match      100.0%; Score 29; DB 4; Length 663;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      534 KAVFFA 539

RESULT 55
US-10-402-212-30
; Sequence 30, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresh, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
```

; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-30

Query Match 100.0%; Score 29; DB 4; Length 663;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPPA 6
Db 534 KAVPPA 539

RESULT 56
US-10-369-493-4873
; Sequence 4873, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4873
; LENGTH: 718
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4873

Query Match 100.0%; Score 29; DB 4; Length 718;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPPA 6
Db 576 KAVPPA 581

RESULT 57
US-10-369-493-7633
; Sequence 7633, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4873
; LENGTH: 718
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4873

; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7633
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-10-369-493-7633

Query Match 100.0%; Score 29; DB 4; Length 737;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPPA 6
Db 576 KAVPPA 581

RESULT 58
US-10-437-963-138526
; Sequence 138526, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 138526
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_39906C.1.pep
US-10-437-963-138526

Query Match 100.0%; Score 29; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPPA 6
Db 555 KAVPPA 560

RESULT 59
US-10-450-763-54358
; Sequence 54358, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO 54358

; LENGTH: 1330

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (579)..(616)

; OTHER INFORMATION: Type II fibronectin collagen-binding domain proteins domain

; OTHER INFORMATION: identified by eMATRIX, accession number BL00023, p-value=4.682e-3

; OTHER INFORMATION: raw score of 24.31

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (271)..(451)

; OTHER INFORMATION: Matrixin domain identified by Pfam, accession name

; OTHER INFORMATION: Peptidase_M10, E-value=3.7e-109, Pfam score of 376.1

US-10-450-763-54358

Query Match

Best Local Similarity 100.0%; Score 29; DB 5; Length 1330;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 768 KAVFFA 773

RESULT 60

US-10-369-493-4941

; Sequence 4941, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 4941

; LENGTH: 383

; TYPE: PRT

; ORGANISM: Burkholderia fungorum

US-10-369-493-4941

Query Match

Best Local Similarity 96.6%; Score 28; DB 4; Length 383;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 167 KAIFFA 172

RESULT 61

US-10-369-493-7699

; Sequence 7699, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 150066

; LENGTH: 61

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 7699

; LENGTH: 383

; TYPE: PRT

; ORGANISM: Burkholderia cepacia

US-10-369-493-7699

Query Match

Best Local Similarity 96.6%; Score 28; DB 4; Length 383;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 164 KAIFFA 169

RESULT 62

US-10-424-599-278606

; Sequence 278606, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 278606

; LENGTH: 49

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_93603C.1.pap

US-10-424-599-278606

Query Match

Best Local Similarity 89.7%; Score 26; DB 4; Length 49;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 15 RAVFFA 20

RESULT 63

US-10-424-599-150066

; Sequence 150066, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 150066

; LENGTH: 61

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_106530C.1.pep
US-10-424-599-150066

Query Match 89.7%; Score 26; DB 4; Length 61;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|:||||
Db 53 KSVFFA 58

RESULT 64

US-10-926-683-1595
; Sequence 1595, Application US/10926683
; Publication No. US20050106595A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: GENSET.025CPI
; CURRENT APPLICATION NUMBER: US/10/926,683
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US/09/471,276
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 09/057,719
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 09/069,047
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: PCT/IB99/00712
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 1595
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-926-683-1595

Query Match 89.7%; Score 26; DB 5; Length 65;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|:||||
Db 54 KAVFFS 59

RESULT 65

US-10-425-115-359391
; Sequence 359391, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 359391
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_90934C.1.pep
US-10-425-115-359391

Query Match 89.7%; Score 26; DB 4; Length 89;

Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|:||||
Db 54 KAVFFS 59

RESULT 66

US-10-424-599-210814
; Sequence 210814, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 210814
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_32392C.1.pep
US-10-424-599-210814

Query Match 89.7%; Score 26; DB 4; Length 103;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|:||||
Db 44 KALFFA 49

RESULT 67

US-10-437-963-114838
; Sequence 114838, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 114838
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(108)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_18490C.1.pep
US-10-437-963-114838

Query Match 89.7%; Score 26; DB 4; Length 108;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||
Db 48 KAVFYA 53

RESULT 68

US-10-424-599-182643
; Sequence 182643, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182643
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(124)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_13593C.1.pep
US-10-424-599-182643

Query Match 89.7%; Score 26; DB 4; Length 124;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||
Db 65 KAVFFS 70

RESULT 69

US-10-767-701-41102
; Sequence 41102, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 41102
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C1929_1.pep
US-10-767-701-41102

Query Match 89.7%; Score 26; DB 4; Length 131;
Best Local Similarity 83.3%; Pred. No. 6.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||
Db 42 KAVFFA 47

RESULT 70

US-10-450-763-39449
; Sequence 39449, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 39449
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-39449

Query Match 89.7%; Score 26; DB 5; Length 138;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
:|||||
Db 49 RAVFFA 54

RESULT 71

US-10-437-963-172959
; Sequence 172959, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172959
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_71044C.1.pep
US-10-437-963-172959

Query Match 89.7%; Score 26; DB 4; Length 172;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
:|||||
Db 145 RAVFFA 150

RESULT 72

US-10-767-701-31699
; Sequence 31699, Application US/10767701